

Package ‘pqrBayes’

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Type Package

Title Bayesian Penalized Quantile Regression

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Description Bayesian regularized quantile regression utilizing sparse priors to promote exact sparsity leads to efficient Bayesian shrinkage estimation, variable selection and statistical inference. In this package, we have implemented robust Bayesian variable selection with spike-and-slab priors under high-dimensional linear regression models (Fan et al. (2024) <[doi:10.3390/e26090794](https://doi.org/10.3390/e26090794)> and Ren et al. (2023) <[doi:10.1111/biom.13670](https://doi.org/10.1111/biom.13670)>), and regularized quantile varying coefficient models (Zhou et al.(2023) <[doi:10.1016/j.csda.2023.107808](https://doi.org/10.1016/j.csda.2023.107808)>). In particular, valid robust Bayesian inferences under both models in the presence of heavy-tailed errors can be validated on finite samples. Additional models with spike-and-slab priors include robust Bayesian group LASSO and robust binary Bayesian LASSO (Fan and Wu (2025) <[doi:10.1002/sta4.70078](https://doi.org/10.1002/sta4.70078)>). The Markov Chain Monte Carlo (MCMC) algorithms of the proposed and alternative models are implemented in C++.

Depends R (>= 3.5.0)

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Encoding UTF-8

URL <https://github.com/cenwu/pqrBayes>

BugReports <https://github.com/cenwu/pqrBayes/issues>

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Imports Rcpp,glmnet,splines, stats

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pqrBayes-package	<i>Bayesian penalized quantile regression for linear, binary LASSO, group LASSO and varying coefficient models</i>
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Description

In this package, we implement Bayesian penalized quantile regression for linear regression (i.e., LASSO), binary LASSO, group LASSO and quantile varying coefficient (VC) models. Point-mass spike-and-slab priors have been incorporated in the Bayesian hierarchical models to facilitate Bayesian shrinkage estimation with exact sparsity in these models. The four default methods are Bayesian regularized quantile regression with spike-and-slab priors under the linear (i.e., LASSO), binary LASSO, group LASSO and VC model, correspondingly. In addition to default methods, users can also choose methods without robustness and/or spike-and-slab priors.

Details

The user friendly, integrated interface **pqrBayes()** allows users to flexibly choose fitting models by specifying the following parameters:

- robust:** whether to fit a robust sparse quantile regression model (LASSO, binary LASSO, group LASSO or Varying Coefficient models) or their non-robust counterparts.
- sparse:** whether to use the spike-and-slab priors to impose exact sparsity.
- model:** whether to fit a linear model (i.e., LASSO), binary LASSO, group LASSO or a varying coefficient model.

The function **pqrBayes()** returns a **pqrBayes** object that stores the posterior estimates of regression coefficients.

References

- Fan, K., Subedi, S., Yang, G., Lu, X., Ren, J. and Wu, C. (2024). Is Seeing Believing? A Practitioner's Perspective on High-dimensional Statistical Inference in Cancer Genomics Studies. *Entropy*, 26(9).794 doi:[10.3390/e26090794](https://doi.org/10.3390/e26090794)
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- Ren, J., Zhou, F., Li, X., Ma, S., Jiang, Y. and Wu, C. (2023). Robust Bayesian variable selection for gene-environment interactions. *Biometrics*, 79(2), 684-694 doi:[10.1111/biom.13670](https://doi.org/10.1111/biom.13670)
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- Zhou, F., Ren, J., Lu, X., Ma, S. and Wu, C. (2021). Gene–Environment Interaction: a Variable Selection Perspective. *Epistasis. Methods in Molecular Biology*. 2212:191–223 https://link.springer.com/protocol/10.1007/978-1-0716-0947-7_13
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- Ren, J., Zhou, F., Li, X., Wu, C. and Jiang, Y. (2019) spinBayes: Semi-Parametric Gene-Environment Interaction via Bayesian Variable Selection. R package version 0.1.0. <https://CRAN.R-project.org/package=spinBayes>
- Wu, C., Jiang, Y., Ren, J., Cui, Y. and Ma, S. (2018). Dissecting gene-environment interactions: A penalized robust approach accounting for hierarchical structures. *Statistics in Medicine*, 37:437–456 doi:[10.1002/sim.7518](https://doi.org/10.1002/sim.7518)
- Wu, C., Shi, X., Cui, Y. and Ma, S. (2015). A penalized robust semiparametric approach for gene-environment interactions. *Statistics in Medicine*, 34 (30): 4016–4030 doi:[10.1002/sim.6609](https://doi.org/10.1002/sim.6609)
- Wu, C., Cui, Y., and Ma, S. (2014). Integrative analysis of gene–environment interactions under a multi–response partially linear varying coefficient model. *Statistics in Medicine*, 33(28), 4988–4998 doi:[10.1002/sim.6287](https://doi.org/10.1002/sim.6287)
- Wu, C., Zhong, P.S. and Cui, Y. (2018). Additive varying–coefficient model for nonlinear gene–environment interactions. *Statistical Applications in Genetics and Molecular Biology*, 17(2) doi:[10.1515/sagmb-20170008](https://doi.org/10.1515/sagmb-20170008)
- Wu, C., Zhong, P.S. and Cui, Y. (2013). High dimensional variable selection for gene-environment interactions. *Technical Report. Michigan State University*.

See Also

[pqrBayes](#)

coverage	<i>95% empirical coverage probability for a pqrBayes object</i>
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Description

Calculate 95% empirical coverage probabilities for regression coefficients under linear, binary LASSO, group LASSO and VC models, respectively.

Usage

```
coverage(object, coefficient, u.grid=NULL, model="linear")
```

Arguments

object	the pqrBayes object.
coefficient	the vector of true regression coefficients under a linear model (i.e., LASSO), binary LASSO, group LASSO, or the matrix of true varying coefficients evaluated on the grid points under a varying coefficient model.
u.grid	the vector of grid points under a varying coefficient model. When assessing empirical coverage probabilities under a linear model (i.e., LASSO), binary LASSO or group LASSO, u.grid = NULL.
model	the model to be fitted. Users can also choose "linear" for a linear model (i.e., LASSO), "binary" for binary LASSO, "group" for group LASSO, and "VC" for a varying coefficient model.

Value

c

See Also

[pqrBayes](#)

Examples

```
## The quantile regression model
data(data)
data = data$data_linear
g=data$g
y=data$y
e=data$e
coeff = data$coeff
fit1=pqrBayes(g,y,u=NULL,e,d=NULL,quant=0.5,spline=NULL, model="linear")
coverage=coverage(fit1,coeff,model="linear")
```

data	<i>Simulated data under high-dimensional linear, binary, group LASSO and quantile varying coefficient models</i>
------	--

Description

Simulated data under high-dimensional linear, binary, group LASSO and quantile varying coefficient models

Format

The data_linear object consists of 4 components: g, y, e and coeff. coeff contains the true values of parameters used for generating the response variable y . The data_binary object consists of 4 components: g, y, e and coeff. coeff contains the true values of parameters used for generating the response variable y . The data_group object consists of 4 components: g, y, e and coeff. coeff contains the true values of parameters used for generating the response variable y . The data_varying object consists of five components: g, y, u, e and coeff. coeff contains the true values of parameters used for generating the response variable y .

Details

Generating Y using a sparse linear (quantile) regression model

The true data generating model under sparse linear regression:

$$Y_i = \beta_0 + \beta_1 X_{i1} + \beta_2 X_{i2} + \beta_3 X_{i3} + \epsilon_i,$$

where $\epsilon_i \sim N(0, 1)$, $\beta_0 = 0$, $\beta_1 = 1$, $\beta_2 = 1.5$ and $\beta_3 = 2$.

Generating Y using a sparse binary (quantile) regression model

The true data generating model under sparse linear regression:

$$\tilde{Y}_i = \beta_0 + \beta_1 X_{i1} + \beta_2 X_{i2} + \beta_3 X_{i3} + \epsilon_i,$$

where $\epsilon_i \sim N(0, 1)$, $\beta_0 = 0$, $\beta_1 = 0.22$, $\beta_2 = 0.18$ and $\beta_3 = 0.14$.

$Y_i = 1$ if $\tilde{Y}_i > 0$ and $Y_i = 0$ otherwise.

Generating Y using a high-dimensional group LASSO model

The true data generating model under a group LASSO model:

$$Y_i = \beta_0 + \beta_1 X_{i1} + \beta_2 X_{i2} + \beta_3 X_{i3} + \beta_7 X_{i7} + \beta_8 X_{i8} + \beta_9 X_{i9} + \epsilon_i,$$

where $\epsilon_i \sim N(0, 1)$, $\beta_0 = 0$, $\beta_1 = 0.6$, $\beta_2 = 0.7$, $\beta_3 = 0.8$, $\beta_7 = 0.65$, $\beta_8 = 0.75$ and $\beta_9 = 0.85$.

Generating Y using a (quantile) varying coefficient model

Data generation under sparse (quantile) VC model:

$$Y_i = \gamma_0(v_i) + \gamma_1(v_i)X_{i1} + \gamma_2(v_i)X_{i2} + \gamma_3(v_i)X_{i3} + \epsilon_i,$$

where $\epsilon_i \sim N(0, 1)$, $\gamma_0(v_i) = 1.5 \sin(0.2\pi * v_i)$, $\gamma_1(v_i) = 2 \exp(0.2v_i - 1) - 1.5$, $\gamma_2(v_i) = 2 - 2v_i$ and $\gamma_3(v_i) = -4 + (v_i - 2)^3/6$.

See Also[pqrBayes](#)**Examples**

```
data(data)
data = data$data_linear
g=data$g
dim(g)
y=data$y
coeff=data$coeff
print(coeff)
```

```
data = data$data_binary
g=data$g
dim(g)
y=data$y
coeff=data$coeff
print(coeff)
```

```
data = data$data_group
g=data$g
dim(g)
y=data$y
coeff=data$coeff
print(coeff)
```

```
data = data$data_varying
g=data$g
dim(g)
coeff=data$coeff
print(coeff)
```

estimation.pqrBayes	<i>Estimation and estimation accuracy for a pqrBayes object</i>
---------------------	---

Description

Calculate estimated regression coefficients with estimation accuracy from linear, binary LASSO, group LASSO and quantile VC models, respectively.

Usage

```
estimation.pqrBayes(object,coefficient,u.grid=NULL,model="linear")
```

Arguments

object	an object of class 'pqrBayes'.
coefficient	the vector of quantile regression coefficients under a linear model (i.e., LASSO), binary LASSO and group LASSO or the matrix of true varying coefficients evaluated on the grid points under a varying coefficient model.
u.grid	the vector of grid points under a varying coefficient model. When fitting a linear regression model (i.e., LASSO), binary LASSO or group LASSO, u.grid = NULL.
model	the model to be fitted. Users can choose "linear" for a linear model (i.e., LASSO), "binary" for binary LASSO, "group" for group LASSO or "VC" for a varying coefficient model.

Value

an object of class 'pqrBayes.est' is returned, which is a list with components:

error	mean square error or integrated mean square errors and total integrated mean square error.
coeff.est	estimated values of the regression coefficients or the varying coefficients.

See Also

[pqrBayes](#)

Examples

```
## The quantile regression model
data(data)
data = data$data_linear
g=data$g
y=data$y
e=data$e
coeff = data$coeff
fit1=pqrBayes(g,y,u=NULL,e,d = NULL,quant=0.5,spline=NULL,model="linear")
estimation=estimation.pqrBayes(fit1,coeff,model="linear")
```

pqrBayes	<i>fit Bayesian penalized quantile regression for linear, binary LASSO, group LASSO, or varying coefficient models</i>
----------	--

Description

fit Bayesian penalized quantile regression for linear, binary LASSO, group LASSO, or varying coefficient models

Usage

```
pqrBayes(
  g,
  y,
  u = NULL,
  e,
  d = NULL,
  quant = 0.5,
  iterations = 10000,
  burn.in = NULL,
  spline = NULL,
  robust = TRUE,
  sparse = TRUE,
  model = "linear",
  hyper = NULL,
  debugging = FALSE
)
```

Arguments

<code>g</code>	the matrix of predictors (subject to selection). Users do not need to specify an intercept which will be automatically included.
<code>y</code>	the response variable.
<code>u</code>	a vector of effect modifying variable of the quantile varying coefficient model. When fitting a linear model or group LASSO, <code>u = NULL</code> .
<code>e</code>	a matrix of clinical covariates not subject to selection.
<code>d</code>	a positive integer denotes the group size. When fitting a linear model or varying coefficient model, <code>d = NULL</code> .
<code>quant</code>	the quantile level specified by users. The default value is 0.5.
<code>iterations</code>	the number of MCMC iterations. The default value is 10,000.
<code>burn.in</code>	the number of burn-in iterations. If <code>NULL</code> , the first half of MCMC iterations will be used as burn-ins.
<code>spline</code>	a list of the number of interior knots (<code>kn</code>) for B-spline and the degree of B-spline basis (degree). When fitting LASSO, binary LASSO and group LASSO, <code>spline = NULL</code> .
<code>robust</code>	logical flag. If <code>TRUE</code> , robust methods will be used. Otherwise, non-robust methods will be used. The default value is <code>TRUE</code> .
<code>sparse</code>	logical flag. If <code>TRUE</code> , spike-and-slab priors will be adopted to impose exact sparsity on regression coefficients. Otherwise, Laplacian shrinkage will be adopted. The default value is <code>TRUE</code> .
<code>model</code>	the model to be fitted. Users can specify "linear" for a linear model (i.e., LASSO), "binary" for binary LASSO, "group" for group LASSO and "VC" for a varying coefficient model.
<code>hyper</code>	a named list of hyper-parameters. The default value is <code>NULL</code> .
<code>debugging</code>	logical flag. If <code>TRUE</code> , progress will be output to the console and extra information will be returned. The default value is <code>FALSE</code> .

Details

The linear quantile regression model described in "data" is:

$$Y_i = \sum_{k=1}^q E_{ik} \beta_k + \sum_{j=0}^p X_{ij} \gamma_j + \epsilon_i,$$

where β_k 's are the regression coefficients for clinical covariates and γ_j 's are the regression coefficients of $\mathbf{X}$.

The binary quantile regression model described in "data" is:

$$\tilde{Y}_i = \sum_{k=1}^q E_{ik} \beta_k + \sum_{j=0}^p X_{ij} \gamma_j + \epsilon_i,$$

where β_k 's are the regression coefficients for clinical covariates and γ_j 's are the regression coefficients of $\mathbf{X}$.

$Y_i = 1$ if $\tilde{Y}_i > 0$ and $Y_i = 0$ otherwise.

The group LASSO model described in "data" is:

$$Y_i = \sum_{k=1}^q E_{ik} \beta_k + X_{i0} \gamma_0 + \sum_{j=1}^m \mathbf{X}_{ij}^\top \boldsymbol{\gamma}_j + \epsilon_i,$$

where β_k 's are the regression coefficients for clinical covariates and $\boldsymbol{\gamma}_j = (\gamma_{j1}, \dots, \gamma_{jd})^\top$ is the vector of regression coefficients of the $n \times d$ matrix $\mathbf{X}_j$.

The quantile varying coefficient model described in "data" is:

$$Y_i = \sum_{k=1}^q E_{ik} \beta_k + \sum_{j=0}^p \gamma_j(V_i) X_{ij} + \epsilon_i,$$

where β_k 's are the regression coefficients for the clinical covariates, and γ_j 's are the varying intercept and varying coefficients for predictors (e.g. genetic factors), respectively.

Users can modify the hyper-parameters by providing a named list of hyper-parameters via the argument 'hyper'. The list can have the following named components

a0, b0: shape parameters of the Beta priors $(\pi^{a_0-1}(1-\pi)^{b_0-1})$ on π_0 .

c1, c2: the shape parameter and the rate parameter of the Gamma prior on ν .

Please check the references for more details about the prior distributions.

Value

an object of class "pqrBayes" is returned, which is a list with components:

obj	a list of posterior samples from the MCMC and other parameters
coefficients	a list of posterior estimates of coefficients

References

- Fan, K., Subedi, S., Yang, G., Lu, X., Ren, J. and Wu, C. (2024). Is Seeing Believing? A Practitioner's Perspective on High-dimensional Statistical Inference in Cancer Genomics Studies. *Entropy*, 26(9).794 doi:[10.3390/e26090794](https://doi.org/10.3390/e26090794)
- Zhou, F., Ren, J., Ma, S. and Wu, C. (2023). The Bayesian regularized quantile varying coefficient model. *Computational Statistics & Data Analysis*, 107808 doi:[10.1016/j.csda.2023.107808](https://doi.org/10.1016/j.csda.2023.107808)
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Examples

```
## The quantile (linear and binary) regression model
data(data)
data = data$data_linear
g=data$g
y=data$y
e=data$e
data(data)
data_1=data$data_binary
g_1=data_1$g
y_1=data_1$y
e_1=data_1$e

fit1=pqrBayes(g,y,u=NULL,e,d=NULL,quant=0.5,model="linear")
fit1_1=pqrBayes(g_1,y_1,u=NULL,e_1,d=NULL,quant=0.5,model="binary")

## Non-sparse example (linear model)
sparse <- FALSE
fit2 <- pqrBayes(
  g = g, y = y, u = NULL, e = e, d = NULL,
  quant = 0.5,
  spline = NULL,
  sparse = sparse,
  model = "linear"
)

## Non-robust example (linear model)
robust <- FALSE
fit3 <- pqrBayes(
  g = g, y = y, u = NULL, e = e, d = NULL,
  quant = 0.5,
  spline = NULL,
  robust = robust,
  model = "linear"
```

```

)

## The group LASSO model
data(data)
data = data$data_group
g=data$g
y=data$y
e=data$e

fit1=pqrBayes(g,y,u=NULL,e,d=3,quant=0.5,model="group")

## Non-sparse version
sparse <- FALSE
fit2 <- pqrBayes(
  g = g, y = y, u = NULL, e = e, d = 3,
  quant = 0.5, spline = NULL,
  sparse = sparse,
  model = "group"
)

## Non-robust version
robust <- FALSE
fit3 <- pqrBayes(
  g = g, y = y, u = NULL, e = e, d = 3,
  quant = 0.5, spline = NULL,
  robust = robust,
  model = "group"
)

## The quantile varying coefficient model
data(data)
data = data$data_varying
g=data$g
y=data$y
u=data$u
e=data$e

spline = list(kn=2,degree=2)
fit1=pqrBayes(g,y,u,e,quant=0.5,spline = spline,model="VC")

## Non-sparse example
sparse <- FALSE
fit2 <- pqrBayes(
  g = g, y = y, u = u, e = e,
  quant = 0.5,
  spline = spline,
  sparse = sparse,
  model = "VC"
)

```

```
## Non-robust example
robust <- FALSE
fit3 <- pqrBayes(
  g = g, y = y, u = u, e = e,
  quant = 0.5,
  spline = spline,
  robust = robust,
  model = "VC"
)
```

pqrBayes.select	<i>Variable selection for a pqrBayes object</i>
-----------------	---

Description

Variable selection for a pqrBayes object

Usage

```
pqrBayes.select(object, sparse=T, model="linear")
```

Arguments

object	a pqrBayes object.
sparse	logical flag. If TRUE, the sparse model is used for variable selection. The default value is TRUE.
model	the model to be fitted. Users can also choose "linear" for a linear model, "VC" for a varying coefficient model or "group" for group LASSO.

Details

For class ‘Sparse’, the median probability model (MPM) (Barbieri and Berger, 2004) is used to identify predictors that are significantly associated with the response variable. For class ‘NonSparse’, variable selection is based on 95% credible interval. Please check the references for more details about the variable selection.

Value

an object of class ‘select’ is returned, which includes the indices of the selected predictors (e.g. genetic factors).

References

Ren, J., Zhou, F., Li, X., Ma, S., Jiang, Y. and Wu, C. (2023). Robust Bayesian variable selection for gene-environment interactions. *Biometrics*, 79(2), 684-694 doi:[10.1111/biom.13670](https://doi.org/10.1111/biom.13670)

Barbieri, M.M. and Berger, J.O. (2004). Optimal predictive model selection. *Ann. Statist.*, 32(3):870–897

See Also[pqrBayes](#)**Examples**

```
## The quantile regression model
data(data)
data = data$data_linear
g=data$g
y=data$y
e=data$e

fit1=pqrBayes(g,y,u=NULL,e,d = NULL,quant=0.5,spline=NULL,model="linear")
sparse=TRUE
select=pqrBayes.select(obj = fit1,sparse = sparse,model="linear")

## The quantile varying coefficient model
data(data)
data = data$data_varying
g=data$g
y=data$y
u=data$u
e=data$e
spline = list(kn=2,degree=2)
fit1=pqrBayes(g,y,u,e,d = NULL,quant=0.5,spline = spline,model="VC")
sparse=TRUE
select=pqrBayes.select(obj = fit1,sparse = sparse,model="VC")
select

## Non-sparse example with VC model
sparse <- FALSE
spline <- list(kn = 2, degree = 2)

fit2 <- pqrBayes(
  g = g, y = y, u = u, e = e, d = NULL,
  quant = 0.5,
  spline = spline,
  sparse = sparse,
  model = "VC"
)

select <- pqrBayes.select(obj = fit2, sparse = FALSE, model = "VC")
select
```

Description

Make predictions from a pqrBayes object

Usage

```
predict_pqrBayes(object, g.new, u.new, e.new, y.new, quant, model, ...)
```

Arguments

<code>object</code>	a pqrBayes object.
<code>g.new</code>	a matrix of new predictors (e.g. genetic factors) at which predictions are to be made. When being applied to the linear model (i.e., LASSO), binary LASSO or group LASSO, <code>g.new = g</code> .
<code>u.new</code>	a vector of new environmental factor at which predictions are to be made. When being applied to the linear model (i.e., LASSO), binary LASSO or group LASSO, <code>u.new = NULL</code> .
<code>e.new</code>	a vector or matrix of new clinical covariates at which predictions are to be made. When being applied to the linear model (i.e., LASSO), <code>e.new = e</code> .
<code>y.new</code>	a vector of the response of new observations. When being applied to the linear model (i.e., LASSO), binary LASSO or group LASSO, <code>y.new = y</code> .
<code>quant</code>	the quantile level. The default is 0.5.
<code>model</code>	the model to be fitted. The default is "VC" for a quantile varying coefficient model. Users can also specify "linear" for a linear model (i.e., LASSO), "binary" for binary LASSO and "group" for a group LASSO.
<code>...</code>	other predict arguments

Details

`g.new` (`u.new`) must have the same number of columns as `g` (`u`) used for fitting the model. By default, the clinical covariates are `NULL` unless provided. The predictions are made based on the posterior estimates of coefficients in the pqrBayes object.

Value

an object of class 'pqrBayes.pred' is returned, which is a list with components:

<code>error</code>	prediction error.
<code>y.pred</code>	predicted values of the new observations.

See Also

[pqrBayes](#)

Examples

```
## The quantile regression model
data(data)
data = data$data_linear
g=data$g
y=data$y
e=data$e
fit1=pqrBayes(g,y,u=NULL,e,d = NULL,quant=0.5,spline=NULL,model="linear")
prediction=predict_pqrBayes(fit1,g,u.new=NULL,e.new = e, y.new = y,model="linear")
```

print.pqrBayes	<i>print a pqrBayes result</i>
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Description

Print a pqrBayes result

Usage

```
## S3 method for class 'pqrBayes'
print(x, digits = max(3, getOption("digits") - 3), ...)
```

Arguments

x	pqrBayes result.
digits	significant digits in printout.
...	other print arguments.

Value

No return value, called for side effects.

See Also

[pqrBayes](#)

print.pqrBayes.pred *print a pqrBayes.pred object*

Description

Print a summary of a pqrBayes.pred object

Usage

```
## S3 method for class 'pqrBayes.pred'  
print(x, digits = max(3, getOption("digits") - 3), ...)
```

Arguments

x	pqrBayes.pred object.
digits	significant digits in printout.
...	other print arguments

Value

No return value, called for side effects.

See Also

[predict_pqrBayes](#)

print.pqrBayes.select *print a select.pqrBayes object*

Description

Print a summary of a select.pqrBayes object

Usage

```
## S3 method for class 'pqrBayes.select'  
print(x, digits = max(3, getOption("digits") - 3), ...)
```

Arguments

x	pqrBayes.select object.
digits	significant digits in printout.
...	other print arguments

Value

No return value, called for side effects.

See Also

[pqrBayes.select](#)

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