

# Package ‘Blend’

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**Type** Package

**Title** Bayesian Longitudinal Regularized Semiparametric Quantile Mixed Models

**Version** 0.1.0

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**Description** Our recently developed fully Bayesian semiparametric quantile mixed-effect model for high-dimensional longitudinal studies with heterogeneous observations can be implemented through this package. This model can distinguish between time-varying interactions and constant-effect-only cases to avoid model misspecifications. Facilitated by spike-and-slab priors, this model leads to superior performance in estimation, identification and statistical inference. In particular, robust Bayesian inferences in terms of valid Bayesian credible intervals on both parametric and nonparametric effects can be validated on finite samples. The Markov chain Monte Carlo algorithms of the proposed and alternative models are efficiently implemented in ‘C++’.

**Depends** R ( $\geq 4.2.0$ )

**License** GPL-2

**Encoding** UTF-8

**URL** <https://github.com/kunfa/Blend>

**LinkingTo** Rcpp, RcppArmadillo

**Imports** Rcpp, splines, stats, ggplot2

**RoxygenNote** 7.3.2

**NeedsCompilation** yes

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**Repository** CRAN

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Blend-package	<i>Bayesian Longitudinal Regularized Semiparametric Quantile Mixed Model</i>
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## Description

In this package, we further extend the sparse Bayesian quantile mixed models to nonlinear longitudinal interactions. Specifically, the proposed Bayesian quantile semiparametric model is robust not only to outliers and heavy-tailed distributions of the response variable, but also to the misspecification of interaction effect in the forms other than non-linear interactions. We have developed the Gibbs sampler with the spike-and-slab priors to promote sparse identification of appropriate forms of main and interaction effects. In addition to the default method, users can also choose different selection structures for separation of constant and varying effects or not, methods without spike-and-slab priors and non-robust methods. In total, *Blend* provides 8 different methods (4 robust and 4 non-robust) under the random intercept and slope model. All the methods in this package are developed for the first time. Please read the Details below for how to configure the method used.

## Details

The user friendly, integrated interface **Blend()** allows users to flexibly choose the fitting methods by specifying the following parameter:

- robust: whether to use robust methods for modelling.
- quant: to specify different quantiles when using robust methods.
- structural: whether to incorporate structural identification(separation of constant and varying effects) .
- sparse: whether to use the spike-and-slab priors to impose sparsity.

The function `Blend()` returns a `Blend` object that contains the posterior estimates of each coefficients and other useful information for `selection()`. S3 generic functions `selection()` and `print()` are implemented for `Blend` objects. `selection()` takes a `Blend` object and returns the variable selection results.

## References

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- 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
- Wu, C., Zhong, P.S. and Cui, Y. (2013). High dimensional variable selection for gene-environment interactions. *Technical Report. Michigan State University*.

## See Also

[Blend](#)

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Blend	<i>fit a Bayesian longitudinal regularized semi-parametric quantile mixed model</i>
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### Description

fit a Bayesian longitudinal regularized semi-parametric quantile mixed model

### Usage

```
Blend(
  y,
  x,
  t,
  J,
  kn,
  degree,
  iterations = 10000,
  burn.in = NULL,
  robust = TRUE,
  quant = 0.5,
  sparse = "TRUE",
  structural = TRUE
)
```

### Arguments

y	the vector of repeated - measured response variable. The current version of mixed only supports continuous response.
x	the matrix of repeated - measured predictors (genetic factors) with intercept. Each row should be an observation vector for each measurement.
t	the vector of scheduled time points.
J	the vector of number of repeated measurement for each subject.
kn	the number of interior knots for B-spline.
degree	the degree of B spline basis.
iterations	the number of MCMC iterations.
burn.in	the number of iterations for burn-in.
robust	logical flag. If TRUE, robust methods will be used.
quant	specify different quantiles when applying robust methods.
sparse	logical flag. If TRUE, spike-and-slab priors will be used to shrink coefficients of irrelevant covariates to zero exactly.
structural	logical flag. If TRUE, the coefficient functions with varying effects and constant effects will be penalized separately.

**Details**

Consider the data model described in "data":

$$Y_{ij} = \alpha_0(t_{ij}) + \sum_{k=1}^m \beta_k(t_{ij}) X_{ijk} + \mathbf{Z}_{ij}^\top \boldsymbol{\zeta}_i + \epsilon_{ij}.$$

The basis expansion and changing of basis with B splines will be done automatically:

$$\beta_k(\cdot) \approx \gamma_{k1} + \sum_{u=2}^q B_{ku}(\cdot) \gamma_{ku}$$

where  $B_{ku}(\cdot)$  represents B spline basis.  $\gamma_{k1}$  and  $(\gamma_{k2}, \dots, \gamma_{kq})^\top$  correspond to the constant and varying parts of the coefficient functional, respectively.  $q=kn+degree+1$  is the number of basis functions. By default,  $kn=degree=2$ . User can change the values of  $kn$  and  $degree$  to any other positive integers. When 'structural=TRUE' (default), the coefficient functions with varying effects and constant effects will be penalized separately. Otherwise, the coefficient functions with varying effects and constant effects will be penalized together.

When 'sparse="TRUE"' (default), spike-and-slab priors are imposed on individual and/or group levels to identify important constant and varying effects. Otherwise, Laplacian shrinkage will be used.

When 'robust=TRUE' (default), the distribution of  $\epsilon_{ij}$  is defined as a Laplace distribution with density.

$f(\epsilon_{ij}|\theta, \tau) = \theta(1 - \theta) \exp\{-\tau\rho_\theta(\epsilon_{ij})\}$ , ( $i = 1, \dots, n, j = 1, \dots, J_i$ ), which leads to a Bayesian formulation of quantile regression. If 'robust=FALSE',  $\epsilon_{ij}$  follows a normal distribution.

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

**Value**

an object of class 'Blend' is returned, which is a list with component:

posterior	the posteriors of coefficients.
coefficient	the estimated coefficients.
burn.in	the total number of burn-ins.
iterations	the total number of iterations.

**See Also**

[data](#)

**Examples**

```
data(dat)

## default method
fit = Blend(y,x,t,J,kn,degree)
fit$coefficient
```

```
## alternative: robust non-structural
fit = Blend(y,x,t,J,kn,degree, structural=FALSE)
fit$coefficient

## alternative: non-robust structural
fit = Blend(y,x,t,J,kn,degree, robust=FALSE)
fit$coefficient

## alternative: non-robust non-structural
fit = Blend(y,x,t,J,kn,degree, robust=FALSE, structural=FALSE)
fit$coefficient
```

---

Coverage

*95% coverage for a Blend object with structural identification*

---

### Description

calculate 95% coverage for varying effects and constant effects under example data

### Usage

```
Coverage(x)
```

### Arguments

x                    Blend object.

### Value

coverage

### See Also

[Blend](#)

### Examples

```
data(dat)
fit = Blend(y,x,t,J,kn,degree)
Coverage(fit)
```

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 data

 simulated data for demonstrating the features of Blend
 

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## Description

Simulated gene expression data for demonstrating the features of Blend.

## Format

The data object consists of 8 components: y, x, t, J, kn and degree.

## Details

### The data and model setting

Consider a longitudinal study on  $n$  subjects with  $J_i$  repeated measurements for each subject. Let  $Y_{ij}$  be the measurement for the  $i$ -th subject at each time point  $t_{ij}$ , ( $1 \leq i \leq n, 1 \leq j \leq J_i$ ). We use an  $m$ -dimensional vector  $X_{ij}$  to denote the genetic factors, where  $X_{ij} = (X_{ij1}, \dots, X_{ijm})^\top$ .  $Z_{ij}$  is a  $2 \times 1$  covariate associated with random effects and  $\zeta_i$  is a  $2 \times 1$  vector of random effects corresponding to the random intercept and slope model. We have the following semi-parametric quantile mixed-effects model:

$$Y_{ij} = \alpha_0(t_{ij}) + \sum_{k=1}^m \beta_k(t_{ij})X_{ijk} + Z_{ij}^\top \zeta_i + \epsilon_{ij}, \zeta_i \sim N(0, \Lambda)$$

where the fixed effects include: (a) the varying intercept  $\alpha_0(t_{ij})$ , and (b) the varying coefficients  $\beta(t_{ij})$ .

The varying intercept and the varying coefficients for the genetic factors can be further expressed as  $\alpha_0(t_{ij})$  and  $\beta(t_{ij}) = (\beta_1(t_{ij}), \dots, \beta_m(t_{ij}))^\top$ .

For the random intercept and slope model,  $Z_{ij}^\top = (1, j)$  and  $\zeta_i = (\zeta_{i1}, \zeta_{i2})^\top$ .

Furthermore,  $Z_{ij}^\top \zeta_i$  can be expressed as  $(b_i^\top \otimes Z_{ij}^\top)J_2\delta$ , where  $\zeta_i = \Delta b_i$ ,  $\Lambda = \Delta\Delta^\top$ , and

$$b_i^\top \otimes Z_{ij}^\top = (b_{i1}Z_{ij1}, b_{i1}Z_{ij2}, b_{i2}Z_{ij1}, b_{i2}Z_{ij2})^\top.$$

In the simulated data,

$$Y = \alpha_0(t) + \beta_1(t)X_1 + \beta_2(t)X_2 + \beta_3(t)X_3 + \beta_4(t)X_4 + 0.8X_5 - 1.2X_6 + 0.7X_7 - 1.1X_8 + \epsilon$$

where  $\epsilon \sim N(0, 1)$ ,  $\alpha_0(t) = 2 + \sin(2\pi t)$ ,  $\beta_1(t) = 2.5 \exp(2.5t - 1)$ ,  $\beta_2(t) = 3t^2 - 2t + 2$ ,  $\beta_3(t) = -4t^3 + 3$  and  $\beta_4(t) = 3 - 2t$

## See Also

[Blend](#)

**Examples**

```
data(dat)
length(y)
dim(x)
length(t)
length(J)
print(t)
print(J)
print(kn)
print(degree)
```

---

plot\_Blend

*plot a Blend object*

---

**Description**

plot the identified varying effects

**Usage**

```
plot_Blend(x, sparse, prob=0.95)
```

**Arguments**

x	Blend object.
sparse	sparsity.
prob	probability for credible interval, between 0 and 1. e.g. prob=0.95 leads to 95% credible interval

**Value**

plot

**See Also**

[Blend](#)

**Examples**

```
data(dat)
fit = Blend(y,x,t,J,kn,degree)
plot_Blend(fit,sparse=TRUE)
```



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selection

*Variable selection for a Blend object*

---

## Description

Variable selection for a Blend object

## Usage

```
selection(obj, sparse)
```

## Arguments

obj	Blend object.
sparse	logical flag. If TRUE, spike-and-slab priors will be used to shrink coefficients of irrelevant covariates to zero exactly.

## Details

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

## Value

an object of class ‘selection’ is returned, which is a list with component:

method	posterior samples from the MCMC
indices	a list of indices and names of selected variables
summary	a summary of selected variables

## 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

[Blend](#)

**Examples**

```
data(dat)
## sparse
fit = Blend(y,x,t,J,kn,degree)
selected=selection(fit,sparse=TRUE)
selected

## non-sparse
fit = Blend(y,x,t,J,kn,degree,sparse="FALSE")
selected=selection(fit,sparse=FALSE)
selected
```

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