Package ‘speedglm’

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**Description**

Fits Linear and Generalized Linear Models to large data sets. For data loaded in R memory the fitting is usually fast, especially if R is linked against an optimized BLAS. For data sets of size greater of R memory, the fitting is made by an updating algorithm.

**Details**

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**Author(s)**

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Maintainer: Marco Enea <emarco76@libero.it>

**Description**

These are advised to be used for speedlm and speedglm models fitted on moderately large data sets. It is also possible to use stepAIC function from package MASS.

**Usage**

```r
## S3 method for class 'speedlm'
add1(object, scope, scale = 0, test = c("none", "Chisq", "F"),
     x = NULL, k = 2, data, ...)
```

```r
## S3 method for class 'speedlm'
```
Arguments

object: a `speedlm` or `speedglm` object for which `model=TRUE` was previously set.
fit: a `speedlm` or `speedglm` object
scope: see `add1` from package stats.
scale: see `add1` from package stats.
all.cols: see `drop1` from package stats.
test: see `add1` from package stats.
x: see `add1` from package stats.
k: see `add1` from package stats.
data: the data that the model was previously fitted to. If not provided, these will be searched in the parent environment.
weights: the model weights, if provided in the `speedglm` object
use.fallback: logical. Should fallback methods be used to try to guess the value?
... further optional arguments.

Details

It is possible to use functions `step()` and `stepAIC()` for both `speedlm` and `speedglm` objects but objects fitted using `updateWithMoreData()`

Warnings

Note that these functions have been poorly tested and need to be checked out more carefully.
Examples

```r
## Not run:
set.seed(10)
n <- 1000
k <- 3
x <- round(matrix(rnorm(n * k), n, k), digits = 3)
beta <- c(0.05, 0.5, 0.8, 1.3, 1.8)
y <- drop(tcrossprod(cbind(1, x[, 2] * x[, 3]), t(beta))) + rnorm(n, 0.2)
colnames(x) <- c("s1", "s2", "s3")
da <- data.frame(y, x)

m0 <- speedlm(y ~ 1, data = da, model = TRUE, y = TRUE)
m0.1 <- add1(m0, scope = ~(s1 + s2 + s3)^2, data = da)
m1 <- step(m0, scope = ~(s1 + s2 + s3)^3)
m1

m2 <- speedglm(y ~ 1, data = da, model = TRUE, y = TRUE)
m2.1 <- add1(m2, scope = ~(s1 + s2 + s3)^2, data = da)
m3 <- step(m2, scope = ~(s1 + s2 + s3)^3)
m3

## End(Not run)
```

### control

**Miscellanea of functions**

**Description**

Utility functions for least squares estimation in large data sets.

**Usage**

```r
ccontrol(B, symmetric = TRUE, tol.values = 1e-7, tol.vectors = 1e-7,
          out.B = TRUE, method = c("eigen", "Cholesky"))
```

**Arguments**

- `B` a squared matrix.
- `symmetric` logical, is B symmetric?
- `tol.values` tolerance to be consider eigenvalues equals to zero.
- `tol.vectors` tolerance to be consider eigenvectors equals to zero.
control

out.B
method
Have the matrix B to be returned?
the method to check for singularity. By default is "eigen", and an eigendecomposition of X'X is made. The "Cholesky" method is faster than "eigen" and does not use tolerance, but the former seems to be more stable for opportune tolerance values.

X
the model matrix.
w
a weights vector.
sparse
logical, is X sparse?
sparselim
a real in the interval [0; 1]. It indicates the minimal proportion of zeroes in the data matrix X in order to consider X as sparse eigendec Logical. Do you want to investigate on rank of X? You may set to
row.chunk
an integer which indicates the total rows number compounding each of the first g-1 blocks. If row.chunk is not a divisor of nrow(X), the g-th block will be formed by the remaining data.
camp
the sample proportion of elements of X on which the survey will be based.

Details
Function control makes an eigendecomposition of B according established values of tolerance. Function cp makes the cross-product X'X by partitioning X in row-blocks. When an optimized BLAS, such as ATLAS, is not installed, the function represents an attempt to speed up the calculation and avoid overflows with medium-large data sets loaded in R memory. The results depending on processor type. Good results are obtained, for example, with an AMD Athlon dual core 1.5 Gb RAM by setting row.chunk to some value less than 1000. Try the example below by changing the matrix size and the value of row.chunk. If the matrix X is sparse, it will have class "dgCMatrix" (the package Matrix is required) and the cross-product will be made without partitioning. However, good performances are usually obtained with a very high zeroes proportion. Function is.sparse makes a quick sample survey on sample proportion of zeroes in X.

Value
for the function control, a list with the following elements:

XTX
the matrix product B without singularities (if there are).
rank
the rank of B
pivot
an ordered set of column indeces of B with, if the case, the last rank + 1, ..., p columns which indicate possible linear combinations.

for the function cp:
new.B
the matrix product X'X (weighted, if w is given).

for the function is.sparse:
sparse
a logical value which indicates if the sample proportion of zeroes is greater than sparselim, with the sample proportion as attribute.
Author(s)

Marco ENEA

See Also

eigen, chol, qr, crossprod

Examples

#### example 1.

n <- 100000
k <- 100
x <- round(matrix(rnorm(n*k),n,k),digits=4)
y <- rnorm(n)

# if an optimized BLAS is not installed, depending on processor type, cp() may be
# faster than crossprod() for large matrices.

system.time(a1 <- crossprod(x))
system.time(a2 <- cp(x,,row.chunk = 500))
all.equal(a1, a2)

#### example 2.1.

n <- 100000
k <- 10
x <- matrix(rnorm(n*k),n,k)
x[,2] <- x[,1] + 2*x[,3] # x has rank 9
y <- rnorm(n)

# estimation by least squares
A <- function(){
  A1 <- control(crossprod(x))
  ok <- A1$pivot[1:A1$rank]
  as.vector(solve(A1$XTX,crossprod(x[,ok],y)))
}

# estimation by QR decomposition
B <- function(){
  B1 <- qr(x)
  qr.solve(x[,B1$pivot[1:B1$rank]],y)
}

system.time(a <- A())
system.time(b <- B())
all.equal(a,b)

### example 2.2

x <- matrix(c(1:5, (1:5)^2), 5, 2)
x <- cbind(x, x[, 1] + 3*x[, 2])
m <- crossprod(x)

qr(m)$rank # is 2, as it should be
control(m,method="eigen")$rank # is 2, as it should be
control(m, method="Cholesky")$rank # is wrong

### example 3.
n <- 10000
fat1 <- gl(20, 500)
y <- rnorm(n)
da <- data.frame(y, fat1)
m <- model.matrix(y ~ factor(fat1), data = da)

---

**data1**

**A toy dataset**

**Description**

The data1 dataset has 100 rows and 4 columns.

**Usage**

data(data1)

**Format**

A data frame with 100 observations on the following 4 variables.

- **y**: a gamma-distributed response variable
- **fat1**: a four-level factor
- **x1**: a numeric covariate
- **x2**: a numeric covariate

**Details**

This is a toy dataset used to show how function shglm works.

**Examples**

data(data1)
predict.speedglm

Predict method for a speedglm object

Description

summary The method is currently under construction but some functionalities are available.

Usage

## S3 method for class 'speedglm'
predict(object, newdata, type = c("link", "response"),
         na.action = na.pass, ...)

Arguments

object an object of class 'speedglm'.
newdata An optional data frame with new data or the original data.
type Type of prediction.
na.action function determining what should be done with missing values in newdata.
... further optional arguments

Details

If newdata is omitted prediction are based on the data used for the fit only if argument fitted was previously set to TRUE in the speedglm object. Currently the method does not work for function shglm.

Value

pred a vector of predictions.

Author(s)

Tomer Kalimi and Marco Enea

See Also

speedglm
Examples

```r
set.seed(10)
y <- rgamma(20, 1.5, 1)
x <- round(matrix(rnorm(20*2), 20, 2), digits=3)
colnames(x) <- c("s1", "s2")
da <- data.frame(y, x)
mod <- speedglm(y~s1+s2, data=da, family=Gamma(log), fitted=TRUE)
predict(mod)
```

predict.speedlm $ Predict method for a speedlm object$

Description

summary The method is currently under construction but some functionalities are available.

Usage

```r
## S3 method for class 'speedlm'
predict(object, newdata, na.action = na.pass, ...)
```

Arguments

- `object` an object of class 'speedlm'.
- `newdata` An optional data frame with new data or the original data.
- `na.action` function determining what should be done with missing values in `newdata`.
- `...` further optional arguments

Details

If `newdata` is omitted prediction are based on the data used for the fit only if argument `fitted` was previously set to TRUE in the speedlm object.

Value

- `predictor` a vector of predictions.

Author(s)

Tomer Kalimi and Marco Enea

See Also

speedlm
Examples

```r
set.seed(10)
x <- round(matrix(rnorm(20*3),20,3),digits=3)
colnames(x) <-c("y","s1","s2")
da <- as.data.frame(x)
mod <- speedlm(y~s1+s2, data=da, fitted=TRUE)
predict(mod)
```

---

### speedglm

**Fitting Generalized Linear Models for Large Data Sets**

**Description**

`speedglm` and `speedglm.wfit` fit GLMs to medium-large data sets, that is those storable into the R memory. The highest performances, in terms of computation time, are obtained when R is linked against an optimized BLAS, such as ATLAS. The function `shglm` is for a data set stored into a file of size greater than the available memory, and takes as argument a function to manipulate connections.

**Usage**

```r
## S3 method for class 'data.frame':
speedglm(formula, data, family = gaussian(), weights = NULL, start = NULL,
etastart = NULL, mustart = NULL, offset = NULL, maxit = 25, k = 2,
sparse = NULL, set.default = list(), trace = FALSE,
method = c("eigen", "Cholesky", "qr"), model = FALSE, y = FALSE,
fitted = FALSE,...)

## S3 method for class 'matrix':
speedglm.wfit(y, X, intercept = TRUE, weights = NULL, row.chunk = NULL,
family = gaussian(), start = NULL, etastart = NULL, mustart = NULL,
offset = NULL, acc = 1e-08, maxit = 25, k = 2,
sparselim = .9, camp = .01, eigendec = TRUE, tol.values = 1e-7,
tol.vectors = 1e-7, tol.solve = .Machine$double.eps,
sparse = NULL, method = c("eigen", "Cholesky", "qr"),
trace = FALSE,...)

## S3 method for class 'function':
shglm(formula, datafun, family = gaussian(), weights.fo = NULL, start = NULL,
etastart = NULL, mustart = NULL, offset = NULL, maxit = 25, k = 2,
chunksize = 5000, sparse = NULL, trace = FALSE, all.levels = FALSE,
set.default = list(),...)
```
Arguments

Most of arguments are the same of `glm` or `bigglm` but with some difference.

- **formula**: a data frame.
- **datafun**: a function which uses connections. See the example below.
- **family**: the same of `glm`, but it must be specified with brackets.
- **start**: the same of `glm`.
- **weights**: the same of `glm`, but it must be specified as `data$weights`.
- **weights.fo**: weights for the response. It must be specified as a formula (see the example below).
- **etastart**: the same of `glm`.
- **mustart**: the same of `glm`.
- **offset**: the same of `glm`.
- **intercept**: the same of `glm`.
- **X**: the same of `x` in `glm.fit`.
- **y**: the same of `glm` and `glm.fit`.
- **maxit**: the same of `glm`.
- **k**: numeric, the penalty per parameter to be used; the default $k = 2$ is the classical AIC.
- **trace**: logical. Do you want to be informed about the model estimation progress?
- **sparse**: logical. Is the model matrix sparse? By default is NULL, so a quickly sample survey will be made.
- **chunksize**: an integer indicates the number of rows of the data file to read at time.
- **all.levels**: logical, are all factor's levels present in each data chunk?
- **set.default**: a list in which to specify the below parameters.
- **sparselim**: a real in the interval $[0, 1]$. It indicates the minimal proportion of zeroes in the data matrix $X$ in order to consider $X$ as sparse.
- **camp**: see the function `is.sparse`.
- **eigendec**: logical. Do you want to check the rank of $X$? You may set it to false if you are sure that $X$ is full rank.
- **row.chunk**: an integer, see the function `cp` for details.
- **acc**: tolerance to be used for the estimation.
- **tol.solve**: see the function `solve`.
- **tol.values**: see the function `control`.
- **tol.vectors**: see the function `control`.
- **method**: the chosen method to detect for singulatity.
- **model**: logical. If TRUE the model frame will be returned.
- **fitted**: logical. If TRUE the fitted values will be returned.
- **...**: further optional arguments.
Details

The function `shglm` works like `biglm`, but it checks for singularity and does not impose restrictions on factors. Since during the IWLS estimation `shglm` uses repeated accesses to data file stored, for example, into the hard disk, the estimation time could be very long. Unlike from `glm` or `biglm`, the functions of class `speedglm` do not use the QR decomposition, but directly solve the equations in the form of Iterative(-ly) (Re-)Weighted Least Squares (IWLS). The memory size of an object of class `speedglm` is $O(p^2)$, where $p$ is the number of covariates, unless one or more of argument `model`, `y` and `fitted` are set to TRUE. If an optimized BLAS is not installed, an attempt to speed up calculations might be done by setting `row.chunk` to some value, usually less than 1000, in `set.default`. See the function `cp` for details.

If the model matrix is (very) sparse, the package `Matrix` could be used. Note that if method `qr` is chosen, then the qr decomposition will not be applied on matrix X, as in `lm`, but on $X'WX$.

Value

coefficients the estimated coefficients.
logLik the log likelihood of the fitted model.
iter the number of iterations of IWLS used.
tol the maximal value of tolerance reached.
convergence a logical value which indicates if convergence was reached.
family the family object used.
link the link function used.
df the degrees of freedom of the model.
XTX the product $X'X$ (weighted, if the case).
dispersion the estimated dispersion parameter of the model.
ok the set of column indeces of the model matrix where the model has been fitted.
rank the rank of the model matrix.
RSS the estimated residual sum of squares of the fitted model.
aic the estimated Akaike Information Criterion.
sparse a logical value which indicates if the model matrix is sparse.
device the estimated deviance of the fitted model.
nulldf the degrees of freedom of the null model.
nulldev the estimated deviance of the null model.
goodobs the number of non-zero weighted observations.
n the number of observations.
intercept a logical value which indicates if an intercept has been used.
terms the terms object used.
call the matched call.
model Either NULL or, if `model` was previously set to TRUE, the model frame.
y Either NULL or, if `y` was previously set to TRUE, the response variable.
linear.predictors Either NULL or, if `fitted` was previously set to TRUE, the fitted values.
Note

All the above functions make an object of class ‘speedglm’.
In the current package version, arguments start, mustart and etastart of function shglm have been disabled. These will be restored in future.

Author(s)

Marco Enea. Ronen Meiri contributed with method ‘qr’

References


See Also

speedlm, bigglm, glm

Examples

## Not run:

# The following comparison among glm(), bigglm() and speedglm() cannot be considered rigorous
# and exhaustive, but it is only to give an idea of the computation time.
# It may take a long time.
require(biglm)
n <- 50000
k <- 80
y <- rgamma(n,1.5,1)
x <- round(matrix(rnorm(n*k),n,k),digits=3)
colnames(x) <- paste("s",1:k,sep="")
da <- data.frame(y,x)
fo <- as.formula(paste("y~",paste(paste("s",1:k,sep=""),collapse="+")))

system.time(m1 <- glm(fo,data=da,family=Gamma(log)))

system.time(m2 <- bigglm(fo,data=da,family=Gamma(log)))

system.time(m3 <- speedglm(fo,data=da,family=Gamma(log)))

# You may also try speedglm when R is linked against an optimized BLAS,
# otherwise try to run the following function. In some computers, it is
# faster for large data sets.

system.time(m4 <- speedglm(fo,data=da,family=Gamma(log),set.default=list(row.chunk=1000)))
## End(Not run)

### Example of function using a connection to an out-memory file

This is a slightly modified version of the function from the bigglm's help page.

```r
make.data<-function(filename, chunksize,...){
  conn<-NULL
  function(reset=FALSE){
    if(reset){
      if(!is.null(conn)) close(conn)
      conn<<-file(filename,open="r")
    } else{
      rval<-read.table(conn, nrow=chunksize,...)
      if (nrow(rval)==0) {
        close(conn)
        conn<<-NULL
        rval<-NULL
      }
      return(rval)
    }
  }
}
```

# datal is a small toy dataset

data(datal)
write.table(datal,"datal.txt",row.names=FALSE,col.names=FALSE)
rm(datal)

da<-make.data("datal.txt",chunksize=50,col.names=c("y","fat1","x1","x2"))

# Caution! make sure to close the connection once you have run command #1

da(reset=T) #1: opens the connection to "datal.txt"
da(reset=F) #2: reads the first 50 rows (out of 100) of the dataset
da(reset=F) #3: reads the second 50 rows (out of 100) of the dataset
da(reset=F) #4: is NULL: this latter command closes the connection

require(biglm)

# fat1 is a factor with four levels
b1<-shglm(y~factor(fat1)+x1,weights~-I(x2^2),datafun=da,family=Gamma(log))
b2<-bigglm(y~factor(fat1)+x1,weights~-I(x2^2),data=da,family=Gamma(log))
summary(b1)
summary(b2)

file.remove("datal.txt")

## End(Not run)
speedlm

Description

The functions of class 'speedlm' may speed up the fitting of LMs to large data sets. High performances can be obtained especially if R is linked against an optimized BLAS, such as ATLAS.

Usage

# S3 method of class 'data.frame'
speedlm(formula, data, weights = NULL, offset = NULL, sparse = NULL,
        set.default = list(), method=c('eigen','Cholesky','qr'),
        model = FALSE, y = FALSE, fitted = FALSE, subset=NULL, ...)

# S3 method of class 'matrix'
speedlm.fit(y, X, intercept = FALSE, offset = NULL, row.chunk = NULL,
            sparselim = 0.9, camp = 0.01, eigendec = TRUE,
            tol.solve = .Machine$double.eps, sparse = NULL, tol.values = 1e-07,
            tol.vectors = 1e-07, method=c('eigen','Cholesky','qr'), ...)

speedlm.wfit(y, X, w, intercept = FALSE, offset = NULL, row.chunk = NULL,
              sparselim = 0.9, camp = 0.01, eigendec = TRUE,
              tol.solve = .Machine$double.eps, sparse = NULL, tol.values = 1e-07,
              tol.vectors = 1e-07, method=c('eigen','Cholesky','qr'), ...)

# S3 method of class 'speedlm' (object) and 'data.frame' (data)
## S3 method for class 'speedlm'
update(object, formula, data, add=TRUE, evaluate=TRUE,
       subset=NULL, offset=NULL, weights=NULL,...)

# S3 method of class 'speedlm' (object) and 'data.frame' (data)
updateWithMoreData(object, data, weights = NULL, offset = NULL, sparse = NULL,
                   all.levels = FALSE, set.default = list(), subset=NULL,...)

Arguments

Most of arguments are the same of functions lm but with some difference.

the same of function lm.

formula the same of function lm, but it must always specified.
weights the same of function lm, but it must be specified as data$weights.
w the same of weights.
intercept a logical value which indicates if an intercept is used.
offset the same of function lm.
X the same of x in function lm.
y the same of lm,lm.wfit and lm.fit.
sparse logical. Is the model matrix sparse? By default is NULL, so a quickly sample survey will be made.
set.default a list in which to specify the parameters to pass to the functions cp, control and is.sparse.
sparselim a value in the interval [0, 1]. It indicates the minimal proportion of zeroes, in the model matrix X, in order to consider X as sparse.
camp see function is.sparse.
eigendec logical. Do you want to investigate on rank of X? You may set it to false if you are sure that X is full rank.
row.chunk an integer, see the function cp for details.
tol.solve see function solve.
tol.values see function control.
tol.vectors see function control.
method see function control.
object an object of class 'speedlm'.
all.levels are all levels of eventual factors present in each data chunk? If so, set all.levels to true to speed up the fitting.
model logical. Should the model frame be returned?
fitted logical. Should the fitted values be returned?
subset the same of function lm
add logical. Are additional data coming from a new chunk provided?
evaluate logical. If true evaluate the new call else return the call.
... further optional arguments.

Details

Unlikely from lm or biglm, the functions of class 'speedlm' do not use the QR decomposition but directly solve the normal equations. Further, the most recent version of the package include method 'qr'. However such qr decomposition is not applied directly on matrix X, but on X'WX. In some extreme case, this might have some problem of numerical stability but may take advantage from the use of an optimized BLAS. The memory size of an object of class 'speedlm' is $O(p^2)$, where $p$ is the number of covariates. If an optimized BLAS library is not installed, an attempt to speed up calculations may be done by setting row.chunk to some value, usually less than 1000, in set.default. See the function cp for details. Factors are permitted without limitations.

In the most recent versions, function update.speedlm is now a wrapper to call either updateWithMoreData (the new name of the old update.speedlm, for additional data chunks), or update from package stats.

Value

coefficients the estimated coefficients.
df.residual the residual degrees of freedom.
XTX the product X'X (weighted, if the case).
A the product X'X (weighted, if the case) not checked for singularity.
Xy the product X'y (weighted, if the case).
ok the set of column indeces of the model matrix where the model has been fitted.
`speedlm`

- `rank`: the numeric rank of the fitted linear model.
- `pivot`: see the function `control`.
- `RSS`: the estimated residual sums of squares of the fitted model.
- `sparse`: a logical value indicating if the model matrix is sparse.
- `deviance`: the estimated deviance of the fitted model.
- `weigths`: the weights used in the last updating.
- `zero.w`: the number of non-zero weighted observations.
- `nobs`: the number of observations.
- `nvar`: the number of independent variables.
- `terms`: the terms object used.
- `intercept`: a logical value which indicates if an intercept has been used.
- `call`: the matched call.
- `model`: Either NULL or the model frame, if `model` was previously set to TRUE.
- `y`: Either NULL or the response variable, if `y` was previously set to TRUE.
- `fitted.values`: Either NULL or the fitted values, if `fitted` was previously set to TRUE.
- `offset`: the model offset.
- `...`: others values necessary to update the estimation.

**Note**

All the above functions make an object of class `speedlm`.

**Author(s)**

Marco Enea, with contribution from Ronen Meiri.

**References**


**See Also**

`summary.speedlm`, `speedglm`, `lm`, and `biglm`
Examples

```r
## Not run:
n <- 1000
k <- 3
y <- rnorm(n)
x <- round(matrix(rnorm(n * k), n, k), digits = 3)
colnames(x) <- c("s1", "s2", "s3")
da <- data.frame(y, x)
d01 <- da[1:300,]
d02 <- da[301:700,]
d03 <- da[701:1000,]

m1 <- speedlm(y ~ s1 + s2 + s3, data = d01)
m1 <- update(m1, data = d02)
m1 <- update(m1, data = d03)

m2 <- lm(y ~ s1 + s2 + s3, data = da)
summary(m1)
summary(m2)

## End(Not run)

## Not run:
# as before but recursively
make.data <- function(filename, chunksize,...){
  conn <- NULL
  function(reset=FALSE, header=TRUE){
    if(reset){
      if(!is.null(conn)) close(conn)
      conn <<- file(filename,open="r")
    } else{
      rval <- read.table(conn, nrows=chunksize,header=header,...)
      if (nrow(rval)==0) {
        close(conn)
        conn <<- NULL
        rval <<- NULL
      }
      return(rval)
    }
  }
}

write.table(da,"da.txt",col.names=TRUE,row.names=FALSE,quote=FALSE)
x.names <- c("s1", "s2", "s3")
dat <- make.data("da.txt",chunksize=300,col.names=c("y",x.names))
dat(reset=TRUE)
da2 <- dat(reset=FALSE)

# the first model runs on the first 300 rows.
m3 <- speedlm(y ~ s1 + s2 + s3, data=da2)

# the last three models run on the subsequent 300, 300 and 100 rows, respectively
```
for (i in 1:3){
  da2 <- dat(reset=FALSE, header=FALSE)
  m3 <- update(m3, data=da2, add=TRUE)
}
all.equal(coef(m1),coef(m3))
file.remove("da.txt")

## End(Not run)

---

**Methods to summarize Generalized Linear Models fits**

**Description**

summary method for the class 'speedglm'.

**Usage**

```r
## S3 method for class 'speedglm'
summary(object, correlation=FALSE, ...)
## S3 method for class 'speedglm'
coef(object, ...)
## S3 method for class 'speedglm'
vcov(object, ...)
## S3 method for class 'speedglm'
logLik(object, ...)
## S3 method for class 'speedglm'
AIC(object, ...)
```

**Arguments**

- `object` an object of class 'speedglm'.
- `correlation` logical. Do you want to print the correlation matrix? By default it is false.
- `...` further optional arguments

**Value**

- `coefficients` the matrix of coefficients, standard errors, z-statistics and two-side p-values.
- `df.residual` the component from object.
- `df.null` the component from object.
- `null.deviance` the component from object.
- `deviance` the component from object.
- `family` the component from object.
- `call` the component from object.
AIC  the Akaike Information Criterion.
RSS  Residuals sums of squares.
correlation (only if correlation is true.) The correlations of the estimated coefficients.
logLik the log-likelihood value.
rank  the component from object.
dispersion the estimated dispersion parameter of the fitted model.
convergence the component from object.
iter  the component from object.
tol   the component from object.

Author(s)
Marco ENEA

See Also
speedglm

Examples

n<‐1000
k<‐5
y <- rgamma(n,1.5,1)
x <- round(matrix(rnorm(n*k),n,k),digits=3)
colnames(x) <- paste("s",1:k,sep = "")
da<- data.frame(y,x)
fo <- as.formula(paste("y~",paste(paste("s",1:k,sep=""),collapse="+")))

m4 <- speedglm(fo,data=da,family=Gamma(log))
summary(m4)

summary.speedlm  Methods to summarize Linear Models fits

Description

  summary method for class ’speedlm’.

Usage

## S3 method for class ’speedlm’
summary(object, correlation = FALSE,...)
## S3 method for class ’speedlm’
coef(object,...)
## S3 method for class ’speedlm’
vcov(object,...)
## S3 method for class 'speedlm'
logLik(object,...)
## S3 method for class 'speedlm'
AIC(object,...,k = 2)

### Arguments

- **object**: an object of class 'speedlm'.
- **correlation**: logical. Do you want to print the correlation matrix? By default it is false.
- **k**: numeric, the penalty per parameter to be used; the default k = 2 is the classical AIC.
- **...**: further optional arguments

### Value

- **coefficients**: the matrix of coefficients, standard errors, t-statistics and two-side p-values.
- **rdf**: degrees of freedom of the fitted model. It is a component from object.
- **call**: the component from object.
- **r.squared**: R^2, the fraction of variance explained by the model.
- **adj.r.squared**: the "adjusted" R^2 statistic, penalizing for higher p.
- **fstatistic**: (for models including non-intercept terms) a 3-vector with the value of the F-statistic with its numerator and denominator degrees of freedom.
- **f.pvalue**: p-value of the F-statistic.
- **RSS**: Residual sum of squares.
- **var.res**: estimated variance of residuals.
- **rank**: the component from object.
- **correlation**: (only if correlation is true) the correlations of the estimated parameters.
- **...**: the results from the functions logLik, AIC and vcov.

### Author(s)

Marco ENEA

### See Also

- speedlm

### Examples

```r
y <- rnorm(100,1.5,1)
x <- round(matrix(rnorm(200), 100, 2), digits = 3)
colnames(x) <- c("s1","s2")
da <- data.frame(y, x)

m <- speedlm(y ~ s1 + s2,da)
summary(m)
```
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