Package ‘bayesQR’

September 8, 2023

Version 2.4
Date 2023-09-08
Title Bayesian Quantile Regression
Author Dries F. Benoit, Rahim Al-Hamzawi, Keming Yu, Dirk Van den Poel
Maintainer Dries F. Benoit <Dries.Benoit@UGent.be>
Depends R (>= 4.2), graphics, methods, stats, utils
Description Bayesian quantile regression using the asymmetric Laplace distribution, both continuous as well as binary dependent variables are supported. The package consists of implementations of the methods of Yu & Moyeed (2001) <doi:10.1016/S0167-7152(01)00124-9>, Benoit & Van den Poel (2012) <doi:10.1002/jae.1216> and Al-Hamzawi, Yu & Benoit (2012) <doi:10.1177/1471082X1101200304>. To speed up the calculations, the Markov Chain Monte Carlo core of all algorithms is programmed in Fortran and called from R.
License GPL (>= 2)
NeedsCompilation yes
Repository CRAN
Date/Publication 2023-09-08 17:30:02 UTC

R topics documented:

bayesQR ................................................................. 2
Churn ................................................................. 5
plot.bayesQR .......................................................... 6
predict.bayesQR ..................................................... 7
print.bayesQR ........................................................ 9
print.bayesQR.summary .......................................... 10
prior ................................................................. 11
Prostate ............................................................. 13
summary.bayesQR .................................................. 14

Index 16
bayesQR

Bayesian quantile regression

Description

bayesQR implements a Bayesian method for estimating quantile regression models (see references). To improve the speed of the routine, the Markov Chain Monte Carlo (MCMC) part of the algorithm is programmed in Fortran and is called from within the R function bayesQR.

Usage

bayesQR(formula, data, quantile, alasso, normal.approx, ndraw, keep, prior)

Arguments

formula  a symbolic description of the model to be fit.
data     an optional data frame containing the variables in the model.
quantile numerical scalar or vector containing quantile(s) of interest (default=0.5).
alasso   logical flag for adaptive lasso variable selection (default=FALSE).
normal.approx   logical flag for normal approximation of posterior distribution (default=TRUE).
ndraw number of MCMC draws.
keep     thinning parameter, i.e. keep every keepth draw (default=1).
prior     an S3 object of class "prior". If omitted, a diffuse prior will be assumed (see prior).

Details

The function bayesQR can estimate four types of models, depending on whether the dependent variable is continuous or binary and whether adaptive lasso variable selection is used.

• Continuous dependent variable without adaptive lasso variable selection:

  Model: \[ y = X\beta + e \]
  \[ e \sim \text{ALD}(\text{location}=0, \text{scale}=\sigma, \text{quantile}=p) \]
  Priors: \[ \beta \sim N(\beta_0, V_0) \]
  \[ \sigma \sim \text{invGamma}(\text{shape}=s, \text{scale}=c) \]

• Continuous dependent variable with adaptive lasso variable selection:

  Model: \[ y = X\beta + e \]
  \[ e \sim \text{ALD}(\text{location}=0, \text{scale}=\sigma, \text{quantile}=p) \]
  Priors: \[ \beta \sim \text{ALD}(\text{location}=0, \text{scale}=\sigma/\lambda, p=0.5) \]
  \[ \sigma \sim \text{InvGamma}(\text{shape}=s, \text{scale}=c) \]
  \[ (\lambda/\sigma)^2 \sim \text{Gamma}(\text{shape}=s_0, \text{scale}=c_0) \]
• Binary dependent variable without adaptive lasso variable selection:

Model: $y^* = X\beta + e$
$e \sim ALD(\text{location}=0, \text{scale}=1, \text{quantile}=p)$
$y = 1, \text{ if } (y^* > 0); \ y = 0, \text{ otherwise}$

Priors: $\beta \sim N(\beta_0, V_0)$

• Binary dependent variable with adaptive lasso variable selection:

Model: $y^* = X\beta + e$
$e \sim ALD(\text{location}=0, \text{scale}=1, \text{quantile}=p)$
$y = 1, \text{ if } (y^* > 0); \ y = 0, \text{ otherwise}$

Priors: $\beta \sim ALD(\text{location}=0, \text{scale}=1/\lambda, p=0.5)$
$\lambda^2 \sim \text{Gamma}(\text{shape}=\text{lambdasq\_shape}, \text{scale}=\text{lambdasq\_scale})$

Value

An object of class `bayesQR`, basically a list of lists. For every estimated quantile a list is created containing the following elements:

- `method` a string containing the method that was used, i.e. indicating whether the dependent variable was continuous or binary and whether adaptive lasso variable selection was used.
- `normal.approx` logical flag for normal approximation of posterior distribution.
- `quantile` the quantile that was estimated.
- `names` character vector containing the names of the independent variables in the model.
- `betadraw` ndraw/keep x nvar(X) matrix of beta draws.
- `sigmadraw` ndraw/keep vector of sigma draws (only in case of continuous dependent variable).

Author(s)

Dries F. Benoit, Rahim Al-Hamzawi, Keming Yu and Dirk Van den Poel

References

• Paper about the `bayesQR` package:

• Continuous dependent variable without adaptive lasso variable selection:
Also see:

- Continuous dependent variable with adaptive lasso variable selection:
  Also see:

- Binary dependent variable without adaptive lasso variable selection:

- Binary dependent variable with adaptive lasso variable selection:

**Examples**

```r
# Simulate data from heteroskedastic regression
set.seed(66)
n <- 200
X <- runif(n=n, min=0, max=10)
y <- 1 + 2*X + rnorm(n=n, mean=0, sd=.6*X)

# Estimate series of quantile regressions with adaptive lasso
# NOTE: to limit execution time of the example, ndraw is set
to a very low value. Set value to 5000 for a better
approximation of the posterior distribution.
out <- bayesQR(y~X, quantile=c(.05,.25,.5,.75,.95), alasso=TRUE, ndraw=500)

# Initiate plot
## Plot datapoints
plot(X, y, main="", cex=.6, xlab="X")
## Add quantile regression lines to the plot (exclude first 500 burn-in draws)
sum <- summary(out, burnin=50)
for (i in 1:length(sum)){
  abline(a=sum[[i]]$betadraw[1,1],b=sum[[i]]$betadraw[2,1],lty=i,col=i)
}

# Estimate and plot OLS model
outOLS = lm(y~X)
abline(outOLS,lty=1, lwd=2, col=6)

# Add legend to plot
```
Description

This dataset is a stratified random sample from all active customers (at the end of June 2006) of a European financial services company. The dependent variable in this dataset is the churn behavior of the customers in the period from July 1st until December 31th 2006. Here a churned customer is defined as someone who closed all his/her bank accounts with the company. Note that all predictor variables are standardized. This dataset is a small subset of the dataset used in Benoit and Van den Poel (2013). The dataset is structured as a dataframe with 400 observations and 5 variables.

Usage

data("Churn")

Format

The data frame has the following components:

• **churn** : churn (yes/no)
• **gender** : gender of the customer (male = 1)
• **Social_Class_Score** : social class of the customer
• **lor** : length of relationship with the customer
• **recency** : number of days since last purchase

Source


References


Description

plot.bayesQR is an S3 method that produces quantile plots, traceplots or posterior histograms based on the estimates obtained by the bayesQR function. For quantile plots, note that the more quantiles are estimated with bayesQR, the more detailed the quantile plot will be.

Usage

```r
## S3 method for class 'bayesQR'
plot(x, var=NULL, quantile=NULL, burnin=0, credint=c(0.025, 0.975), plottype=NULL, main=NULL, xlab=NULL, ylab=NULL, xlim=NULL, ylim=NULL, ...)
```

Arguments

- `x` an output object of the bayesQR function, i.e. an S3 object of class bayesQR.
- `var` vector containing the index or name of the variable(s) that has to be plotted (default=all variables).
- `quantile` vector containing the quantile(s) that has to be plotted (default=all quantiles).
- `burnin` the number of burnin draws that should be discarded (default=0, meaning all draws are included).
- `credint` the width of the credible interval (default=c(0.025, 0.975)).
- `plottype` should be ‘quantile’, ‘trace’ or ‘hist’.
- `main` Main title of the plot (default="").
- `xlab` Label of the x-axis; if omitted, the value chosen based on the input data.
- `ylab` Label of the y-axis; if omitted, the value chosen based on the input data.
- `xlim` Plot region of the x-axis; if omitted, the value chosen based on the input data.
- `ylim` Plot region of the y-axis; if omitted, the value chosen based on the input data.
- `...` additional arguments that are passed to the generic `plot` function

Details

A quantile plot shows how the value of the regression parameter changes over a range of quantiles together with the associated credible interval. When the normal approximation was requested, the credible regions represent the adjusted credible intervals. Note that the more quantiles are estimated, the more detailed the quantile plot will be. The minimum number of quantiles to plot is 2. A posterior histogram provides a graphical representation of the marginal posterior distribution of the regression parameters. When the normal approximation was requested, the histogram will be overlaid with the adjusted credible intervals. A traceplot gives the evolution of the MCMC chain and can be used as graphical check of convergence. Note that more formal checks of convergence exist (see, for example, the coda package).
**Value**

A (series of) quantile plot(s) or a (series of) traceplot(s).

**Author(s)**

Dries F. Benoit

**Examples**

```r
# Simulate data from heteroskedastic regression
set.seed(66)
n <- 200
X <- runif(n=n, min=0, max=10)
y <- 1 + 2 * X + rnorm(n=n, mean=0, sd=.6*X)

# Analyze 5 quantiles using default prior
# NOTE: to limit execution time of the example, ndraw is set
to a very low value. Set value to 5000 for a better
approximation of the posterior distribution.
out <- bayesQR(y ~ X, quantile=c(.05,.25,.5,.75,.95), ndraw=500)

# Check traceplot of first variable of .75 quantile regression
plot(out, var=1, quantile=.75, plottype="trace")

# Check posterior histogram of first variable of .5 quantile regression
plot(out, var=1, quantile=.5, plottype="hist")

# Create default quantile plot of first variable
plot(out, var=1, plottype="quantile")

# Create quantile plot of second variable with 90% credible interval
plot(out, var="X", credint=c(.05, .95), plottype="quantile", main="This is an example")
```

---

**predict.bayesQR**

*Calculate predicted probabilities for binary quantile regression*

**Description**

*predict.bayesQR* is an S3 method that calculates predicted probabilities for binary quantile regression, both with or without adaptive lasso.

**Usage**

```r
## S3 method for class 'bayesQR'
predict(object, X, burnin=0, ...)
```
Arguments

object an output object of the `bayesQR` function, S3 class `bayesQR`, with binary dependent variable, with or without adaptive lasso. At least 9 estimated quantiles are required.

X matrix of predictors (should be of the same type as the variables used to estimate the model).

burnin the number of burnin draws that should be discarded (default=0, meaning all draws are included).

... additional parameters passed to the generic `predict` function.

Details

`predict.bayesQR` is an S3 method that calculates the predicted probabilities based on a matrix of predictors `X` and an object containing the parameter estimates of a sequence of binary quantile regressions. The rationale behind the approach is described in Kordas (2006) and applied in Migueis, V.L., Benoit, D.F. and Van den Poel, D. (2012). Note that the more quantiles are estimated, the more fine-grained the predicted probabilities will be.

Value

A vector containing the predicted probabilities.

Author(s)

Dries F. Benoit

References


Examples

```r
# Simulate data from binary regression model
set.seed(1234)
n <- 200
X <- matrix(runif(n=n*2, min=-5, max=5),ncol=2)
ystar <- cbind(1,X)%*% c(1,1.5,-.5) + rnorm(n=n, mean=0, sd=abs(2*X[,1]))
y <- as.numeric(ystar>0)

# Estimate a sequence of binary quantile regression models
# NOTE: to limit execution time of the example, ndraw is set
# to a very low value. Set value to 4000 for a better
# approximation of the posterior distribution.
out <- bayesQR(y ~ X, quantile=seq(.1,.9,.1), ndraw=400)
```
# Calculate predicted probabilities
pred <- predict(object=out, X=cbind(1,X), burnin=20)

# Make histogram of predicted probabilities
hist(pred, breaks=10)

# Calculate Percentage Correctly Classified (PCC)
mean(y==as.numeric(pred>.5))

# Compare with logit model
mylogit <- glm(y ~ X, family=binomial(logit))

# Make histogram of predicted probabilities
hist(mylogit$fit, breaks=10)

# Calculate Percentage Correctly Classified (PCC)
mean(y==as.numeric(mylogit$fit>.5))

print.bayesQR

Prints the contents of a bayesQR object to the console

Description

print.bayesQR is an S3 method that prints the content of an S3 object of class bayesQR to the console.

Usage

## S3 method for class 'bayesQR'
print(x, digits=3, ...)

Arguments

x an output object of the bayesQR function, i.e. an S3 object of class bayesQR.
digits the number of printed digits of the estimates (default=3).
... additional arguments that are passed to the generic print function

Value

Formatted output of a bayesQR object.

Author(s)

Dries F. Benoit
Examples

```r
# Simulate data from heteroskedastic regression
set.seed(666)
n <- 200
X <- runif(n=n, min=0, max=10)
y <- 1 + 2*X + rnorm(n=n, mean=0, sd=.6*X)

# Analyze 0.5 quantile using default prior
out <- bayesQR(y ~ X, ndraw=5000)

# Print the bayesQR object
print(out)
```

---

**print.bayesQR.summary**  
*Prints the contents of bayesQR.summary object to the console*

### Description

`print.bayesQR.summary` is an S3 method that prints the content of an S3 object of class `bayesQR.summary` to the console.

### Usage

```r
## S3 method for class 'bayesQR.summary'
print(x, digits=3, ...)
```

### Arguments

- **x**: an output object of the `summary.bayesQR` function, i.e. an S3 object of class `bayesQR.summary`.
- **digits**: the number of printed digits of the estimates (default=3).
- **...**: additional arguments that are passed to the generic `print` function

### Value

Formatted output of a `bayesQR.summary` object.

### Author(s)

Dries F. Benoit
Examples

```r
# Simulate data from heteroskedastic regression
set.seed(666)
n <- 200
X <- runif(n=n, min=0, max=10)
y <- 1 + 2*X + rnorm(n=n, mean=0, sd=.6*X)

# Analyze 0.5 quantile using default prior and adaptive lasso
out <- bayesQR(y ~ X, alasso=TRUE, ndraw=5000)

# Return Bayes estimates and credible intervals
sum <- summary(out, burnin=1000)

# Print the bayesQR.summary object
sum
```

prior

Create prior for Bayesian quantile regression

Description

prior creates an S3 object of class bayesQR.prior that contains all necessary prior information to estimate a Bayesian quantile regression model.

Usage

```r
prior(formula, data, alasso, ...)
```

Arguments

- `formula`: a symbolic description of the model to be fit.
- `data`: an optional data frame containing the variables in the model.
- `alasso`: logical flag for adaptive lasso variable selection (default=FALSE).
- `...`: the prior parameters that are dependent on the method that is used. If omitted, a standard diffuse prior will be used (see details section).

Details

The function prior builds the prior for four types of models, depending on whether the dependent variable is continuous or binary and whether adaptive lasso variable selection is used. Every non-specified prior parameter will get the default value.

Continuous dependent variable without adaptive lasso variable selection:

- `beta0`: nvar(X) x 1 vector of prior means (default: 0)
- `V0`: nvar(X) x nvar(X) prior covariance matrix (default: 100*diag(ncol(X)))
- `shape0`: shape parameter for inverse Gamma prior for sigma (default: 0.01)
• **scale0**: scale parameter for inverse Gamma prior for sigma (default: 0.01)

Continuous dependent variable with adaptive lasso variable selection:

• **sigma_shape**: shape parameter for the inverse gamma prior on sigma (default: 0.01)
• **sigma_scale**: scale parameter for the inverse gamma prior on sigma (default: 0.01)
• **etasq_shape**: shape parameter for the gamma prior on etasq (default: 0.01)
• **etasq_scale**: scale parameter for the gamma prior on etasq (default: 0.01)

Binary dependent variable without adaptive lasso variable selection:

• **beta0**: nvar(X) x 1 vector of prior means (default: 0)
• **V0**: nvar(X) x nvar(X) prior covariance matrix (default: 100*diag(ncol(X)))

Binary dependent variable with adaptive lasso variable selection:

• **lambdasq_shape**: shape parameter for the gamma prior on lambdasq (default: 0.01)
• **lambdasq_scale**: scale parameter for the gamma prior on lambdasq (default: 0.01)

**Value**

An object of class bayesQR, basically a list containing the following elements:

- **method**: a string containing the method that was used, i.e. indicating whether the dependent variable was continuous or binary and whether adaptive lasso variable selection was used.
- **...**: the prior parameters that are dependent on the method that is used (see details section).

**Author(s)**

Dries F. Benoit

**Examples**

```r
# Load the Prostate cancer dataset
data(Prostate)

# Create informative prior object
prior <- prior(lpsa~., data=Prostate, beta0=rep(5,9), V0=diag(9))

# Estimate the model parameters with informative prior
out <- bayesQR(lpsa~., data=Prostate, prior=prior, ndraw=5000)

# Print results
summary(out)
```
Prostate Cancer Data

Description

These data come from a study that examined the correlation between the level of prostate specific antigen and a number of clinical measures in men who were about to receive a radical prostatectomy. It is a data frame with 97 rows and 9 columns.

Usage

data("Prostate")

Format

The data frame has the following components:

- \texttt{lcvol} : log(cancer volume)
- \texttt{lweight} : log(prostate weight)
- \texttt{age} : age
- \texttt{lbph} : log(benign prostatic hyperplasia amount)
- \texttt{svi} : seminal vesicle invasion
- \texttt{lcp} : log(capsular penetration)
- \texttt{gleason} : Gleason score
- \texttt{pgg45} : percentage Gleason scores 4 or 5
- \texttt{lpsa} : log(prostate specific antigen)

Source


References


This dataset also appears in the R-package: \texttt{lasso2}.

**summary.bayesQR**

*Summarize the output of the bayesQR function*

**Description**

summary.bayesQR is an S3 method that summarizes the output of the bayesQR function in an object of class bayesQR.summary. For every estimated beta and sigma, this object contains the Bayes estimate and the posterior credible interval is calculated. The object also contains other relevant information about the estimation procedure, such as the quantile, the variable names, etc.

**Usage**

```r
## S3 method for class 'bayesQR'
summary(object, burnin=0, credint=c(.025,.975), quantile=NULL, ...)
```

**Arguments**

- `object` an output object of the bayesQR function, i.e. an S3 object of class bayesQR.
- `burnin` the number of burnin draws that should be discarded (default=0, meaning all draws are included).
- `credint` the width of the credible interval (default=c(0.025, 0.975)).
- `quantile` the quantile(s) of the quantile regressions that have to be summarized (default: all estimated quantiles in QRobj).
- `...` additional arguments passed to the generic `summary` function.

**Value**

An object of class bayesQR.summary, basically a list including elements:

- `method` a string containing the method that was used, i.e. indicating whether the dependent variable was continuous or binary and whether adaptive lasso variable selection was used.
- `normal.approx` logical flag for normal approximation of posterior distribution.
- `quantile` the quantile that was estimated.
- `names` character vector containing the names of the independent variables in the model.
- `burnin` the number of burnin draws that were discarded.
- `retained` the number of draws that were retained and used to calculate the summary statistics.
- `credint` the width of the credible interval.
- `betadraw` the Bayes estimate, credible interval and, if `normal.approx=TRUE`, the adjusted credible intervals of the beta draws.
- `sigmadraw` the Bayes estimate and credible interval of the sigma draws.
Author(s)
Dries F. Benoit

Examples

# Load the Prostate cancer dataset
data(Churn)

# Estimate the model parameters with default prior
out <- bayesQR(churn~gender+recency, data=Churn, ndraw=2000)

# Return Bayes estimates and credible intervals
sum <- summary(out, burnin=1000)

# Inspect structure of bayesQR.summary object
str(sum)

# Print bayesQR.summary object
sum
Index

* datasets
  Churn, 5
  Prostate, 13

bayesQR, 2

Churn, 5

plot.bayesQR, 6
predict.bayesQR, 7
print.bayesQR, 9
print.bayesQR.summary, 10
prior, 2, 11
Prostate, 13

summary.bayesQR, 14