The ar data frame has 60 rows and 4 columns.

Usage

data(ar)

Format

This data frame contains the following columns:

- x1  a numeric vector
- x2  a numeric vector
- x3  a numeric vector
- y   a numeric vector
bliss

References


---

bliss  Bliss data

Description

The bliss data frame has 8 rows and 4 columns.

Usage

data(bliss)

Format

This data frame contains the following columns:

- **Dose**  a numeric vector
- **Killed**  a numeric vector
- **Total**  a numeric vector
- **y**  a numeric vector

References


---

calcium  Calcium data

Description

Calcium uptake of cells suspended in a solution of radioactive calcium. The calcium data frame has 27 rows and 2 columns.

Usage

data(calcium)

Format

This data frame contains the following columns:

- **Time**  a numeric vector
- **y**  a numeric vector
### References


---

**carinsuk**  
*Car insurance data*

**Description**

The `carinsuk` data frame has 128 rows and 5 columns.

**Usage**

```r
data(carinsuk)
```

**Format**

This data frame contains the following columns:

- **OwnerAge**: a factor with levels: 17-20, 21-24, 25-29, 30-34, 35-39, 40-49, 50-59, 60+
- **Model**: a factor with levels: A, B, C, D
- **CarAge**: a factor with levels: 0-3, 10+, 4-7, 8-9
- **NClaims**: a numeric vector
- **AvCost**: a numeric vector

**References**


---

**carr**  
*n-Pentane data*

**Description**

Reaction rate for Catalytic Isomerization of n-Pentane to Isopentane

The `carr` data frame has 24 rows and 4 columns.

**Usage**

```r
data(carr)
```
```
Format

This data frame contains the following columns:

- **hydrogen** partial pressure of hydrogen
- **npentane** partial pressure of n-pentane
- **isopentane** partial pressure of iso-pentane
- **rate** rate of disappearance of n-pentane

References

```

```
Description

The **cellular** data frame has 16 rows and 3 columns.

Usage

data(cellular)

Format

This data frame contains the following columns:

- **TNF** Dose of TNF (U/ml)
- **IFN** Dose of IFN (U/ml)
- **y** Number of cells differentiating

References

```
chapman

Description
The chapman data frame has 200 rows and 7 columns.

Usage
data(chapman)

Format
This data frame contains the following columns:

- age  a numeric vector
- highbp  a numeric vector
- lowbp  a numeric vector
- chol  a numeric vector
- height  a numeric vector
- weight  a numeric vector
- y  a numeric vector

References

derailme

Description
These data are obtained from Atkinson and Riani (2000), which is a simplified version of the data in Evans (2000). The outcome is the number of deaths that occurred in a train accident with a categorical covariate describing the type of rolling stock, and an exposure variable giving the annual distance travelled by trains in that year, and was originally analysed using a Poisson model. As the data does not include observations with zero deaths, it will be analysed here as a zero-truncated Poisson with an offset of log of the train distance. The derailme data frame has 67 rows and 5 columns.

Usage
data(derailme)
**dialectric**

**Format**
This data frame contains the following columns:

- **Month**  Month of accident
- **Year**  Year of accident
- **Type**  Type of rolling stock 1=Mark 1 train, 2=Post-Mark 1 train, 3=Non-passenger
- **TrainKm**  Amount of traffic on the railway system (billions of train km)
- **y**  Number of deaths that occurred in the train accident

**Source**
Atkinson and Riani (2000)

**References**

---

**dialectric**  
*Dialectic data*

**Description**
The dialectric data frame has 128 rows and 3 columns.

**Usage**
data(dialectric)

**Format**
This data frame contains the following columns:

- **time**  Time (weeks)
- **temp**  Temperature (degrees Celsius)
- **y**  dialectric breakdown strength in kilovolts

**References**
fwd.combn  
*Generate all combinations of elements of x taken m at a time*

**Description**
Generate all combinations of the elements of x taken m at a time. If x is a positive integer, returns all combinations of the elements of seq(x) taken m at a time. If argument fun is not null, applies a function given by the argument to each point. If simplify is FALSE, returns a list; else returns a vector or an array. Optional arguments ... are passed unchanged to the function given by argument fun, if any.

**Usage**
```r
fwd.combn(x, m, fun = NULL, simplify = TRUE, ...)
fwd.nCm(n, m, tol = 1e-08)
```

**Arguments**
- `x` a vector or a single value.
- `n` a positive integer.
- `m` a positive integer.
- `fun` a function to be applied to each combination.
- `simplify` logical, if TRUE returns a vector or an array, otherwise a list.
- `tol` optional, tolerance value.
- `...` optional arguments passed to fun.

**Value**
Returns a vector or an array if simplify = TRUE, otherwise a list.

**Note**
Renamed by Kjell Konis for inclusion in the Forward Library 11/2002

**Author(s)**
Scott Chasalow

**References**
Examples

```r
fwd.combn(letters[1:4], 2)
fwd.combn(10, 5, min)  # minimum value in each combination
# Different way of encoding points:
fwd.combn(c(1,1,1,1,2,2,2,3,3,4), 3, tabulate, nbins = 4)
# Compute support points and (scaled) probabilities for a
# Multivariate-Hypergeometric(n = 3, N = c(4,3,2,1)) p.f.:
table(t(fwd.combn(c(1,1,1,1,2,2,2,3,3,4), 3, tabulate, nbins=4)))
```

Description

This function applies the forward search approach to robust analysis in generalized linear models.

Usage

```r
fwdglm(formula, family, data, weights, na.action, contrasts = NULL, bsb = NULL,
        balanced = TRUE, maxit = 50, epsilon = 1e-06, nsamp = 100, trace = TRUE)
```

Arguments

- **formula**: a symbolic description of the model to be fit. The details of the model are the same as for glm.
- **family**: a description of the error distribution and link function to be used in the model. See `family` for details.
- **data**: an optional data frame containing the variables in the model. By default the variables are taken from the environment from which the function is called.
- **weights**: an optional vector of weights to be used in the fitting process.
- **na.action**: a function which indicates what should happen when the data contain NA's. The default is set by the `na.action` setting of options, and is `na.fail` if that is unset. The default is `na.omit`.
- **contrasts**: an optional list. See the `contrasts.arg` of `model.matrix.default`.
- **bsb**: an optional vector specifying a starting subset of observations to be used in the forward search. By default the "best" starting subset is chosen using the function `lmsglm` with control arguments provided by `nsamp`.
- **balanced**: logical, for a binary response if `TRUE` the proportion of successes on the full dataset is approximately balanced during the forward search algorithm.
- **maxit**: integer giving the maximal number of IWLS iterations. See `glm.control` for details.
- **epsilon**: positive convergence tolerance epsilon. See `glm.control` for details.
the initial subset for the forward search in generalized linear models is found by the function \texttt{lmsglm}. This argument allows to control how many subsets are used in the robust fitting procedure. The choices are: the number of samples (100 by the default) or "all". Note that the algorithm tries to find \texttt{nsamp} good subsets or a maximum of $2^{\texttt{nsamp}}$ subsets.

logical, if TRUE a message is printed for every ten iterations completed during the forward search.

Value

The function returns an object of class "\texttt{fwdglm}" with the following components:

call
Residuals
Unit
included
Coefficients
$\text{tStatistics}$
Leverage
MaxRes
MinDelRes
ScoreTest
Likelihood
CookDist
ModCookDist
Weights
inibs

logical, equal to TRUE if binary response.

Author(s)

Originally written for S-Plus by: Kjell Konis <kkonis@insightful.com> and Marco Riani <mriani@unipr.it>
Ported to R by Luca Scrucca <luca@stat.unipg.it>

References

See Also

summary.fwdglm, plot.fwdglm, fwdlm, fwdsco.

Examples

data(cellular)
cellular$TNF <- as.factor(cellular$TNF)
cellular$IFN <- as.factor(cellular$IFN)
mod <- fwdglm(y ~ TNF + IFN, data=cellular, family=poisson(log), nsamp=200)
summary(mod)
## Not run: plot(mod)
plot(mod, 1)
plot(mod, 5)
plot(mod, 6, ylim=c(-3, 20))
plot(mod, 7)
plot(mod, 8)

fwdlm

Forward Search in Linear Regression

Description

This function applies the forward search approach to robust analysis in linear regression models.

Usage

fwdlm(formula, data, nsamp = "best", x = NULL, y = NULL, intercept = TRUE,
na.action, trace = TRUE)

Arguments

formula a symbolic description of the model to be fit. The details of the model are the
same as for lm.
data an optional data frame containing the variables in the model. By default the
variables are taken from the environment from which the function is called.
nsamp the initial subset for the forward search in linear regression is found by fitting
the regression model with the R function lmsreg. This argument allows to
control how many subsets are used in the Least Median of Squares regression.
The choices are: the number of samples or "best" (the default) or "exact" or
"sample". For details see lmsreg.
x A matrix of predictors values (if no formula is provided).
y A vector of response values (if no formula is provided).
intercept Logical for the inclusion of the intercept (if no formula is provided).
na.action a function which indicates what should happen when the data contain NA’s. The
default is set by the na.action setting of options, and is na.fail if that is
unset. The default is na.omit.
trace logical, if TRUE a message is printed for every ten iterations completed during the forward search.

Value

The function returns an object of class "fwdlm" with the following components:

call the matched call.
Residuals a $(n \times (n - p + 1))$ matrix of residuals.
Unit a matrix of units added (to a maximum of 5 units) at each step.
included a list with each element containing a vector of units included at each step of the forward search.
Coefficients a $( (n - p + 1) \times p )$ matrix of coefficients.
tStatistics a $( (n - p + 1) \times p )$ matrix of t statistics for the coefficients.
CookDist a $( (n - p) \times 1 )$ matrix of forward Cook's distances.
ModCookDist a $( (n - p) \times 5 )$ matrix of forward modified Cook's distances for the units (to a maximum of 5 units) included at each step.
Leverage a $(n \times (n - p + 1))$ matrix of leverage values.
S2 a $( (n - p + 1) \times 2 )$ matrix with 1st column containing $S^2$ and the 2nd column $R^2$.
MaxRes a $( (n - p) \times 1 )$ matrix of max studentized residuals.
MinDelRes a $( (n - p - 1) \times 1 )$ matrix of minimum deletion residuals.
StartingModel a "lqs" object providing the least Median of Squares regression fit used to select the starting subset.

Author(s)

Originally written for S-Plus by: Kjell Konis <kkonis@insightful.com> and Marco Riani <mriani@unipr.it>
Ported to R by Luca Scrucca <luca@stat.unipg.it>

References


See Also

summary.fwdlm, plot.fwdlm, fwdco, fwdglm, lmsreg.

Examples

library(MASS)
data(forbes)
plot(forbes, xlab="Boiling point", ylab="Pressure")
mod <- fwdlm(I@0*log10(pres) ~ bp, data=forbes)
summary(mod)
## Not run: plot(mod)
plot(mod, 1)
plot(mod, 6, ylim=c(-3, 1000))

---

**fwd sco**

*Forward Search Transformation in Linear Regression*

**Description**

This function applies the forward search approach to the Box-Cox transformation of response in linear regression models.

**Usage**

```r
fwd sco(formula, data, nsamp = "best", lambda = c(-1, -0.5, 0, 0.5, 1),
       x = NULL, y = NULL, intercept = TRUE, na.action, trace = TRUE)
```

**Arguments**

- `formula` a symbolic description of the model to be fit. The details of the model are the same as for `lm`.
- `data` an optional data frame containing the variables in the model. By default the variables are taken from the environment from which the function is called.
- `nsamp` the initial subset for the forward search in linear regression is found by fitting the regression model with the R function `lmsreg`. This argument allows to control how many subsets are reused in the Least Median of Squares regression. The choices are: the number of samples or "best" (the default) or "exact" or "sample". For details see `lmsreg`.
- `lambda` a vector (or a single numerical value) of lambda values for the response transformation.
- `x` A matrix of predictors values (if no formula is provided).
- `y` A vector of response values (if no formula is provided).
- `intercept` Logical for the inclusion of the intercept (if no formula is provided).
- `na.action` a function which indicates what should happen when the data contain NA’s. The default is set by the `na.action` setting of `options`, and is `na.fail` if that is unset. The default is `na.omit`.
- `trace` logical, if TRUE a message is printed for every ten iterations completed during the forward search.

**Value**

The function returns an object of class "fwd sco" with the following components:

- `call` the matched call.
- `Likelihood` a \((n - p + 1)x n.lambda\) matrix of likelihood values.
- `Score Test` a \((n - p + 1)x n.lambda\) matrix of score test statistic values.
Unit a list with an element for each lambda values. Each element provides a matrix of units added (to a maximum of 5 units) at each step of the forward search.

Input a list with \( n, p \) and the vector of lambda values used.

\( x \) The design matrix.

\( y \) The vector for the response.

Author(s)
Originally written for S-Plus by: Kjell Konis <kkonis@insightful.com> and Marco Riani <mriani@unipr.it>
Ported to R by Luca Scrucca <luca@stat.unipg.it>

References

See Also
summary.fwdsco, plot.fwdsco, fwdlm, fwdglm.

Examples
data(wool)
mod <- fwdsco(y ~ x1 + x2 + x3, data = wool)
summary(mod)
plot(mod, plot.mle=FALSE)
plot(mod, plot.Sco=FALSE, plot.Lik=TRUE)

---

**hawkins**

**Hawkins’ data**

Description
The hawkins data frame has 128 rows and 9 columns.

Usage
data(hawkins)

Format
This data frame contains the following columns:

\( \text{x1} \) a numeric vector

\( \text{x2} \) a numeric vector

\( \text{x3} \) a numeric vector

\( \text{x4} \) a numeric vector
kinetics

\[ x_5 \] a numeric vector
\[ x_6 \] a numeric vector
\[ x_7 \] a numeric vector
\[ x_8 \] a numeric vector
\[ y \] a numeric vector

References


---

<table>
<thead>
<tr>
<th>kinetics</th>
</tr>
</thead>
</table>

**Kinetics data**

Description

Kinetics data (from Becton-Dickenson) The kinetics data frame has 19 rows and 5 columns.

Usage

data(kinetics)

Format

This data frame contains the following columns:

- **Substrate** substrate indicator
- **I0** Inhibitor concentration
- **I3** Inhibitor concentration
- **I10** Inhibitor concentration
- **I30** Inhibitor concentration
- **y** initial velocity

References

The `lakes` data frame has 29 rows and 3 columns.

```r
data(lakes)
```

This data frame contains the following columns:

- **NIN**: average influent nitrogen concentration
- **TW**: water retention time
- **TN**: mean annual nitrogen concentration

References


The `leafpine` data frame has 70 rows and 3 columns.

```r
data(leafpine)
```

This data frame contains the following columns:

- **girth**: girth
- **height**: height
- **volume**: volume

References

Description

This function computes the Least Median Square robust fit for generalized linear models using deviance residuals.

Usage

\texttt{lmsglm(x, y, family, weights, offset, n.samples = 100, max.samples = 200, epsilon = 1e-04, maxit = 50, trace = FALSE)}

Arguments

- \texttt{x}: a matrix or data frame containing the explanatory variables.
- \texttt{y}: the response: a vector of length the number of rows of \texttt{x}.
- \texttt{family}: a description of the error distribution and link function to be used in the model. See \texttt{family} for details.
- \texttt{weights}: an optional vector of weights to be used in the fitting process.
- \texttt{offset}: optional, a priori known component to be included in the linear predictor during fitting.
- \texttt{n.samples}: number of good subsets to fit. It can be a numeric value or "all".
- \texttt{max.samples}: maximal number of subsets to fit. By default is set to twice \texttt{n.samples}.
- \texttt{epsilon}: positive convergence tolerance epsilon. See \texttt{glm.control} for details.
- \texttt{maxit}: integer giving the maximal number of IWLS iterations. See \texttt{glm.control} for details.
- \texttt{trace}: logical, if \texttt{TRUE} a message is printed for every ten iterations completed during the search.

Details

This function is used by \texttt{fwdglm} to select the starting subset for the forward search. For this reason, users do not generally need to use it.

Value

The function returns a list with the following components:

- \texttt{bsb}: a vector giving the best subset found
- \texttt{dev.res}: a vector giving the deviance residuals for all the observations
- \texttt{message}: a short message about the status of the algorithm
- \texttt{model}: the model provided by \texttt{glm.fit} using the units in the best subset found
mice

Author(s)

Originally written for S-Plus by: Kjell Konis <kkonis@insightful.com> and Marco Riani <mriani@unipr.it>
Ported to R by Luca Scrucca <luca@stat.unipg.it>

References


See Also

fwdglm, fwdlm, lmsreg, fwdsc0.

---

### mice

**Mice data**

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<table>
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<tbody>
<tr>
<td></td>
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</tbody>
</table>

**Description**

The *mice* data frame has 14 rows and 4 columns.

**Usage**

data(mice)

**Format**

This data frame contains the following columns:

- **dose** dose level
- **prep** factor preparation: 0= Standard preparation, 1= Test preparation
- **conv** number with convultion
- **total** Total

**References**

molar

---

**Molar data**

**Description**
Radioactivity versus molar concentration of nifedipene
The molar data frame has 15 rows and 2 columns.

**Usage**
data(molar)

**Format**
This data frame contains the following columns:
- \( x \) log10(NIF concentration)
- \( y \) Total counts for \( 5 \times 10^{-10} \) Molar NTD additive

**References**

---

mussels

---

**Mussels data**

**Description**
The mussels data frame has 82 rows and 5 columns.

**Usage**
data(mussels)

**Format**
This data frame contains the following columns:
- \( W \) width
- \( H \) height
- \( L \) length
- \( S \) shell mass
- \( M \) mass
References


---

**ozone**

**Ozone data**

---

**Description**

Ozone concentration at Upland, CA.
The ozone data frame has 80 rows and 9 columns.

**Usage**

data(ozone)

**Format**

This data frame contains the following columns:

- **x1** a numeric vector
- **x2** a numeric vector
- **x3** a numeric vector
- **x4** a numeric vector
- **x5** a numeric vector
- **x6** a numeric vector
- **x7** a numeric vector
- **x8** a numeric vector
- **y** Ozone concentration (ppm)

**References**

plot.fwdglm

Forward Search in Generalized Linear Models

Description

This function plots the results of a forward search analysis in generalized linear models.

Usage

```r
## S3 method for class 'fwdglm'
plot(x, which.plots = 1:11, squared = FALSE, scaled = FALSE,
    ylim = NULL, xlim = NULL, th.Res = 4, th.Lev = 0.25, sig.Tst = 2.58,
    sig.score = 1.96, plot.pf = FALSE, labels.in.plot = TRUE, ...)
```

Arguments

- `x`: a "fwdglm" object.
- `which.plots`: select which plots to draw, by default all. Each graph is addressed by an integer:
  1. deviance residuals
  2. leverages
  3. maximum deviance residuals
  4. minimum deviance residuals
  5. coefficients
  6. t statistics, i.e. coef.est/SE(coef.est)
  7. likelihood matrix: deviance, deviance explained, pseudo R-squared, dispersion parameter
  8. score statistic for the goodness of link test
  9. forward Cook’s distances
  10. modified forward Cook’s distances
  11. weights used at each step of the forward search for the units included
- `squared`: logical, if TRUE plots squared deviance residuals.
- `scaled`: logical, if TRUE plots scaled coefficient estimates.
- `ylim`: a two component vector for the min and max of the y axis.
- `xlim`: a two component vector for the min and max of the x axis.
- `th.Res`: numerical, a threshold for labelling the residuals.
- `th.Lev`: numerical, a threshold for labelling the leverages.
- `sig.Tst`: numerical, a value used to draw the confidence interval on the plot of the t statistic.
- `sig.score`: numerical, a value used to draw the confidence interval on the plot of the score test statistic.
- `plot.pf`: logical, in case of binary response if TRUE graphs contain all the step of the forward search, otherwise only those in which there is no perfect fit.
- `labels.in.plot`: logical, if TRUE units are labelled in the plots when required.
- `...`: further arguments passed to or from other methods.
plot.fwdlm

Author(s)
Originally written for S-Plus by: Kjell Konis <kkonis@insightful.com> and Marco Riani <mriani@unipr.it>
Ported to R by Luca Scrucca <luca@stat.unipg.it>

References

See Also
fwdglm, fwdlm, fwdsco.

Examples

## Not run:
data(cellular)
mod <- fwdglm(y ~ as.factor(TNF) + as.factor(IFN), data=cellular,
              family=poisson(log), nsamp=200)
summary(mod)
plot(mod)
## End(Not run)

plot.fwdlm Forward Search in Linear Regression

Description
This function plots the results of a forward search analysis in linear regression models.

Usage

## S3 method for class 'fwdlm'
plot(x, which.plots = 1:10, squared = FALSE, scaled = TRUE,
ylim = NULL, xlim = NULL, th.Res = 2, th.Lev = 0.25, sig.Tst = 2.58,
      labels.in.plot = TRUE, ...)

Arguments

  x
  a "fwdlm" object.

  which.plots
  select which plots to draw, by default all. Each graph is addressed by an integer:
  1. scaled residuals
  2. leverages
  3. maximum studentized residuals
  4. minimum deletion residuals
5. coefficients
6. statistics
7. forward Cook’s distances
8. modified forward Cook’s distances
9. $S^2$ values
10. $R^2$ values

squared logical, if TRUE plots squared residuals.
scaled logical, if TRUE plots scaled coefficient estimates.
ylim a two component vector for the min and max of the y axis.
xlim a two component vector for the min and max of the x axis.
th.Res numerical, a threshold for labelling the residuals.
th.Lev numerical, a threshold for labelling the leverages.
sig.Tst numerical, a value (on the scale of the t statistics) used to draw the confidence interval on the plot of the t statistics.
labels.in.plot logical, if TRUE units are labelled in the plots when required.
... further arguments passed to or from other methods.

Author(s)

Originally written for S-Plus by: Kjell Konis <kkonis@insightful.com> and Marco Riani <mriani@unipr.it>
Ported to R by Luca Scrucca <luca@stat.unipg.it>

References


See Also

fwdlm, fwdsco, fwdglm.

Examples

```r
library(MASS)
data(forbes)
plot(forbes)
mod <- fwdlm(100*log10(pres) ~ bp, data=forbes)
summary(mod)
## Not run: plot(mod)
```
plot.fwdsco

Forward Search Transformation in Linear Regression

Description

This function plots the results of a forward search analysis for Box-Cox transformation of response in linear regression models.

Usage

## S3 method for class 'fwdsco'
plot(x, plot.Sco = TRUE, plot.Lik = FALSE, th.Sco = 2.58,
     plot.mle = TRUE, ylim = NULL, xlim = NULL, ...)

Arguments

x a "fwdsco" object.
plot.Sco logical, if TRUE plots the score test statistic at each step of the forward search for each lambda value.
plot.Lik logical, if TRUE plots the likelihood value at each step of the forward search for each lambda value.
th.Sco numerical, a value used to draw the confidence interval on the plot of the score test statistic.
plot.mle logical, if TRUE adds a point at the maximum likelihood value for the transformation computed in the final step, i.e. on the full dataset.
ylim a two component vector for the min and max of the y axis.
xlim a two component vector for the min and max of the x axis.
... further arguments passed to or from other methods.

Author(s)

Originally written for S-Plus by: Kjell Konis <kkonis@insightful.com> and Marco Riani <mriani@unipr.it>
Ported to R by Luca Scrucca <luca@stat.unipg.it>

References


See Also

fwdsco, fwdlm, fwdglm.
## poison

### Examples
```r
## Not run:
data(wool)
mod <- fwdsco(y ~ x1 + x2 + x3, data = wool)
plot(mod, plot.mle=FALSE)
plot(mod, plot.Sco=FALSE, plot.Lik=TRUE)
## End(Not run)
```

### Description
Box and Cox poison data. Survival times in 10 hour units of animals in a $3 \times 4$ factorial experiment. The poison data frame has 48 rows and 3 columns.

### Usage
```r
data(poison)
```

### Format
This data frame contains the following columns:

- **time** a numeric vector
- **poison** a factor
- **treat** a factor with levels: A, B, C, D

### References

## rainfall

### Description
Toxoplasmosis data. The rainfall data frame has 34 rows and 3 columns.

### Usage
```r
data(rainfall)
```
**Format**

This data frame contains the following columns:

- **Rain**  mm of rain
- **Cases**  cases of toxoplasmosis
- **Total**  total

**References**


---

**Description**

The salinity data frame has 28 rows and 4 columns.

**Usage**

```r
data(salinity)
```

**Format**

This data frame contains the following columns:

- **lagsalinity**  Lagged salinity
- **trend**  Trend
- **waterflow**  Water flow
- **salinity**  Salinity

**References**

scglm

**Goodness of Link Test in GLM**

**Description**

Computes the score test statistic for the goodness of link test in generalized linear models.

**Usage**

```r
scglm(x, y, family, weights, beta, phi = 1, offset)
```

**Arguments**

- `x`: a matrix or data frame containing the explanatory variables.
- `y`: the response: a vector of length the number of rows of `x`.
- `family`: a description of the error distribution and link function to be used in the model. See `family` for details.
- `weights`: an optional vector of weights to be used in the fitting process.
- `beta`: a vector of coefficients estimates
- `phi`: the dispersion parameter
- `offset`: optional, a priori known component to be included in the linear predictor during fitting.

**Details**


**Value**

Return the value of the score test statistic.

**Author(s)**

Originally written for S-Plus by: Kjell Konis <kkonis@insightful.com> and Marco Riani <mriani@unipr.it>
Ported to R by Luca Scrucca <luca@stat.unipg.it>

**References**


**See Also**

`fwdglm`, `fwdlm`, `score.s`. 
Score test for the Box-Cox transformation of the response

Description

Computes the approximate score test statistic for the Box-Cox transformation

Usage

score.s(x, y, la, tol = 1e-20)
lambda.mle(x, y, init = c(-2, 2), tol = 1e-04)

Arguments

x  
a matrix or data frame containing the explanatory variables.
y  
the response: a vector of length the number of rows of x.
la  
the value of the lambda parameter.
tol  
tolerance value used to check for full rank matrix.
init  
range of values to search for MLE.

Details


Value

Return a list with two components:

Score  
the value of the score test statistic
Likelihood  
the value of the likelihood

Author(s)

Originally written for S-Plus by: Kjell Konis <kkonis@insightful.com> and Marco Riani <mriani@unipr.it>
Ported to R by Luca Scrucca <luca@stat.unipg.it>

References


See Also

fwdsco, fwdlm, fwdglm.
Description

Brownlee's stack loss data.
The stackloss data frame has 21 rows and 4 columns.

Usage

data(stackloss)

Format

This data frame contains the following columns:

- **Air**  Air flow
- **Temp** Cooling water inlet temperature
- **Conc** Acid concentration
- **Loss** Stack loss

References


summary.fwdglm

**Summary Fit of Forward Search in Generalized Linear Regression**

Description

summary method for class "fwdglm".

Usage

```r
## S3 method for class 'fwdglm'
summary(object, steps = "auto", remove.perfect.fit = TRUE, ...)
```

Arguments

- **object** an object of class "fwdglm".
- **steps** the number of forward steps to show.
- **remove.perfect.fit** logical, controlling if perfect fit steps should be removed (only apply to binary responses).
- **...** further arguments passed to or from other methods.
Author(s)

Originally written for S-Plus by: Kjell Konis <kkonis@insightful.com> and Marco Riani <mriani@unipr.it>
Ported to R by Luca Scrucca <luca@stat.unipg.it>

References


See Also

fwdglm.

summary.fwdlm

Summarizing Fit of Forward Search in Linear Regression

Description

summary method for class "fwdlm".

Usage

## S3 method for class 'fwdlm'
summary(object, steps = "auto", ...)

Arguments

object an object of class "fwdlm".
steps the number of forward steps to show.
... further arguments passed to or from other methods.

Author(s)

Originally written for S-Plus by: Kjell Konis <kkonis@insightful.com> and Marco Riani <mriani@unipr.it>
Ported to R by Luca Scrucca <luca@stat.unipg.it>

References


See Also

fwdlm.
**Summary**

**Summary**

Summary method for class "fwdso".

**Usage**

```r
## S3 method for class 'fwdso'
summary(object, steps = "auto", lambdaMLE = FALSE, ...)
```

**Arguments**

- `object`: an object of class "fwdso".
- `steps`: the number of forward steps to show.
- `lambdaMLE`: logical, controlling if the MLE of lambda calculated on the full dataset must be shown.
- `...`: further arguments passed to or from other methods.

**Author(s)**

Originally written for S-Plus by: Kjell Konis <kkonis@insightful.com> and Marco Riani <mriani@unipr.it>
Ported to R by Luca Scrucca <luca@stat.unipg.it>

**References**


**See Also**

- `fwdso`.

---

**Vaso**

**Vaso data**

**Description**

Finney's data on vaso-constriction in the skin of the digits.

The vaso data frame has 39 rows and 3 columns.

**Usage**

```r
data(vaso)
```
Format

This data frame contains the following columns:

- `volume` volume
- `rate` rate
- `y` response: 0= nonoccurrence, 1= occurrence

References


---

### wool

**Wool data**

**Description**

Number of cycles to failure of samples of worsted yarn in a 33 experiment. The wool data frame has 27 rows and 4 columns.

**Usage**

data(wool)

**Format**

This data frame contains the following columns:

- `x1` factor levels: -1, 0, 1
- `x2` factor levels: -1, 0, 1
- `x3` factor levels: -1, 0, 1
- `y` cycles to failure a numeric vector

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