

Package ‘bkmrhat’

May 7, 2026

Title Parallel Chain Tools for Bayesian Kernel Machine Regression

Version 1.1.7

Date 2025-11-19

Description Bayesian kernel machine regression (from the 'bkmr' package) is a Bayesian semi-parametric generalized linear model approach under identity and probit links. There are a number of functions in this package that extend Bayesian kernel machine regression fits to allow multiple-chain inference and diagnostics, which leverage functions from the 'future', 'rstan', and 'coda' packages. Reference: Bobb, J. F., Henn, B. C., Valeri, L., & Coull, B. A. (2018). Statistical software for analyzing the health effects of multiple concurrent exposures via Bayesian kernel machine regression. ; <doi:10.1186/s12940-018-0413-y>.

License GPL (>= 3)

URL <https://github.com/alexpkel1/bkmrhat/>

BugReports <https://github.com/alexpkel1/bkmrhat/issues>

Depends coda, R (>= 3.5.0)

Imports bkmr, data.table, future, rstan

Suggests knitr, markdown

VignetteBuilder knitr

Encoding UTF-8

Language en-US

RoxygenNote 7.3.3

NeedsCompilation no

Author Alexander Keil [aut, cre]

Maintainer Alexander Keil <alex.keil@nih.gov>

Repository CRAN

Date/Publication 2025-11-30 09:20:14 UTC

Contents

as.mcmc.bkmrfit	2
as.mcmc.list.bkmrfit.list	3
ExtractPIPs_parallel	4
kmbayes_combine	5
kmbayes_combine_lowmem	6
kmbayes_continue	8
kmbayes_diagnose	9
kmbayes_parallel	10
kmbayes_parallel_continue	11
OverallRiskSummaries_parallel	12
predict.bkmrfit	12
PredictorResponseBivar_parallel	13
PredictorResponseUnivar_parallel	14
SamplePred_parallel	14
SingVarRiskSummaries_parallel	15
Index	16

as.mcmc.bkmrfit	<i>Convert bkmrfit to mcmc object for coda MCMC diagnostics</i>
-----------------	---

Description

Converts a `kmrfit` (from the `bkmr` package) into an `mcmc` object from the `coda` package. The `coda` package enables many different types of single chain MCMC diagnostics, including `geweke.diag`, `traceplot` and `effectiveSize`. Posterior summarization is also available, such as `HPDinterval` and `summary.mcmc`.

Usage

```
## S3 method for class 'bkmrfit'
as.mcmc(x, iterstart = 1, thin = 1, ...)
```

Arguments

<code>x</code>	object of type <code>kmrfit</code> (from <code>bkmr</code> package)
<code>iterstart</code>	first iteration to use (e.g. for implementing burnin)
<code>thin</code>	keep 1/thin % of the total iterations (at regular intervals)
<code>...</code>	unused

Value

An `mcmc` object

Examples

```
# following example from https://jenfb.github.io/bkmr/overview.html

set.seed(111)
library(coda)
library(bkmr)
dat <- bkmr::SimData(n = 50, M = 4)
y <- dat$y
Z <- dat$Z
X <- dat$X
set.seed(111)
fitkm <- kmbayes(y = y, Z = Z, X = X, iter = 500, verbose = FALSE,
  varsel = FALSE)
mcmcobj <- as.mcmc(fitkm, iterstart=251)
summary(mcmcobj) # posterior summaries of model parameters
# compare with default from bkmr package, which omits first 1/2 of chain
summary(fitkm)
# note this only works on multiple chains (see kmbayes_parallel)
# gelman.diag(mcmcobj)
# lots of functions in the coda package to use
traceplot(mcmcobj)
# will also fail with delta functions (when using variable selection)
try(geweke.plot(mcmcobj))
```

```
as.mcmc.list.bkmrfit.list
```

Convert multi-chain bkmrfit to mcmc.list for coda MCMC diagnostics

Description

Converts a `kmrfit.list` (from the `bkmrhat` package) into an `mcmc.list` object from the `coda` package. The `coda` package enables many different types of MCMC diagnostics, including `geweke.diag`, `traceplot` and `effectiveSize`. Posterior summarization is also available, such as `HPDinterval` and `summary.mcmc`. Using multiple chains is necessary for certain MCMC diagnostics, such as `gelman.diag`, and `gelman.plot`.

Usage

```
## S3 method for class 'list.bkmrfit.list'
as.mcmc(x, ...)
```

Arguments

```
x          object of type kmrfit.list (from bkmrhat package)
...        arguments to as.mcmc.bkmrfit
```

Value

An `mcmc.list` object

Examples

```
# following example from https://jenfb.github.io/bkmr/overview.html

set.seed(111)
library(coda)
dat <- bkmr::SimData(n = 50, M = 4)
y <- dat$y
Z <- dat$Z
X <- dat$X
set.seed(111)

future::plan(strategy = future::multisession, workers=2)
# run 2 parallel Markov chains (more usually better)
fitkm.list <- kmbayes_parallel(nchains=2, y = y, Z = Z, X = X, iter = 1000,
  verbose = FALSE, varsel = FALSE)
mcmcobj = as.mcmc.list(fitkm.list)
summary(mcmcobj)
# Gelman/Rubin diagnostics won't work on certain objects,
# like delta parameters (when using variable selection),
# so the rstan version of this will work better (does not give errors)
try(gelman.diag(mcmcobj))
# lots of functions in the coda package to use
plot(mcmcobj)
# both of these will also fail with delta functions (when using variable selection)
try(gelman.plot(mcmcobj))
try(geweke.plot(mcmcobj))

closeAllConnections()
```

ExtractPIPs_parallel *Posterior inclusion probabilities by chain*

Description

Posterior inclusion probabilities by chain

Usage

```
ExtractPIPs_parallel(x, ...)
```

Arguments

`x` bkmrfit.list object from `kmbayes_parallel`
`...` arguments to `ExtractPIPs`

Value

data.frame with all chains together

kmbayes_combine	<i>Combine multiple BKMR chains</i>
-----------------	-------------------------------------

Description

Combine multiple chains comprising BKMR fits at different starting values.

Usage

```
kmbayes_combine(
  fitkm.list,
  burnin = NULL,
  excludeburnin = FALSE,
  reorder = TRUE
)
```

```
comb_bkmrfits(fitkm.list, burnin = NULL, excludeburnin = FALSE, reorder = TRUE)
```

Arguments

fitkm.list	output from kmbayes_parallel
burnin	(numeric, or default=NULL) add in custom burnin (number of burnin iterations per chain). If NULL, then default to half of the chain
excludeburnin	(logical, default=FALSE) should burnin iterations be excluded from the final chains? Note that all bkmr package functions automatically exclude burnin from calculations.
reorder	(logical, default=TRUE) ensures that the first half of the combined chain contains only the first half of each individual chain - this allows unaltered use of standard functions from bkmr package, which automatically trims the first half of the iterations. This can be used for posterior summaries, but certain diagnostics may not work well (autocorrelation, effective sample size) so the diagnostics should be done on the individual chains #' @param ... arguments to as.mcmc.bkmrfit

Details

Chains are not combined fully sequentially

Value

a bkmrplusfit object, which inherits from bkmrfit (from the [kmbayes](#) function) with multiple chains combined into a single object and additional parameters given by chain and iters, which index the specific chains and iterations for each posterior sample in the bkmrplusfit object

Examples

```

# following example from https://jenfb.github.io/bkmr/overview.html
set.seed(111)
library(bkmr)
dat <- bkmr::SimData(n = 50, M = 4)
y <- dat$y
Z <- dat$Z
X <- dat$X
set.seed(111)

future::plan(strategy = future::multisession, workers=2)
# run 4 parallel Markov chains (low iterations used for illustration)
fitkm.list <- kmbayes_parallel(nchains=2, y = y, Z = Z, X = X, iter = 500,
  verbose = FALSE, varsel = TRUE)
# use bkmr defaults for burnin, but keep them
bigkm = kmbayes_combine(fitkm.list, excludeburnin=FALSE)
ests = ExtractEsts(bigkm) # defaults to keeping second half of samples
ExtractPIPs(bigkm)
pred.resp.univar <- PredictorResponseUnivar(fit = bigkm)
risks.overall <- OverallRiskSummaries(fit = bigkm, y = y, Z = Z, X = X,
  qs = seq(0.25, 0.75, by = 0.05), q.fixed = 0.5, method = "exact")

# additional objects that are not in a standard bkmrfit object:
summary(bigkm$iters) # note that this reflects how fits are re-ordered to reflect burnin
table(bigkm$chain)

closeAllConnections()

```

kmbayes_combine_lowmem

Combine multiple BKMR chains in lower memory settings

Description

Combine multiple chains comprising BKMR fits at different starting values. This function writes some results to disk, rather than trying to process fully within memory which, in some cases, will result in avoiding "out of memory" errors that can happen with kmbayes_combine.

Usage

```

kmbayes_combine_lowmem(
  fitkm.list,
  burnin = NULL,
  excludeburnin = FALSE,
  reorder = TRUE
)

```

```
comb_bkmrfits_lowmem(
  fitkm.list,
  burnin = NULL,
  excludeburnin = FALSE,
  reorder = TRUE
)
```

Arguments

fitkm.list	output from kmbayes_parallel
burnin	(numeric, or default=NULL) add in custom burnin (number of burnin iterations per chain). If NULL, then default to half of the chain
excludeburnin	(logical, default=FALSE) should burnin iterations be excluded from the final chains? Note that all bkmr package functions automatically exclude burnin from calculations.
reorder	(logical, default=TRUE) ensures that the first half of the combined chain contains only the first half of each individual chain - this allows unaltered use of standard functions from bkmr package, which automatically trims the first half of the iterations. This can be used for posterior summaries, but certain diagnostics may not work well (autocorrelation, effective sample size) so the diagnostics should be done on the individual chains #' @param ... arguments to as.mcmc.bkmrfit

Details

Chains are not combined fully sequentially (see "reorder")

Value

a `bkmrplusfit` object, which inherits from `bkmrfit` (from the [kmbayes](#) function) with multiple chains combined into a single object and additional parameters given by `chain` and `iters`, which index the specific chains and iterations for each posterior sample in the `bkmrplusfit` object

Examples

```
# following example from https://jenfb.github.io/bkmr/overview.html
set.seed(111)
library(bkmr)
dat <- bkmr::SimData(n = 50, M = 4)
y <- dat$y
Z <- dat$Z
X <- dat$X
set.seed(111)

future::plan(strategy = future::multisession, workers=2)
# run 4 parallel Markov chains (low iterations used for illustration)
fitkm.list <- kmbayes_parallel(nchains=2, y = y, Z = Z, X = X, iter = 500,
  verbose = FALSE, varsel = TRUE)
# use bkmr defaults for burnin, but keep them
bigkm = kmbayes_combine_lowmem(fitkm.list, excludeburnin=FALSE)
```

```

ests = ExtractEsts(bigkm) # defaults to keeping second half of samples
ExtractPIPs(bigkm)
pred.resp.univar <- PredictorResponseUnivar(fit = bigkm)
risks.overall <- OverallRiskSummaries(fit = bigkm, y = y, Z = Z, X = X,
  qs = seq(0.25, 0.75, by = 0.05), q.fixed = 0.5, method = "exact")

# additional objects that are not in a standard bkrmfit object:
summary(bigkm$iters) # note that this reflects how fits are re-ordered to reflect burnin
table(bigkm$chain)

closeAllConnections()

```

kmbayes_continue	<i>Continue sampling from existing bkrm fit</i>
------------------	---

Description

Use this when you've used MCMC sampling with the [kmbayes](#) function, but you did not take enough samples and do not want to start over.

Usage

```
kmbayes_continue(fit, ...)
```

Arguments

fit	output from kmbayes
...	arguments to kmbayes_continue

Details

Note this does not fully start from the prior values of the MCMC chains. The [kmbayes](#) function does not allow full specification of the kernel function parameters, so this will restart the chain at the last values of all fixed effect parameters, and start the kernel r parameters at the arithmetic mean of all r parameters from the last step in the previous chain.

Value

a `bkrmfit.continued` object, which inherits from `bkrmfit` objects similar to [kmbayes](#) output, and which can be used to make inference using functions from the `bkrm` package.

See Also

[kmbayes_parallel](#)

Examples

```

set.seed(111)
dat <- bkmr::SimData(n = 50, M = 4)
y <- dat$y
Z <- dat$Z
X <- dat$X
## Not run:
fitty1 = bkmr::kmbayes(y=y,Z=Z,X=X, est.h=TRUE, iter=100)
# do some diagnostics here to see if 100 iterations (default) is enough
# add 100 additional iterations (for illustration - still will not be enough)
fitty2 = kmbayes_continue(fitty1, iter=100)
cobj = as.mcmc(fitty2)
varnames(cobj)

## End(Not run)

```

kmbayes_diagnose *MCMC diagnostics using rstan*

Description

Give MCMC diagnostics from the `rstan` package using the `Rhat`, `ess_bulk`, and `ess_tail` functions. Note that `r-hat` is only reported for `bkmrfit.list` objects from `kmbayes_parallel`

Usage

```
kmbayes_diagnose(kmobj, ...)
```

```
kmbayes_diag(kmobj, ...)
```

Arguments

<code>kmobj</code>	Either an object from <code>kmbayes</code> or from <code>kmbayes_parallel</code>
<code>...</code>	arguments to <code>monitor</code>

Examples

```

set.seed(111)
dat <- bkmr::SimData(n = 50, M = 4)
y <- dat$y
Z <- dat$Z
X <- dat$X
set.seed(111)

future::plan(strategy = future::multisession)
fitkm.list <- kmbayes_parallel(nchains=2, y = y, Z = Z, X = X, iter = 1000,
  verbose = FALSE, varsel = TRUE)

```

```
kmbayes_diag(fitkm.list)
kmbayes_diag(fitkm.list[[1]]) # just the first chain

closeAllConnections()
```

kmbayes_parallel *Run multiple BKMR chains in parallel*

Description

Fit parallel chains from the [kmbayes](#) function. These chains leverage parallel processing from the `future` package, which can speed fitting and enable diagnostics that rely on multiple Markov chains from dispersed initial values.

Usage

```
kmbayes_parallel(nchains = 4, ...)
```

Arguments

nchains	number of parallel chains
...	arguments to <code>kmbayes</code>

Value

a "bkmrfit.list" object, which is just an R list object in which each entry is a "bkmrfit" object [kmbayes](#)

Examples

```
set.seed(111)
dat <- bkmr::SimData(n = 50, M = 4)
y <- dat$y
Z <- dat$Z
X <- dat$X
set.seed(111)

future::plan(strategy = future::multisession, workers=2)
# only 50 iterations fit to save installation time
fitkm.list <- kmbayes_parallel(nchains=2, y = y, Z = Z, X = X, iter = 50,
  verbose = FALSE, varsel = TRUE)
closeAllConnections()
```

`kmbayes_parallel_continue`*Continue sampling from existing `bkmr_parallel` fit*

Description

Use this when you've used MCMC sampling with the `kmbayes_parallel` function, but you did not take enough samples and do not want to start over.

Usage

```
kmbayes_parallel_continue(fitkm.list, ...)
```

Arguments

<code>fitkm.list</code>	output from <code>kmbayes_parallel</code>
<code>...</code>	arguments to <code>kmbayes_continue</code>

Value

a `bkmrfit.list` object, which is just a list of `bkmrfit` objects similar to `kmbayes_parallel`

See Also

[kmbayes_parallel](#)

Examples

```
set.seed(111)
dat <- bkmr::SimData(n = 50, M = 4)
y <- dat$y
Z <- dat$Z
X <- dat$X
## Not run:

future::plan(strategy = future::multisession, workers=2)
fitty1p = kmbayes_parallel(nchains=2, y=y,Z=Z,X=X)

fitty2p = kmbayes_parallel_continue(fitty1p, iter=3000)
cobj = as.mcmc.list(fitty2p)
plot(cobj)

## End(Not run)
```

OverallRiskSummaries_parallel
Overall summary by chain

Description

Overall summary by chain

Usage

```
OverallRiskSummaries_parallel(x, ...)
```

Arguments

x bkmrfit.list object from [kmbayes_parallel](#)
 ... arguments to [OverallRiskSummaries](#)

Value

data.frame with all chains together

predict.bkmrfit *Posterior mean/sd predictions*

Description

Provides observation level predictions based on the posterior mean, or, alternatively, yields the posterior standard deviations of predictions for an observation. This function is useful for interfacing with ensemble machine learning packages such as SuperLearner, which utilize only point estimates.

Usage

```
## S3 method for class 'bkmrfit'
predict(object, ptype = c("mean", "sd.fit"), ...)
```

Arguments

object fitted object of class inheriting from "bkmrfit".
 ptype "mean" or "sd.fit", where "mean" yields posterior mean prediction for every observation in the data, and "sd.fit" yields the posterior standard deviation for every observation in the data.
 ... arguments to [SamplePred](#)

Value

vector of predictions the same length as the outcome in the bkrmfit object

Examples

```
# following example from https://jenfb.github.io/bkmr/overview.html

library(bkmr)
set.seed(111)
dat <- bkmr::SimData(n = 50, M = 4)
y <- dat$y
Z <- dat$Z
X <- dat$X
set.seed(111)
fitkm <- kmbayes(y = y, Z = Z, X = X, iter = 200, verbose = FALSE,
  varsel = TRUE)
postmean = predict(fitkm)
postmean2 = predict(fitkm, Znew=Z/2)
# mean difference in posterior means
mean(postmean-postmean2)
```

PredictorResponseBivar_parallel

Bivariate predictor response by chain

Description

Bivariate predictor response by chain

Usage

```
PredictorResponseBivar_parallel(x, ...)
```

Arguments

x	bkrmfit.list object from kmbayes_parallel
...	arguments to PredictorResponseBivar

Value

data.frame with all chains together

PredictorResponseUnivar_parallel

Univariate predictor response summary by chain

Description

Univariate predictor response summary by chain

Usage

PredictorResponseUnivar_parallel(x, ...)

Arguments

x bkmrfit.list object from [kmbayes_parallel](#)
... arguments to [PredictorResponseUnivar](#)

Value

data.frame with all chains together

SamplePred_parallel *Posterior samples of $E(Y|h(Z),X,\beta)$ by chain*

Description

Posterior samples of $E(Y|h(Z),X,\beta)$ by chain

Usage

SamplePred_parallel(x, ...)

Arguments

x bkmrfit.list object from [kmbayes_parallel](#)
... arguments to [SamplePred](#)

Value

data.frame with all chains together

`SingVarRiskSummaries_parallel`
Single variable summary by chain

Description

Single variable summary by chain

Usage

`SingVarRiskSummaries_parallel(x, ...)`

Arguments

`x` `bkmrfit.list` object from [kmbayes_parallel](#)
`...` arguments to [SingVarRiskSummaries](#)

Value

`data.frame` with all chains together

Index

as.mcmc.bkmrfit, [2, 3, 5, 7](#)
as.mcmc.list.bkmrfit.list, [3](#)

comb_bkmrfits (kmbayes_combine), [5](#)
comb_bkmrfits_lowmem
 (kmbayes_combine_lowmem), [6](#)

effectiveSize, [2, 3](#)
ess_bulk, [9](#)
ess_tail, [9](#)
ExtractPIPs, [4](#)
ExtractPIPs_parallel, [4](#)

gelman.diag, [3](#)
gelman.plot, [3](#)
geweke.diag, [2, 3](#)

HPDinterval, [2, 3](#)

kmbayes, [5, 7–10](#)
kmbayes_combine, [5](#)
kmbayes_combine_lowmem, [6](#)
kmbayes_continue, [8, 8, 11](#)
kmbayes_diag (kmbayes_diagnose), [9](#)
kmbayes_diagnose, [9](#)
kmbayes_parallel, [4, 5, 7–9, 10, 11–15](#)
kmbayes_parallel_continue, [11](#)

mcmc, [2](#)
mcmc.list, [3, 4](#)
monitor, [9](#)

OverallRiskSummaries, [12](#)
OverallRiskSummaries_parallel, [12](#)

predict.bkmrfit, [12](#)
PredictorResponseBivar, [13](#)
PredictorResponseBivar_parallel, [13](#)
PredictorResponseUnivar, [14](#)
PredictorResponseUnivar_parallel, [14](#)

Rhat, [9](#)

SamplePred, [12, 14](#)
SamplePred_parallel, [14](#)
SingVarRiskSummaries, [15](#)
SingVarRiskSummaries_parallel, [15](#)
summary.mcmc, [2, 3](#)

traceplot, [2, 3](#)