

Package ‘forward’

October 12, 2009

Version 1.0.3

Date 2009/10/10

Title Forward search

Author 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>

Maintainer Luca Scrucca <luca@stat.unipg.it>

Depends R (>= 2.8), MASS

Description Forward search approach to robust analysis in linear and generalized linear regression models.

License GPL-2

Repository CRAN

Date/Publication 2009-10-12 06:48:35

R topics documented:

ar	2
bliss	3
calcium	3
carinsuk	4
carr	4
cellular	5
chapman	5
derailme	6
dielectric	7
forbes	7
fwd.combn	8
fwdglm	9
fwdlm	11
fwdscs	13

hawkins	14
kinetics	15
lakes	16
leafpine	16
lmsglm	17
mice	18
molar	19
mussels	19
ozone	20
plot.fwdglm	21
plot.fwdlm	22
plot.fwdsco	24
poison	25
rainfall	25
salinity	26
scglm	27
score.s	28
stackloss	29
summary.fwdglm	29
summary.fwdlm	30
summary.fwdsco	31
vaso	31
wool	32
Index	33

ar

ar data

Description

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

References

Atkinson, A.C. and Riani, M. (2000), *Robust Diagnostic Regression Analysis*, First Edition. New York: Springer, Table A.2

bliss	<i>Bliss data</i>
-------	-------------------

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

Atkinson, A.C. and Riani, M. (2000), *Robust Diagnostic Regression Analysis*, First Edition. New York: Springer, Table A.20

calcium	<i>Calcium data</i>
---------	---------------------

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

Atkinson, A.C. and Riani, M. (2000), *Robust Diagnostic Regression Analysis*, First Edition. New York: Springer, Table A.13

carinsuk

Car insurance data

Description

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

Usage

```
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

Atkinson, A.C. and Riani, M. (2000), *Robust Diagnostic Regression Analysis*, First Edition. New York: Springer, Table A.16

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

```
data(carr)
```

Format

This data frame contains the following columns:

x1 partial pressure of hydrogen

x2 partial pressure of n-pentane

x3 partial pressure of iso-pentane

y rate of disappearance of n-pentane

References

Atkinson, A.C. and Riani, M. (2000), *Robust Diagnostic Regression Analysis*, First Edition. New York: Springer, Table A.15

cellular

Cellular differentiation data

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

Atkinson, A.C. and Riani, M. (2000), *Robust Diagnostic Regression Analysis*, First Edition. New York: Springer, Table A.19

chapman

Chapman data

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

Atkinson, A.C. and Riani, M. (2000), *Robust Diagnostic Regression Analysis*, First Edition. New York: Springer, Table A.24

derailme

British Train Accidents.

Description

The derailme data frame has 67 rows and 5 columns.

Usage

```
data(derailme)
```

Format

This data frame contains the following columns:

Month a numeric vector

Year a numeric vector

Type a numeric vector

TrainKm a numeric vector

y a numeric vector

References

Atkinson, A.C. and Riani, M. (2000), *Robust Diagnostic Regression Analysis*, First Edition. New York: Springer, Table A.18

dialectric

Dialectric 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 dielectric breakdown strength in kilovolts

References

Atkinson, A.C. and Riani, M. (2000), *Robust Diagnostic Regression Analysis*, First Edition. New York: Springer, Table A.17

`forbes`*Forbes data*

Description

Forbes' data on air pressure in the Alps and the boiling point of water. The `forbes` data frame has 17 rows and 2 columns.

Usage

```
data(forbes)
```

Format

This data frame contains the following columns:

x Boiling point

y 100 x log(pressure)

References

Atkinson, A.C. and Riani, M. (2000), *Robust Diagnostic Regression Analysis*, First Edition. New York: Springer, Table A.1

`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

```
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

Nijenhuis, A. and Wilf, H.S. (1978) *Combinatorial Computers and Calculators*. NY: Academic Press.

Examples

```
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)))
```

fwdglm

Forward Search in Generalized Linear Models

Description

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

Usage

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

Arguments

<code>formula</code>	a symbolic description of the model to be fit. The details of the model are the same as for <code>glm</code> .
<code>family</code>	a description of the error distribution and link function to be used in the model. See family for details.
<code>data</code>	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.
<code>weights</code>	an optional vector of weights to be used in the fitting process.
<code>na.action</code>	a function which indicates what should happen when the data contain NA's. The default is set by the <code>na.action</code> setting of <code>options</code> , and is <code>na.fail</code> if that is unset. The default is <code>na.omit</code> .
<code>contrasts</code>	an optional list. See the <code>contrasts.arg</code> of <code>model.matrix.default</code> .
<code>bsb</code>	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 <code>lmsglm</code> with control arguments provided by <code>nsamp</code> .
<code>balanced</code>	logical, for a binary response if TRUE the proportion of successes on the full dataset is approximately balanced during the forward search algorithm.
<code>maxit</code>	integer giving the maximal number of IWLS iterations. See <code>glm.control</code> for details.
<code>epsilon</code>	positive convergence tolerance epsilon. See <code>glm.control</code> for details.
<code>nsamp</code>	the initial subset for the forward search in generalized linear models is found by the function <code>lmsglm</code> . 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 <code>nsamp</code> good subsets or a maximum of $2 * nsamp$ subsets.
<code>trace</code>	logical, if TRUE a message is printed for every ten iterations completed during the forward search.

Value

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

<code>call</code>	the matched call.
<code>Residuals</code>	a $(n \times (n - p + 1))$ matrix of residuals.
<code>Unit</code>	a matrix of units added (to a maximum of 5 units) at each step.
<code>included</code>	a list with each element containing a vector of units included at each step of the forward search.
<code>Coefficients</code>	a $((n - p + 1) \times p)$ matrix of coefficients.
<code>tStatistics</code>	a $((n - p + 1) \times p)$ matrix of t statistics for the coefficients, i.e. <code>coef.est/SE(coef.est)</code> .
<code>Leverage</code>	a $(n \times (n - p + 1))$ matrix of leverage values.
<code>MaxRes</code>	a $((n - p) \times 2)$ matrix of max deviance residuals in the best subsets and m -th deviance residuals.

MinDelRes	a $((n - p - 1) \times 2)$ matrix of minimum deviance residuals out of best subsets and $(m + 1)$ -th deviance residuals.
ScoreTest	a $((n - p) \times 1)$ matrix of score test statistics for a goodness of link test.
Likelihood	a $((n - p) \times 4)$ matrix with columns containing: deviance, residual deviance, psuedo R^2 (computed as $1 - \text{deviance}/\text{null.deviance}$), dispersion parameter (computed as $\sum(\text{pearson.residuals}^2)/(m - p)$).
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.
Weights	a $(n \times (n - p))$ matrix of weights used at each step of the forward search.
inibsb	a vector giving the best starting subset chosen by <code>lmsglm</code> .
binary.response	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

Atkinson, A.C. and Riani, M. (2000), *Robust Diagnostic Regression Analysis*, First Edition. New York: Springer, Chapter 6.

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)
```

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

<code>formula</code>	a symbolic description of the model to be fit. The details of the model are the same as for <code>lm</code> .
<code>data</code>	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.
<code>nsamp</code>	the initial subset for the forward search in linear regression is found by fitting the regression model with the R function <code>lmsreg</code> . 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 <code>lmsreg</code> .
<code>x</code>	A matrix of predictors values (if no formula is provided).
<code>y</code>	A vector of response values (if no formula is provided).
<code>intercept</code>	Logical for the inclusion of the intercept (if no formula is provided).
<code>na.action</code>	a function which indicates what should happen when the data contain NA's. The default is set by the <code>na.action</code> setting of <code>options</code> , and is <code>na.fail</code> if that is unset. The default is <code>na.omit</code> .
<code>trace</code>	logical, if <code>TRUE</code> 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:

<code>call</code>	the matched call.
<code>Residuals</code>	a $(n \times (n - p + 1))$ matrix of residuals.
<code>Unit</code>	a matrix of units added (to a maximum of 5 units) at each step.
<code>included</code>	a list with each element containing a vector of units included at each step of the forward search.
<code>Coefficients</code>	a $((n - p + 1) \times p)$ matrix of coefficients.
<code>tStatistics</code>	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 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

Atkinson, A.C. and Riani, M. (2000), *Robust Diagnostic Regression Analysis*, First Edition. New York: Springer, Chapters 2-3.

See Also

[summary.fwdlm](#), [plot.fwdlm](#), [fwdsc0](#), [fwdglm](#), [lmsreg](#).

Examples

```
data(forbes)
plot(forbes, xlab="Boiling point", ylab="100 x log(pressure)")
mod <- fwdlm(y ~ x, data=forbes)
summary(mod)
## Not run: plot(mod)
plot(mod, 1)
plot(mod, 6, ylim=c(-3, 1000))
```

fwdsc0

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

```
fwdsc0(formula, data, nsamp = "best", lambda = c(-1, -0.5, 0, 0.5, 1),
       x = NULL, y = NULL, intercept = TRUE, na.action, trace = TRUE)
```

Arguments

<code>formula</code>	a symbolic description of the model to be fit. The details of the model are the same as for <code>lm</code> .
<code>data</code>	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.
<code>nsamp</code>	the initial subset for the forward search in linear regression is found by fitting the regression model with the R function <code>lmsreg</code> . 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 <code>lmsreg</code> .
<code>lambda</code>	a vector (or a single numerical value) of lambda values for the response transformation.
<code>x</code>	A matrix of predictors values (if no formula is provided).
<code>y</code>	A vector of response values (if no formula is provided).
<code>intercept</code>	Logical for the inclusion of the intercept (if no formula is provided).
<code>na.action</code>	a function which indicates what should happen when the data contain NA's. The default is set by the <code>na.action</code> setting of <code>options</code> , and is <code>na.fail</code> if that is unset. The default is <code>na.omit</code> .
<code>trace</code>	logical, if TRUE a message is printed for every ten iterations completed during the forward search.

Value

The function returns an object of class "fwdsc0" with the following components:

<code>call</code>	the matched call.
<code>Likelihood</code>	a $((n - p + 1) \times n \times \text{lambda})$ matrix of likelihood values.
<code>ScoreTest</code>	a $((n - p + 1) \times n \times \text{lambda})$ matrix of score test statistic values.
<code>Unit</code>	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.
<code>Input</code>	a list with n , p and the vector of lambda values used.
<code>x</code>	The design matrix.
<code>y</code>	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

Atkinson, A.C. and Riani, M. (2000), *Robust Diagnostic Regression Analysis*, First Edition. New York: Springer, Chapter 4.

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:

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 a numeric vector

References

Atkinson, A.C. and Riani, M. (2000), *Robust Diagnostic Regression Analysis*, First Edition. New York: Springer, Table A.4

`kinetics`*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

Atkinson, A.C. and Riani, M. (2000), *Robust Diagnostic Regression Analysis*, First Edition. New York: Springer, Table A.12

`lakes`*Lakes data*

Description

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

Usage

```
data(lakes)
```

Format

This data frame contains the following columns:

x1 average influent nitrogen concentration

x2 a numeric vector

y a numeric vector

References

Atkinson, A.C. and Riani, M. (2000), *Robust Diagnostic Regression Analysis*, First Edition. New York: Springer, Table A.14

leafpine	<i>Pine data</i>
----------	------------------

Description

The leafpine data frame has 70 rows and 3 columns.

Usage

```
data(leafpine)
```

Format

This data frame contains the following columns:

x1 a numeric vector

x2 a numeric vector

y a numeric vector

References

Atkinson, A.C. and Riani, M. (2000), *Robust Diagnostic Regression Analysis*, First Edition. New York: Springer, Table A.10

lmsglm	<i>Forward Search in Generalized Linear Models</i>
--------	--

Description

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

Usage

```
lmsglm(x, y, family, weights, offset, n.samples = 100, max.samples = 200, epsilon =
```

Arguments

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

Details

This function is used by `fdgglm` 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:

<code>bsb</code>	a vector giving the best subset found
<code>dev.res</code>	a vector giving the deviance residuals for all the observations
<code>message</code>	a short message about the status of the algorithm
<code>model</code>	the model provided by <code>glm.fit</code> using the units in the best subset found

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

Atkinson, A.C. and Riani, M. (2000), *Robust Diagnostic Regression Analysis*, First Edition. New York: Springer, Chapter 6.

See Also

[fdgglm](#), [fdglm](#), [lmsreg](#), [fwdsc0](#).

mice	<i>Mice data</i>
------	------------------

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 convulsion

total Total

References

Atkinson, A.C. and Riani, M. (2000), *Robust Diagnostic Regression Analysis*, First Edition. New York: Springer, Table A.21

molar	<i>Molar data</i>
-------	-------------------

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 5×10^{-10} Molar NTD additive

References

Atkinson, A.C. and Riani, M. (2000), *Robust Diagnostic Regression Analysis*, First Edition. New York: Springer, Table A.1

`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

Atkinson, A.C. and Riani, M. (2000), *Robust Diagnostic Regression Analysis*, First Edition. New York: Springer, Table A.9

`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

Atkinson, A.C. and Riani, M. (2000), *Robust Diagnostic Regression Analysis*, First Edition. New York: Springer, Table A.7

plot.fwdglm

Forward Search in Generalized Linear Models

Description

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

Usage

```
## 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 statistics.
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.

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

Atkinson, A.C. and Riani, M. (2000), *Robust Diagnostic Regression Analysis*, First Edition. New York: Springer, Chapter 6.

See Also

[fwdglm](#), [fwdlm](#), [fwdSCO](#).

Examples

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

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: <ol style="list-style-type: none"> 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

Atkinson, A.C. and Riani, M. (2000), *Robust Diagnostic Regression Analysis*, First Edition. New York: Springer, Chapters 2-3.

See Also

[fwdlm](#), [fwdsco](#), [fwdglm](#).

Examples

```
## Not run: data(forbes)
## Not run: plot(forbes)
## Not run: mod <- fwdlm(Log.Pressure ~ Boiling.point, data=forbes)
## Not run: 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

Atkinson, A.C. and Riani, M. (2000), *Robust Diagnostic Regression Analysis*, First Edition. New York: Springer, Chapters 2-3.

See Also

[fwdsc](#), [fwdlm](#), [fwdglm](#).

Examples

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

poison

Poison data

Description

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

Usage

```
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

Atkinson, A.C. and Riani, M. (2000), *Robust Diagnostic Regression Analysis*, First Edition. New York: Springer, Table A.8

`rainfall`*Rainfall data*

Description

Toxoplasmosis data.

The `rainfall` data frame has 34 rows and 3 columns.

Usage

```
data(rainfall)
```

Format

This data frame contains the following columns:

Rain mm of rain

Cases cases of toxoplasmosis

Total total

References

Atkinson, A.C. and Riani, M. (2000), *Robust Diagnostic Regression Analysis*, First Edition. New York: Springer, Table A.22

`salinity`*Salinity data*

Description

The `salinity` data frame has 28 rows and 4 columns.

Usage

```
data(salinity)
```

Format

This data frame contains the following columns:

x1 Lagged salinity

x2 Trend

x3 Water flow

y Salinity

References

Atkinson, A.C. and Riani, M. (2000), *Robust Diagnostic Regression Analysis*, First Edition. New York: Springer, Table A.6

scglm *Goodness of Link Test in GLM*

Description

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

Usage

```
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

See pag. 200–201 of Atkinson and Riani (2000).

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

Atkinson, A.C. and Riani, M. (2000), *Robust Diagnostic Regression Analysis*, First Edition. New York: Springer, Chapter 6.

See Also

[fwdglm](#), [fwdlm](#), [score.s](#).

`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

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

Details

See pag. 82–86 of Atkinson and Riani (2000).

Value

Return a list with two components:

<code>Score</code>	the value of the score test statistic
<code>Likelihood</code>	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

Atkinson, A.C. and Riani, M. (2000), *Robust Diagnostic Regression Analysis*, First Edition. New York: Springer, Chapter 4.

See Also

[fwdsc](#), [fwdlm](#), [fwdglm](#).

stackloss	<i>Stackloss data</i>
-----------	-----------------------

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

Atkinson, A.C. and Riani, M. (2000), *Robust Diagnostic Regression Analysis*, First Edition. New York: Springer, Table A.5

summary.fwdglm	<i>Summarizing Fit of Forward Search in Generalized Linear Regression</i>
----------------	---

Description

summary method for class "fwdglm".

Usage

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

Arguments

<code>object</code>	an object of class "fwdglm".
<code>steps</code>	the number of forward steps to show.
<code>remove.perfect.fit</code>	logical, controlling if perfect fit steps should be removed (only apply to binary responses).
<code>...</code>	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

Atkinson, A.C. and Riani, M. (2000), *Robust Diagnostic Regression Analysis*, First Edition. New York: Springer, Chapter 6.

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

Atkinson, A.C. and Riani, M. (2000), *Robust Diagnostic Regression Analysis*, First Edition. New York: Springer, Chapters 2-3.

See Also

[fwdlm](#).

summary.fwdsco	<i>Summarizing Fit of Forward Search Transformation in Linear Regression</i>
----------------	--

Description

summary method for class "fwdsco".

Usage

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

Arguments

object	an object of class "fwdsco".
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

Atkinson, A.C. and Riani, M. (2000), *Robust Diagnostic Regression Analysis*, First Edition. New York: Springer, Chapter 4.

See Also

[fwdsco](#).

vaso	<i>Vaso data</i>
------	------------------

Description

Finney's data on vaso-contraction in the skin of the digits.
The `vaso` data frame has 39 rows and 3 columns.

Usage

```
data(vaso)
```

Format

This data frame contains the following columns:

volume volume

rate rate

y response: 0= nonoccurrence, 1= occurrence

References

Atkinson, A.C. and Riani, M. (2000), *Robust Diagnostic Regression Analysis*, First Edition. New York: Springer, Table A.23

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

References

Atkinson, A.C. and Riani, M. (2000), *Robust Diagnostic Regression Analysis*, First Edition. New York: Springer, Table A.3

Index

*Topic **datasets**

- ar, 1
- bliss, 2
- calcium, 3
- carinsuk, 3
- carr, 4
- cellular, 4
- chapman, 5
- derailme, 6
- dielectric, 6
- forbes, 7
- hawkins, 14
- kinetics, 15
- lakes, 15
- leafpine, 16
- mice, 18
- molar, 18
- mussels, 19
- ozone, 19
- poison, 24
- rainfall, 25
- salinity, 25
- stackloss, 28
- vaso, 30
- wool, 31

*Topic **math**

- fwd.combn, 7

*Topic **models**

- fwdglm, 8
- fwdlm, 11
- fwdscs, 12
- lmsglm, 16
- plot.fwdglm, 20
- plot.fwdlm, 22
- plot.fwdscs, 23
- scglm, 26
- score.s, 27
- summary.fwdglm, 28
- summary.fwdlm, 29

- summary.fwdscs, 30

*Topic **regression**

- fwdglm, 8
- fwdlm, 11
- fwdscs, 12
- lmsglm, 16
- plot.fwdglm, 20
- plot.fwdlm, 22
- plot.fwdscs, 23
- scglm, 26
- score.s, 27
- summary.fwdglm, 28
- summary.fwdlm, 29
- summary.fwdscs, 30

*Topic **robust**

- fwdglm, 8
- fwdlm, 11
- fwdscs, 12
- lmsglm, 16
- plot.fwdglm, 20
- plot.fwdlm, 22
- plot.fwdscs, 23
- scglm, 26
- score.s, 27
- summary.fwdglm, 28
- summary.fwdlm, 29
- summary.fwdscs, 30

- ar, 1

- bliss, 2

- calcium, 3
- carinsuk, 3
- carr, 4
- cellular, 4
- chapman, 5
- derailme, 6
- dielectric, 6

family, 9, 26
forbes, 7
fwd.combn, 7
fwd.nCm(*fwd.combn*), 7
fwdglm, 8, 12, 14, 17, 21, 23, 24, 26, 27, 29
fwdlm, 10, 11, 14, 17, 21, 23, 24, 26, 27, 29
fwdscs, 10, 12, 12, 17, 21, 23, 24, 27, 30

hawkins, 14

kinetics, 15

lakes, 15
lambda.mle(*score.s*), 27
leafpine, 16
lmsglm, 9, 10, 16
lmsreg, 11–13, 17

mice, 18
molar, 18
mussels, 19

ozone, 19

plot.fwdglm, 10, 20
plot.fwdlm, 12, 22
plot.fwdscs, 14, 23
poison, 24
print.fwdglm(*fwdglm*), 8
print.fwdlm(*fwdlm*), 11
print.fwdscs(*fwdscs*), 12
print.summary.fwdglm
 (*summary.fwdglm*), 28
print.summary.fwdlm
 (*summary.fwdlm*), 29
print.summary.fwdscs
 (*summary.fwdscs*), 30

rainfall, 25

salinity, 25
scglm, 26
score.s, 26, 27
stackloss, 28
summary.fwdglm, 10, 28
summary.fwdlm, 12, 29
summary.fwdscs, 14, 30

vaso, 30

wool, 31