

# Package ‘spexvb’

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**Type** Package

**Title** Parameter Expanded Variational Bayes for High-Dimensional Linear Regression

**Version** 0.1.0

**Description** Implements a parameter expanded variational Bayes algorithm for linear regression models with high-dimensional variable selection. The methodology utilizes spike-and-slab priors to perform simultaneous estimation and selection. Details can be found in Olejua et al. (2024) <[doi:10.21203/rs.3.rs-7208847/v1](https://doi.org/10.21203/rs.3.rs-7208847/v1)>.

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**VignetteBuilder** knitr

**NeedsCompilation** yes

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cv.spexvb	<i>Cross-validation for Sparse Parameter Expanded Variational Bayes (spexvb)</i>
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### Description

Performs k-fold cross-validation for the spexvb model, allowing for evaluation of model performance across different tau\_alpha values.

### Usage

```
cv.spexvb(
  k = 5,
  X,
  Y,
  mu_0 = NULL,
  omega_0 = NULL,
  c_pi_0 = NULL,
  d_pi_0 = NULL,
  tau_e = NULL,
  update_order = NULL,
  mu_alpha = 1,
  tau_alpha = c(0, 10^(3:7)),
  tau_b = 400,
  standardize = TRUE,
  intercept = TRUE,
  max_iter = 100L,
  tol = 1e-05,
  seed = 12376,
  verbose = TRUE,
  parallel = TRUE
)
```

### Arguments

k	Integer, the number of folds for cross-validation. Must be greater than 2.
X	A design matrix.
Y	A response vector.
mu_0	Initial variational mean (posterior expectation of beta_j   s_j = 1). If NULL, initialized automatically.
omega_0	Initial variational probability (posterior expectation of s_j). If NULL, initialized automatically.
c_pi_0	Prior parameter for pi (beta distribution shape1). If NULL, initialized automatically.

d_pi_0	Prior parameter for pi (beta distribution shape2). If NULL, initialized automatically.
tau_e	Initial precision of errors. If NULL, initialized automatically.
update_order	A numeric vector specifying the order of updates for coefficients. If NULL, initialized automatically.
mu_alpha	Mean for the prior on alpha (expansion parameter).
tau_alpha	A numeric vector of tau_alpha values to cross-validate over. Must have at least two values.
tau_b	Initial precision for beta_j (when s_j = 1).
standardize	Logical. Center Y, and center and scale X. Default is TRUE.
intercept	Logical. Whether to include an intercept. Default is TRUE. After the model is fit on the centered and scaled data, the final coefficients are "unscaled" to put them back on the original scale of your data. The intercept is then calculated separately using the means and the final coefficients.
max_iter	Maximum number of outer loop iterations for each spexvb fit.
tol	Convergence tolerance for each spexvb fit.
seed	Seed for reproducibility of data splitting and glmnet initials.
verbose	Logical, if TRUE, prints progress messages during cross-validation.
parallel	Logical, if TRUE, search in parallel.

## Details

This function performs k-fold cross-validation to find the optimal tau\_alpha for the spexvb model. It iterates through different tau\_alpha values, trains the model on training folds, and evaluates performance on the held-out test fold. To leverage parallel processing, ensure a parallel backend (e.g., from doParallel or doSNOW packages) is registered using registerDoParallel() or similar before calling this function.

## Value

A list containing cross-validation results:

ordered_tau_alpha	The sorted vector of tau_alpha values used.
epe_test_k	A matrix of prediction errors (MSE) for each fold (rows) and each tau_alpha (columns).
CVE	Cross-Validation Error (mean MSE) for each tau_alpha.
tau_alpha_opt	The tau_alpha value that minimizes the CVE.

## Examples

```
n <- 50
p <- 100
X <- matrix(rnorm(n * p), n, p)
Y <- X[,1] * 2 + rnorm(n)
```

```
# Run cross-validation only (returns errors and optimal tau_alpha)
cv_res <- cv.spexvb(k = 3, X = X, Y = Y)

# Inspect the optimal tau_alpha
print(cv_res$tau_alpha_opt)
```

---

`cv.spexvb.fit`*Cross-validation and Final Model Fitting for SPEVXB*

---

### Description

This function performs k-fold cross-validation to determine the optimal `tau_alpha` parameter for the `spexvb` model, and then fits a final `spexvb` model to the full dataset using this optimal `tau_alpha`. Initial values for the final model are also derived from the full dataset.

### Usage

```
cv.spexvb.fit(
  k = 5,
  X,
  Y,
  mu_0 = NULL,
  omega_0 = NULL,
  c_pi_0 = NULL,
  d_pi_0 = NULL,
  tau_e = NULL,
  update_order = NULL,
  mu_alpha = 1,
  tau_alpha = c(0, 10^(3:7)),
  tau_b = 400,
  standardize = TRUE,
  intercept = TRUE,
  max_iter = 100L,
  tol = 1e-05,
  seed = 12376,
  verbose = TRUE,
  parallel = TRUE
)
```

### Arguments

<code>k</code>	Integer, the number of folds to use for cross-validation. Must be greater than 2.
<code>X</code>	A design matrix.
<code>Y</code>	A response vector.

mu_0	Initial variational mean (posterior expectation of $\beta_j \mid s_j = 1$ ). If NULL, initialized automatically by <code>get.initials</code> .
omega_0	Initial variational probability (posterior expectation of $s_j$ ). If NULL, initialized automatically by <code>get.initials</code> .
c_pi_0	Prior parameter for pi (beta distribution shape1). If NULL, initialized automatically by <code>get.initials</code> .
d_pi_0	Prior parameter for pi (beta distribution shape2). If NULL, initialized automatically by <code>get.initials</code> .
tau_e	Initial precision of errors. If NULL, initialized automatically by <code>get.initials</code> .
update_order	A numeric vector specifying the order of updates for coefficients. If NULL, initialized automatically by <code>get.initials</code> .
mu_alpha	Mean for the prior on alpha (expansion parameter).
tau_alpha	A numeric vector of tau_alpha values to cross-validate over. Must have at least two values.
tau_b	Initial precision for $\beta_j$ (when $s_j = 1$ ).
standardize	Logical. Center Y, and center and scale X. Default is TRUE.
intercept	Logical. Whether to include an intercept. Default is TRUE. After the model is fit on the centered and scaled data, the final coefficients are "unscaled" to put them back on the original scale of your data. The intercept is then calculated separately using the means and the final coefficients.
max_iter	Maximum number of outer loop iterations for both CV fits and the final fit.
tol	Convergence tolerance for both CV fits and the final fit.
seed	Seed for reproducibility of data splitting and <code>glmnet</code> initials.
verbose	Logical, if TRUE, prints progress messages during cross-validation.
parallel	Logical, if TRUE, search in parallel.

## Details

This function orchestrates the cross-validation process and the final model fit. It first gets initial values for the full dataset, then uses `cv.spexvb` to find the `tau_alpha` that minimizes cross-validation error, and finally calls `spexvb` on the complete dataset with the chosen `tau_alpha`.

## Value

The final fitted `spexvb` model, which is a list containing the approximate posterior parameters and convergence information for the full dataset using the optimal `tau_alpha` determined by cross-validation.

## See Also

[cv.spexvb](#), [spexvb](#)

### Examples

```
# Generate simple synthetic data
n <- 50
p <- 100
X <- matrix(rnorm(n * p), n, p)
Y <- X[,1] * 2 + rnorm(n)

# Run cross-validation and fit final model
# (Setting k=3 to keep it quick for the example)
fit <- cv.spexvb.fit(k = 3, X = X, Y = Y)
```

---

get.initials	<i>Get initial values for spexvb</i>
--------------	--------------------------------------

---

### Description

This function initializes parameters for the spexvb model.

### Usage

```
get.initials(
  X,
  Y,
  mu_0 = NULL,
  omega_0 = NULL,
  c_pi_0 = NULL,
  d_pi_0 = NULL,
  tau_e = NULL,
  update_order = NULL,
  seed = 12376
)
```

### Arguments

X	A design matrix.
Y	A response vector.
mu_0	Initial mean.
omega_0	Initial omega.
c_pi_0	Initial c_pi.
d_pi_0	Initial d_pi.
tau_e	Initial tau_e.
update_order	Initial update order.
seed	Seed for reproducibility.

## Details

### Generate Initial Values for Variational Inference in Sparse Regression

This helper function estimates initial values for variational parameters such as regression coefficients ( $\mu$ ), spike probabilities ( $\omega$ ), and hyperparameters like  $\tau_e$ ,  $c_\pi$ , and  $d_\pi$  using LASSO and Ridge regression fits.

## Value

A list of initialized parameters.

## Examples

```
n <- 50
p <- 100
X <- matrix(rnorm(n * p), n, p)
Y <- X[,1] * 2 + rnorm(n)

initials <- get.initials(X, Y)

# Check estimated noise precision (tau_e)
print(initials$tau_e)
```

---

get.initials.logistic *Get initial values for spexvb*

---

## Description

This function initializes parameters for the spexvb model.

## Usage

```
get.initials.logistic(
  X,
  Y,
  mu_0 = NULL,
  omega_0 = NULL,
  c_pi_0 = NULL,
  d_pi_0 = NULL,
  update_order = NULL,
  seed = 12376
)
```

**Arguments**

<code>X</code>	A design matrix.
<code>Y</code>	A response vector.
<code>mu_0</code>	Initial mean.
<code>omega_0</code>	Initial omega.
<code>c_pi_0</code>	Initial <code>c_pi</code> .
<code>d_pi_0</code>	Initial <code>d_pi</code> .
<code>update_order</code>	Initial update order.
<code>seed</code>	Seed for reproducibility.

**Details****Generate Initial Values for Variational Inference in Sparse Logistic Regression**

This helper function estimates initial values for variational parameters such as regression coefficients ( $\mu$ ), spike probabilities ( $\omega$ ), and hyperparameters like `c_pi`, and `d_pi` using LASSO regression.

**Value**

A list of initialized parameters.

**Examples**

```
n <- 50
p <- 100
X <- matrix(rnorm(n * p), n, p)
# Generate binary response
Y <- rbinom(n, 1, plogis(X[,1]))

initials <- get.initials.logistic(X, Y)

# View the initial mu (posterior means)
head(initials$mu_0)
```

---

hspvb

*Hierarchical Spike-and-Slab Variational Bayes (HSPVB) for High-Dimensional Linear Regression*

---

**Description**

Fits a sparse linear regression model using variational inference with a Gamma prior on the slab precision ( $\tau_b$ ). The model uses spike-and-slab priors where the slab scale is adaptively learned.

**Usage**

```

hspvb(
  X,
  Y,
  mu_0 = NULL,
  omega_0 = NULL,
  c_pi_0 = NULL,
  d_pi_0 = NULL,
  a_prior_tau_b = 0.1,
  b_prior_tau_b = 1,
  tau_e = NULL,
  update_order = NULL,
  standardize = TRUE,
  intercept = TRUE,
  max_iter = 1000,
  tol = 1e-05,
  seed = 12376
)

```

**Arguments**

X	A numeric matrix. The design matrix (n observations $\times$ p predictors).
Y	A numeric vector. The response vector of length n.
mu_0	Optional numeric vector. Initial variational means for regression coefficients.
omega_0	Optional numeric vector. Initial spike probabilities.
c_pi_0	Optional numeric. Prior Beta(a, b) parameter a for the spike probability $\pi$ .
d_pi_0	Optional numeric. Prior Beta(a, b) parameter b for the spike probability $\pi$ .
a_prior_tau_b	Optional numeric. Gamma prior shape parameter (a) for the slab precision $\tau_b$ . Default is 1.
b_prior_tau_b	Optional numeric. Gamma prior rate parameter (b) for the slab precision $\tau_b$ . Default is 0.01.
tau_e	Optional numeric. Known or estimated error precision $\tau_e$ .
update_order	Optional integer vector. The coordinate update order (0-indexed for C++).
standardize	Logical. Center Y, and center and scale X. Default is TRUE.
intercept	Logical. Whether to include an intercept. Default is TRUE.
max_iter	Maximum number of iterations for the variational update. Default is 1000.
tol	Convergence threshold for entropy change. Default is 1e-5.
seed	Integer seed for initialization, passed to <code>get.initials</code> . Default is 12376.

**Details**

This function acts as a wrapper for the C++ implementation of the variational Bayes algorithm with a hierarchical Gamma prior on the slab precision,  $\tau_b$ .

**Value**

A list with posterior summaries including estimated coefficients ( $\mu$ ), inclusion probabilities ( $\omega$ ), final expected slab precision ( $\tau_b$ ), intercept (if applicable), convergence status, etc.

**Examples**

```
n <- 50
p <- 100
X <- matrix(rnorm(n * p), n, p)
Y <- X[,1] * 2 + rnorm(n)
result <- hspvb(X = X, Y = Y)
```

---

 spexvb

*Parameter Expanded Variational Bayes for Well-Calibrated High-Dimensional Linear Regression with Spike-and-Slab Priors*

---

**Description**

Fits a sparse linear regression model using variational inference with an alpha expansion step. The model uses spike-and-slab priors.

**Usage**

```
spexvb(
  X,
  Y,
  mu_0 = NULL,
  omega_0 = NULL,
  c_pi_0 = NULL,
  d_pi_0 = NULL,
  tau_e = NULL,
  update_order = NULL,
  mu_alpha = 1,
  tau_alpha = 1000,
  tau_b = 400,
  standardize = TRUE,
  intercept = TRUE,
  max_iter = 1000,
  tol = 1e-05,
  seed = 12376
)
```

**Arguments**

**X** A numeric matrix. The design matrix ( $n$  observations  $\times$   $p$  predictors).

**Y** A numeric vector. The response vector of length  $n$ .

<code>mu_0</code>	Optional numeric vector. Initial variational means for regression coefficients.
<code>omega_0</code>	Optional numeric vector. Initial spike probabilities.
<code>c_pi_0</code>	Optional numeric. Prior Beta(a, b) parameter a for the spike probability.
<code>d_pi_0</code>	Optional numeric. Prior Beta(a, b) parameter b for the spike probability.
<code>tau_e</code>	Optional numeric. Known or estimated error precision.
<code>update_order</code>	Optional integer vector. The coordinate update order (0-indexed for C++).
<code>mu_alpha</code>	Prior mean for alpha. Default is 1.
<code>tau_alpha</code>	Prior precision for alpha. Default is 1000.
<code>tau_b</code>	Slab prior precision. Default is 400.
<code>standardize</code>	Logical. Center Y, and center and scale X. Default is TRUE.
<code>intercept</code>	Logical. Whether to include an intercept. Default is TRUE. After the model is fit on the centered and scaled data, the final coefficients are "unscaled" to put them back on the original scale of your data. The intercept is then calculated separately using the means and the final coefficients.
<code>max_iter</code>	Maximum number of iterations for the variational update. Default is 1000.
<code>tol</code>	Convergence threshold for entropy and alpha change. Default is 1e-5.
<code>seed</code>	Integer seed for cross-validation in glmnet. Default is 12376.

## Details

This function acts as a wrapper for a C++ implementations of the SPEVXB algorithm.

## Value

A list with posterior summaries including estimated coefficients (`mu`), inclusion probabilities (`omega`), intercept (if applicable), alpha path, convergence status, etc.

## Examples

```
n <- 50
p <- 100
X <- matrix(rnorm(n * p), n, p)
Y <- X[,1] * 2 + rnorm(n)
result <- spexvb(X = X, Y = Y)
```

---

 spexvb.logistic

*Parameter Expanded Variational Bayes for Sparse Logistic Regression*


---

## Description

Fits a sparse logistic regression model using variational inference with an alpha expansion step.

## Usage

```
spexvb.logistic(
  X,
  Y,
  mu_0 = NULL,
  omega_0 = NULL,
  c_pi_0 = NULL,
  d_pi_0 = NULL,
  update_order = NULL,
  mu_alpha = 1,
  tau_alpha = 10,
  tau_b = 1,
  max_iter = 300,
  tol = 1e-04
)
```

## Arguments

X	A numeric matrix. The design matrix (n observations $\times$ p predictors).
Y	A numeric vector. The response vector (0/1).
mu_0	Optional numeric vector. Initial variational means.
omega_0	Optional numeric vector. Initial spike probabilities.
c_pi_0	Optional numeric. Prior Beta(a, b) parameter a.
d_pi_0	Optional numeric. Prior Beta(a, b) parameter b.
update_order	Optional integer vector. Coordinate update order (0-indexed).
mu_alpha	Prior mean for alpha. Default is 1.
tau_alpha	Prior precision for alpha. Default is 10.
tau_b	Slab prior precision. Default is 1.
max_iter	Maximum iterations. Default is 300.
tol	Convergence tolerance. Default is 1e-4.

## Value

A list with posterior summaries including estimated coefficients (mu), inclusion probabilities (omega), final expected slab precision (tau\_b), intercept (if applicable), convergence status, etc.

**Examples**

```
n <- 50
p <- 100
X <- matrix(rnorm(n * p), n, p)
# Generate binary response
Y <- rbinom(n, 1, plogis(X[,1] * 2))

fit <- spexvb.logistic(X, Y)

# Check convergence
print(fit$converged)
```

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