Package 'fkbma'

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Contents

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coef.rjMCMC   *Extract Posterior Mean Coefficients from rjMCMC Results*

Description

This function extracts the posterior means of the intercept, exposure parameters, and binary parameters from the results of an rjMCMC model.

Usage

```
## S3 method for class 'rjMCMC'
coef(object, ...)
```

Arguments

object   An object of class rjMCMC containing the output from the rjMCMC procedure,
                which includes:

   fixed_param Matrix of posterior samples for exposure intercept and main ef-
            fect.

   binary_param Matrix of posterior samples for binary variable parameters.

   sigma_sq Matrix of posterior samples for the residual variance (sigma squared).

   vars_prop_summ Posterior inclusion probabilities for candidate variables.

   splines_fitted List of matrices containing fitted values for spline terms across
            iterations.

   data_fit Original dataset used in the rjMCMC procedure.

   candsplineinter Names of continuous candidate predictive spline variables.

   candsplinevars Names of continuous candidate spline variables.

   candbinaryvars Names of binary candidate variables.

   candinter Names of interaction terms, which can include spline variables.

   mcmc_specs MCMC sampler specifications, including the number of itera-
            tions, burn-in, thinning, and chains.

...   Additional arguments to be passed to other methods or functions.

Value

A numeric vector containing the posterior mean of the intercept, exposure, and binary parameters.

Examples

```
# Example dataset
data("simulated_data")

candsplinevars <- c("X_1")
candbinaryvars <- paste0("Z_", 1:5)
candinter <- c(candsplinevars, candbinaryvars)


results <- rjMCMC(simulated_data, candsplinevars, candbinaryvars, candinter,
                  outcome = "Y", factor_var = "trt")
coef(results)
```

---

credint   *Credible Intervals for rjMCMC Results*

Description

This function calculates the posterior mean and credible intervals for parameters from the rjMCMC results, including both intercept/exposure parameters and binary parameters. The credible intervals are computed based on the specified confidence level.

Usage

```
credint(results, level = 0.95)
```

Arguments

results   An object of class rjMCMC containing the output from the rjMCMC procedure, including posterior samples.

level   The level for the credible intervals (default is 0.95).

Value

A data frame with estimates, lower, and upper bounds of the credible intervals.

Examples

```
# Example dataset
data("simulated_data")

candsplinevars <- c("X_1")
candbinaryvars <- paste0("Z_", 1:5)
```

```
candinter <- c(candsplinevars, candbinaryvars)


results <- rjMCMC(simulated_data, candsplinevars, candbinaryvars, candinter,
                  outcome = "Y", factor_var = "trt")
credint(results)
```

---

fitted.rjMCMC   *Fitted values from Reversible Jump MCMC (rjMCMC) Model Results*

Description

This function generates posterior fitted values from an rjMCMC model based on the provided data. It combines the fixed effects, spline terms, and binary parameters.

Usage

```
## S3 method for class 'rjMCMC'
fitted(object, newdata = NULL, ...)
```

Arguments

object   An object of class rjMCMC containing the output from the rjMCMC procedure, which includes:

fixed_param Matrix of posterior samples for exposure intercept and main effect.

binary_param Matrix of posterior samples for binary variable parameters.

sigma_sq Matrix of posterior samples for the residual variance (sigma squared).

vars_prop_summ Posterior inclusion probabilities for candidate variables.

splines_fitted List of matrices containing fitted values for spline terms across iterations.

data_fit Original dataset used in the rjMCMC procedure.

candsplineinter Names of continuous candidate predictive spline variables.

candsplinevars Names of continuous candidate spline variables.

candbinaryvars Names of binary candidate variables.

candinter Names of interaction terms, which can include spline variables.

mcmc_specs MCMC sampler specifications, including the number of iterations, burn-in, thinning, and chains.

newdata   A data frame for which fitted values are to be computed. If NA, the original fitted data is used.

...   Additional arguments to be passed to other methods or functions.

Value

A matrix of fitted values.

Examples

```
# Example dataset
data("simulated_data")

candsplinevars <- c("X_1")
candbinaryvars <- paste0("Z_", 1:5)
candinter <- c(candsplinevars, candbinaryvars)

results <- rjMCMC(simulated_data, candsplinevars, candbinaryvars, candinter,
          outcome = "Y", factor_var = "trt")

newdata = data.frame(Z_1 = 1, Z_2 = 1, Z_3 = 1, Z_4 = 1, Z_5 = 1,
                trt = 1, X_1 = seq(0,1,by=0.01))
fitted(results)
fitted(results,newdata)
```

---

fittedExposureEff *Fitted exposure effect values from Reversible Jump MCMC (rjMCMC) Model Results*

Description

This function generates posterior fitted exposure effects from an rjMCMC model based on the provided data. It combines the fixed effects, spline terms, and binary parameters.

Usage

```
fittedExposureEff(results, newdata = NULL)
```

Arguments

results   An object of class rjMCMC containing the output from the `rjMCMC` procedure, which includes:

   fixed_param Matrix of posterior samples for exposure intercept and main effect.

   binary_param Matrix of posterior samples for binary variable parameters.

   sigma_sq Matrix of posterior samples for the residual variance (sigma squared).

   vars_prop_summ Posterior inclusion probabilities for candidate variables.

   splines_fitted List of matrices containing fitted values for spline terms across iterations.

   data_fit Original dataset used in the `rjMCMC` procedure.

   candsplineinter Names of continuous candidate predictive spline variables.

   candsplinevars Names of continuous candidate spline variables.

   candbinaryvars Names of binary candidate variables.

   candinter Names of interaction terms, which can include spline variables.

mcmc_specs MCMC sampler specifications, including the number of itera-
tions, burn-in, thinning, and chains.

newdata   A data frame for which fitted values are to be computed. If NA, the original
                 fitted data is used.

Value

A matrix of fitted values.

Examples

```
# Example dataset
data("simulated_data")

candsplinevars <- c("X_1")
candbinaryvars <- paste0("Z_", 1:5)
candinter <- c(candsplinevars, candbinaryvars)
results <- rjMCMC(simulated_data, candsplinevars, candbinaryvars, candinter,
                  outcome = "Y", factor_var = "trt")
newdata = data.frame(Z_1 = 1, Z_2 = 1, Z_3 = 1, Z_4 = 1, Z_5 = 1,
                     trt = 1, X_1 = seq(0,1,by=0.01))
fittedExposureEff(results)
fittedExposureEff(results,newdata)
```

---

getEffectiveSubspace   *Get Effective Subspace*

Description

This function identifies the "effective subspace" where exposure is effective based on posterior
inference results from the FK-BMA model. It analyzes interaction terms between exposure and
covariates, allowing for both binary and continuous variables.

Usage

```
getEffectiveSubspace(results, newdata = NULL, alpha = 0.05, pip_cutoff = 0.1)
```

Arguments

results   A fitted model object from rjMCMC.

newdata   Optional. A new dataset for evaluating the effective subspace. If NULL, the
                 function uses results$data_fit.

alpha   Numeric. The alpha level used for computing quantiles. Default is 0.05.

pip_cutoff   Numeric. The minimum Posterior Inclusion Probability (PIP) threshold for se-
                 lecting covariates. Default is 0.1.

Details

- The function computes the posterior exposure effect for each observation in the dataset using the `fittedExposureEff` function and evaluates its quantiles at the specified `alpha` level.

- Binary variables with high posterior inclusion probabilities (PIP) are used to define subgroups, and the corresponding effective subspaces for a continuous variable are identified by checking where the exposure effect quantiles are strictly positive.

- If the number of binary variables is <= 3 and there is exactly one continuous variable, the function describes the effective subspace in terms of disjoint intervals.

- For more complex cases, a warning is issued suggesting alternative methods such as Bayesian regression trees for interpretation.

Value

A list with the following components:

quantiles   A vector of quantile values for the exposure effect in the new dataset.

is_effective_subspace

A logical vector indicating whether the exposure effect is positive in the effective subspace.

Examples

```
# Example dataset
data("simulated_data")

candsplinevars <- c("X_1")
candbinaryvars <- paste0("Z_", 1:5)
candinter <- c(candsplinevars, candbinaryvars)

results <- rjMCMC(simulated_data, candsplinevars, candbinaryvars, candinter,
                  outcome = "Y", factor_var = "trt")
getEffectiveSubspace(results)
```

---

pip   *Compute Posterior Inclusion Probabilities (PIPs) for rjMCMC Results*

Description

This function returns the posterior inclusion probabilities (PIPs) for all variables, including the intercept and exposure, based on the results from an rjMCMC model.

Usage

```
pip(results)
```

Arguments

results   An object of class rjMCMC containing the output from the `rjMCMC` procedure,
               which includes:

               fixed_param Matrix of posterior samples for exposure intercept and main ef-
                          fect.

               binary_param Matrix of posterior samples for binary variable parameters.

               sigma_sq Matrix of posterior samples for the residual variance (sigma squared).

               vars_prop_summ Posterior inclusion probabilities for candidate variables.

               splines_fitted List of matrices containing fitted values for spline terms across
                          iterations.

               data_fit Original dataset used in the `rjMCMC` procedure.

               candsplineinter Names of continuous candidate predictive spline variables.

               candsplinevars Names of continuous candidate spline variables.

               candbinaryvars Names of binary candidate variables.

               candinter Names of interaction terms, which can include spline variables.

               mcmc_specs MCMC sampler specifications, including the number of itera-
                          tions, burn-in, thinning, and chains.

Value

A numeric vector with the PIPs for the intercept, exposure, and other variables.

Examples

```
# Example dataset
data("simulated_data")

candsplinevars <- c("X_1")
candbinaryvars <- paste0("Z_", 1:5)
candinter <- c(candsplinevars, candbinaryvars)

results <- rjMCMC(simulated_data, candsplinevars, candbinaryvars, candinter,
                  outcome = "Y", factor_var = "trt")
pip(results)
```

---

plot.rjMCMC   *Plotting function for* rjMCMC *results*

Description

This function generates plots for model results from `rjMCMC` based on specified sample type, effect
type, and plot type. The function is flexible for various combinations of sample_type, effect_type,
and plot_type, as outlined below.

Usage

```
## S3 method for class 'rjMCMC'
plot(
  x,
  ...,
  variables = NULL,
  sample_type = "fitted",
  effect_type = "exposure_effect",
  plot_type = "cred",
  level = 0.95,
  aux_vars = list(),
  facet_by = NULL,
  pip_cutoff = 0.1
)
```

Arguments

x	A fitted model object from `rjMCMC`.
...	Additional arguments to be passed to other methods or functions.
variables	A vector of variable names to include in the plot. Automatically set to continuous variables if `NULL`.
sample_type	Character string specifying the type of sample: "fitted", "predictive", or "estimand". "fitted" and "predictive" are compatible with `plot_type = "cred"`. "estimand" is compatible with `plot_type = "hist"` or "trace" (only used for individual parameter trajectories).
effect_type	Character string indicating the effect type: "exposure_effect" or "outcome". For "exposure_effect", the function plots the fitted or predictive effect of exposure; for "outcome", it plots outcome values without interaction with exposure.
plot_type	Character string specifying the plot type: "cred" for credible interval plots, or "hist"/"trace" for histogram or trace plots of individual parameters (only for `sample_type = "estimand"`).
level	Numeric value for the credible interval level (default is 0.95).
aux_vars	A list of auxiliary variables and their fixed values. Each element name must match a model variable.
facet_by	A vector of variable names to facet by in the plot. Automatically set to binary model variables if `NULL`.
pip_cutoff	Numeric threshold for the posterior inclusion probability (PIP) of model variables to include in the plot.

Details

- **Sample and Plot Compatibility**:
  - For `sample_type = "estimand"`, only `plot_type = "hist"` or "trace" is allowed, as these are designed to visualize the posterior distribution or MCMC trajectory of individual parameters. Parameters like `intercept`, `trt`, and `sigma` are agnostic to `effect_type` as they do not interact with exposure.

- – plot_type = "cred" is designed for use with sample_type = "fitted" or "predictive" and shows credible intervals for the outcome (y-axis) across biomarker values (x-axis) by covariate pattern. effect_type controls whether the exposure effect or main effect is displayed.

- **Effect Types**:
  - – outcome plots either the fitted or predictive values without exposure interaction, allowing for exposure (trt) values to be specified.
  - – exposure_effect plots the interaction of the exposure effect across different covariate patterns.

Value

A ggplot2 object or a grid of plots.

Examples

```
# Example dataset
data("simulated_data")

candsplinevars <- c("X_1")
candbinaryvars <- paste0("Z_", 1:5)
candinter <- c(candsplinevars, candbinaryvars)

results <- rjMCMC(simulated_data, candsplinevars, candbinaryvars, candinter,
                  outcome = "Y", factor_var = "trt")
plot(results, sample_type = "fitted", effect_type = "exposure_effect", plot_type = "cred")
plot(results, sample_type = "estimand", plot_type = "hist")
```

---

predict.rjMCMC   *Predict from Reversible Jump MCMC (rjMCMC) Model Results*

Description

This function generates posterior predictions from an rjMCMC model based on the provided data. It combines the fixed effects, spline terms, and binary parameters, and includes residual variance in the predictions.

Usage

```
## S3 method for class 'rjMCMC'
predict(object, newdata = NULL, ...)
```

Arguments

object	An object of class rjMCMC containing the output from the rjMCMC procedure, which includes:

> **fixed_param** Matrix of posterior samples for exposure intercept and main effect.
>
> **binary_param** Matrix of posterior samples for binary variable parameters.
>
> **sigma_sq** Matrix of posterior samples for the residual variance (sigma squared).
>
> **vars_prop_summ** Posterior inclusion probabilities for candidate variables.
>
> **splines_fitted** List of matrices containing fitted values for spline terms across iterations.
>
> **data_fit** Original dataset used in the rjMCMC procedure.
>
> **candsplineinter** Names of continuous candidate predictive spline variables.
>
> **candsplinevars** Names of continuous candidate spline variables.
>
> **candbinaryvars** Names of binary candidate variables.
>
> **candinter** Names of interaction terms, which can include spline variables.
>
> **mcmc_specs** MCMC sampler specifications, including the number of iterations, burn-in, thinning, and chains.

newdata	A data frame for which predictions are to be made. If NA, the original fitted data is used.
...	Additional arguments to be passed to other methods or functions.

Value

A matrix of predicted values.

Examples

```
# Example dataset
data("simulated_data")

candsplinevars <- c("X_1")
candbinaryvars <- paste0("Z_", 1:5)
candinter <- c(candsplinevars, candbinaryvars)

results <- rjMCMC(simulated_data, candsplinevars, candbinaryvars, candinter,
          outcome = "Y", factor_var = "trt")
predict(results)
```

---

predictExposureEff	*Predict Exposure Effect*

Description

This function predicts the exposure effect for new data based the Reversible Jump MCMC (rjM-CMC) results.

Usage

```
predictExposureEff(results, newdata = NULL)
```

Arguments

results   An object of class rjMCMC containing the output from the rjMCMC procedure,
                which includes:

> **fixed_param** Matrix of posterior samples for exposure intercept and main effect.
>
> **binary_param** Matrix of posterior samples for binary variable parameters.
>
> **sigma_sq** Matrix of posterior samples for the residual variance (sigma squared).
>
> **vars_prop_summ** Posterior inclusion probabilities for candidate variables.
>
> **splines_fitted** List of matrices containing fitted values for spline terms across iterations.
>
> **data_fit** Original dataset used in the rjMCMC procedure.
>
> **candsplineinter** Names of continuous candidate predictive spline variables.
>
> **candsplinevars** Names of continuous candidate spline variables.
>
> **candbinaryvars** Names of binary candidate variables.
>
> **candinter** Names of interaction terms, which can include spline variables.
>
> **mcmc_specs** MCMC sampler specifications, including the number of iterations, burn-in, thinning, and chains.

newdata   A data frame for which predicted values are to be computed If NA, the original
                fitted data is used.

Details

The function:

- Checks if the required columns in results$candinter are present in newdata.

- Computes the fitted posterior exposure effect based on main exposure effects, spline interactions, and binary interactions.

- Adds noise to the fitted posterior using the residual variance results$sigma_sq to generate predictive posterior samples.

Spline interactions are handled by interpolating the spline coefficients for the values in newdata.

Value

A matrix of predictive posterior samples for the exposure effect, where each row corresponds to a posterior sample and each column corresponds to an observation in newdata.

Examples

```
# Example dataset
data("simulated_data")

candsplinevars <- c("X_1")
```

```
candbinaryvars <- paste0("Z_", 1:5)
candinter <- c(candsplinevars, candbinaryvars)

results <- rjMCMC(simulated_data, candsplinevars, candbinaryvars, candinter,
                  outcome = "Y", factor_var = "trt")
newdata = data.frame(Z_1 = 1, Z_2 = 1, Z_3 = 1, Z_4 = 1, Z_5 = 1,
                     trt = 1, X_1 = seq(0,1,by=0.01))
predictExposureEff(results)
predictExposureEff(results,newdata)
```

---

print.rjMCMC   *Print a summary of results from from Reversible Jump MCMC (rjMCMC)*

Description

This function provides a detailed summary of the results from the rjMCMC procedure, including model information, parameter estimates, posterior inclusion probabilities, convergence diagnostics, and plots for spline terms. The function also prints the model formula with fbs() notation for spline terms, indicating the use of free-knot B-splines.

Usage

```
## S3 method for class 'rjMCMC'
print(x, ...)
```

Arguments

x   An object of class rjMCMC containing the output from the rjMCMC procedure, which includes:

    fixed_param Matrix of posterior samples for exposure intercept and main effect.

    binary_param Matrix of posterior samples for binary variable parameters.

    sigma_sq Matrix of posterior samples for the residual variance (sigma squared).

    vars_prop_summ Posterior inclusion probabilities for candidate variables.

    splines_fitted List of matrices containing fitted values for spline terms across iterations.

    data_fit Original dataset used in the rjMCMC procedure.

    candsplineinter Names of continuous candidate predictive spline variables.

    candsplinevars Names of continuous candidate spline variables.

    candbinaryvars Names of binary candidate variables.

    candinter Names of interaction terms, which can include spline variables.

    mcmc_specs MCMC sampler specifications, including the number of iterations, burn-in, thinning, and chains.

...   Additional arguments to be passed to other methods or functions.

Details

The function produces detailed summaries similar to those from `brms`, including diagnostics, estimates, posterior inclusion probabilities, and spline effects. The spline terms are wrapped in `fbs()` notation, indicating the use of free-knot B-splines in the model. If the sampler did not converge, a warning is issued. The function also allows the user to view diagnostic plots for fitted exposure effects.

Value

Prints the following summary information:

Model Formula The model formula with spline terms wrapped in `fbs()`, indicating free-knot B-splines, and interaction terms appropriately formatted.

Convergence Diagnostics Reports any convergence issues based on Geweke diagnostics.

MCMC Sampler Arguments Displays MCMC sampler arguments, including the number of posterior samples, burn-in, thinning, and chains.

Parameter Estimates Posterior mean, standard error, 95% credible intervals, effective sample size (ESS), Gelman-Rubin statistic (Rhat), and posterior inclusion probabilities (PIP) for binary parameters, exposure intercept, and exposure effect.

Gaussian Family Parameters Posterior summary for the residual standard error (sigma).

Posterior Inclusion Probabilities for Splines Prints the posterior inclusion probabilities for spline terms.

Plots for Fitted Exposure Effects Plots the mean and 95% credible intervals for each spline term vs fitted exposure effects.

Examples

```
# Example dataset
data("simulated_data")

candsplinevars <- c("X_1")
candbinaryvars <- paste0("Z_", 1:5)
candinter <- c(candsplinevars, candbinaryvars)


results <- rjMCMC(simulated_data, candsplinevars, candbinaryvars, candinter,
          outcome = "Y", factor_var = "trt")
print(results)
```

---

rhats   *Calculate and Print Rhat Diagnostics for rjMCMC Results*

Description

This function calculates the Rhat diagnostic for convergence based on the posterior samples of individual exposure effects, intercept, and main exposure effect from an rjMCMC model. It prints the median, minimum, and maximum Rhat values for the exposure effects, as well as the Rhat for the intercept and exposure effect.

Usage

```
rhats(results)
```

Arguments

results
An object of class rjMCMC containing the output from the `rjMCMC` procedure, which includes:

fixed_param Matrix of posterior samples for exposure intercept and main effect.

binary_param Matrix of posterior samples for binary variable parameters.

sigma_sq Matrix of posterior samples for the residual variance (sigma squared).

vars_prop_summ Posterior inclusion probabilities for candidate variables.

splines_fitted List of matrices containing fitted values for spline terms across iterations.

data_fit Original dataset used in the `rjMCMC` procedure.

candsplineinter Names of continuous candidate predictive spline variables.

candsplinevars Names of continuous candidate spline variables.

candbinaryvars Names of binary candidate variables.

candinter Names of interaction terms, which can include spline variables.

mcmc_specs MCMC sampler specifications, including the number of iterations, burn-in, thinning, and chains.

Details

This function calculates R-hat statistics to assess MCMC convergence for both exposure effects and model parameters. Diagnostic plots are generated to visually inspect the chains across iterations.

Value

A list containing:

Rhat_trt_eff_posterior Vector of R-hat values for each individual's exposure effect.

Rhat_inter R-hat value for the intercept parameter.

Rhat_factor_var R-hat value for the main effect of exposure.

Examples

```
# Example dataset
data("simulated_data")

candsplinevars <- c("X_1")
candbinaryvars <- paste0("Z_", 1:5)
candinter <- c(candsplinevars, candbinaryvars)

results <- rjMCMC(simulated_data, candsplinevars, candbinaryvars, candinter,
                  outcome = "Y", factor_var = "trt")
rhats(results)
```

---

rjMCMC   *Run Reversible Jump MCMC (rjMCMC) Procedure*

Description

This function performs a Reversible Jump MCMC (rjMCMC) procedure to generate the posterior distribution, using Bayesian model averaging and free-knot B-splines.

Usage

```
rjMCMC(
  data,
  candsplinevars,
  candbinaryvars,
  candinter,
  outcome,
  factor_var,
  mcmc_specs = NULL,
  prior_params = NULL
)
```

Arguments

data	A data frame containing the observations, including the following columns:
	factor_var Exposure group binary indicator.
	outcome Continuous-valued outcome.
	candsplinevars All candidate spline variables as described in candsplinevars.
	candbinaryvars All candidate binary variables as described in candbinaryvars.
candsplinevars	A vector of names for continuous predictive candidate variables (default = NULL).
candbinaryvars	A vector of names for binary predictive candidate variables (default = NULL).
candinter	A vector indicating which of the candidate variables are tailoring (default = NULL).
outcome	A string indicating the name of the continuous outcome variable in data.

factor_var   A string indicating the name of the binary exposure variable in data.

mcmc_specs   A list containing:

> **iter** Number of total iterations per chain (including warmup; default = 4000).
>
> **warmup** Number of warmup/burn-in samples per chain (default = 2000).
>
> **thin** Thinning parameter (default = 1).
>
> **chain** Number of chains (default = 4).
>
> **sigma_v** Proposal variance for "jump" terms (default = 0.1).
>
> **bma** Boolean indicating whether to include Bayesian model averaging step (default = TRUE).

prior_params   A list containing prior parameters:

> **lambda_1** Prior parameter for the number of terms in the model (default = 0.1).
>
> **lambda_2** Prior parameter for the number of knots in each spline (default = 1).
>
> **a_0** Shape parameter for inverse gamma prior on individual-level variance (default = 0.01).
>
> **b_0** Rate parameter for inverse gamma prior on individual-level variance (default = 0.01).
>
> **degree** Degree of B-splines (default = 3).
>
> **k_max** Maximum number of knots for each spline term (default = 9).
>
> **w** Window for proposing knot location changes (default = 1).
>
> **sigma_B** Prior normal variance for model coefficients (default = sqrt(20)).

Value

An rjMCMC object with the following components:

accept_var Matrix indicating the acceptance of variable inclusion/removal for each iteration.

accept_add_knot Matrix indicating acceptance of knot addition for each spline term across iterations.

accept_remove_knot Matrix indicating acceptance of knot removal for each spline term across iterations.

accept_move_knot Matrix indicating acceptance of knot movement for each spline term across iterations.

splines_fitted List of matrices, one per spline interaction term, containing fitted spline values across iterations.

binary_param Matrix containing posterior samples of binary variable parameters.

inter_trt_param Matrix containing posterior samples of the treatment intercept and main effect.

sigma_sq Matrix of posterior samples for the residual variance (sigma squared).

vars_prop Matrix indicating the inclusion of variables across iterations (1 for included, 0 for excluded).

vars_prop_summ Posterior inclusion probabilities for all candidate variables (spline and binary).

k Matrix indicating the number of knots for each spline term across iterations.

trt_eff_posterior Matrix of posterior treatment effect estimates, including spline effects.

data_fit The original dataset passed to the function.

candsplineinter A character vector indicating the spline interaction terms.

candsplinevars A character vector of candidate spline variables.

candbinaryvars A character vector of candidate binary variables.

candinter A character vector of interaction terms with treatment (can include splines and binary variables).

mcmc_specs The MCMC specifications used in the procedure.

prior_params The prior parameters used in the procedure.

References

Maleyeff, L., Golchi, S., Moodie, E. E. M., & Hudson, M. (2024) "An adaptive enrichment design using Bayesian model averaging for selection and threshold-identification of predictive variables" doi:10.1093/biomtc/ujae141

Examples

```
# Example dataset
data("simulated_data")

candsplinevars <- c("X_1")
candbinaryvars <- paste0("Z_", 1:5)
candinter <- c(candsplinevars, candbinaryvars)

results <- rjMCMC(simulated_data, candsplinevars, candbinaryvars, candinter,
                  outcome = "Y", factor_var = "trt")
```

---

simulated_data	*A synthetic dataset with continuous and binary covariates and a binary treatment variable (`trt`).*

Description

This dataset was generated using the formula: $Y = 2*Z_1 + 2*X_1 + 2*Z_1*trt + \cos(X_1 \cdot 2\pi)*trt + \epsilon$, where $\epsilon \sim N(0, 0.5)$.

Usage

```
data(simulated_data)
```

Format

A data frame with 1000 rows and 8 variables:

X_1 A continuous variable sampled from `U(0, 1)`.

Z_1 A binary variable sampled from `Bernoulli(0.35)`.

Z_2 A binary variable sampled from `Bernoulli(0.5)`.

Z_3 A binary variable sampled from `Bernoulli(0.65)`.

Z_4 A binary variable sampled from `Bernoulli(0.2)`.

Z_5 A binary variable sampled from `Bernoulli(0.35)`.

trt A binary treatment variable sampled from `Bernoulli(0.5)`.

Y The outcome variable calculated using the formula above.

Examples

```
data(simulated_data)
head(simulated_data)
```

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summary.rjMCMC *Summarize Results from Reversible Jump MCMC (rjMCMC)*

Description

This function provides a detailed summary of the results from the `rjMCMC` procedure, including model information, parameter estimates, posterior inclusion probabilities, convergence diagnostics, and plots for spline terms. The function also prints the model formula with `fbs()` notation for spline terms, indicating the use of free-knot B-splines.

Usage

```
## S3 method for class 'rjMCMC'
summary(object, digits = 3, level = 0.95, pip_cutoff = 0.1, ...)
```

Arguments

object   An object of class rjMCMC containing the output from the `rjMCMC` procedure,
              which includes:

              fixed_param Matrix of posterior samples for exposure intercept and main ef-
                  fect.

              binary_param Matrix of posterior samples for binary variable parameters.

              sigma_sq Matrix of posterior samples for the residual variance (sigma squared).

              vars_prop_summ Posterior inclusion probabilities for candidate variables.

              splines_fitted List of matrices containing fitted values for spline terms across
                  iterations.

              data_fit Original dataset used in the `rjMCMC` procedure.

> **candsplineinter** Names of continuous candidate predictive spline variables.
>
> **candsplinevars** Names of continuous candidate spline variables.
>
> **candbinaryvars** Names of binary candidate variables.
>
> **candinter** Names of interaction terms, which can include spline variables.
>
> **mcmc_specs** MCMC sampler specifications, including the number of iterations, burn-in, thinning, and chains.

`digits`	Number of digits in summary output (default = 3)
`level`	Credible interval level (default = 0.95)
`pip_cutoff`	Posterior inclusion probability cutoff for reporting effective sample size and R-squared (default = 0.10)
`...`	Additional arguments to be passed to other methods or functions.

Details

The function produces detailed summaries similar to those from `brms`, including diagnostics, estimates, posterior inclusion probabilities, and spline effects. The spline terms are wrapped in `fbs()` notation, indicating the use of free-knot B-splines in the model. If the sampler did not converge, a warning is issued. The function also allows the user to view diagnostic plots for fitted exposure effects.

Value

Prints the following summary information:

Model Formula The model formula with spline terms wrapped in `fbs()`, indicating free-knot B-splines, and interaction terms appropriately formatted.

Convergence Diagnostics Reports any convergence issues based on Geweke diagnostics.

MCMC Sampler Arguments Displays MCMC sampler arguments, including the number of posterior samples, burn-in, thinning, and chains.

Parameter Estimates Posterior mean, standard error, 95% credible intervals, effective sample size (ESS), Gelman-Rubin statistic (Rhat), and posterior inclusion probabilities (PIP) for binary parameters, exposure intercept, and exposure effect.

Gaussian Family Parameters Posterior summary for the residual standard error (sigma).

Posterior Inclusion Probabilities for Splines Prints the posterior inclusion probabilities for spline terms.

Plots for Fitted Exposure Effects Plots the mean and 95% credible intervals for each spline term vs fitted exposure effects.

Examples

```
# Example dataset
data("simulated_data")

candsplinevars <- c("X_1")
candbinaryvars <- paste0("Z_", 1:5)
candinter <- c(candsplinevars, candbinaryvars)
```

```
results <- rjMCMC(simulated_data, candsplinevars, candbinaryvars, candinter,
                  outcome = "Y", factor_var = "trt")
summary(results)
```

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