Manual of the \textit{BayesPSA} Package

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\section*{bpsa()}

\subsection*{Description}

The first step in performing a Bayesian propensity score analysis. Runs a Bayesian logistic regression on the treatment factor, either via MCMC or Bayesian Model Averaging (BMA).

\subsection*{Usage}

\begin{verbatim}
bpsa(x, response, treatment, treatment.success.level = 1, vars = names(x), exclude = NULL, prior.b0 = 0, prior.B0 = 0, mcmc.burnin = 1250, mcmc.iter = 1e+05, mcmc.thin = 100, mcmc.logfun = TRUE, mcmc.tune = 0.25, method = c("MCMC", "BMA"))
\end{verbatim}

\subsection*{Arguments}

- \texttt{\textbf{x}} a data frame containing the response, treatment and covariates for the propensity score estimation.

- \texttt{response} the name of the dependent variable one is interested in for the causal model. Can be either a column name (entered as a character string) or a column number (entered as an integer).

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treatment  the treatment variable. It is expected that ‘treatment’ will be a two-level factor. Can be either a column name (entered as a character string) or a column number (entered as an integer).

treatment.success.level which level (1 or 2) of the ‘treatment’ factor is considered to be the ‘success’ or ‘treatment’ level. Default is set to 1.

vars names of the variables to be used to calculate the propensity score. Default is set to be all the columns in x (other than ‘response’ and ‘treatment’). Can be either a vector of column names or a vector of column numbers.

exclude an optional vector of column names or vector of column indices to exclude from the logistic regression.

prior.b0 prior mean of beta under a multivariate normal prior. This can either be a scalar or a column vector with dimension equal to the number of betas. If this takes a scalar value, then that value will serve as the prior mean for all of the betas.

prior.B0 prior precision of beta under a multivariate normal prior. This can either be a scalar or a square matrix with dimensions equal to the number of betas. If this takes a scalar value, then that value times an identity matrix serves as the prior precision of beta. Default value of 0 is equivalent to an improper uniform prior for beta.

mcmc.burnin if method == ‘MCMC’, the number of iterations to throw away before sampling from the chain. Default is set to 5,000. Ignored if method == ‘BMA’.

mcmc.iter if method == ‘MCMC’, the number of iterations in the MCMC chain. Default is set to 400,000. Ignored if method == ‘BMA’.

mcmc.thin if method == ‘MCMC’, the thinning interval of the MCMC chain. Default is set to 400, which yields 1000 posterior draws in 400,000 iterations. Ignored if method == ‘BMA’.

mcmc.logfun default to TRUE. See ?MCMClogit for more details.

mcmc.tune tuning parameter for the MCMC sampling. Default to 0.25. See ?MCMClogit for more details.

Returned Values

p.score a matrix containing the estimated propensity scores.

mcmc.model if method == ‘MCMC’, the model created by MCMClogit. Otherwise NULL.

mcmc.model.matrix if method == ‘MCMC’, the model created by MCMClogit. Otherwise NULL.
\textbf{x.data} \hspace{1em} the original data frame used to in the bpsa() call.

\textbf{x.vars} \hspace{1em} a vector containing the names of the variables used as co-variates in creating the propensity score.

\textbf{response} \hspace{1em} the name of the response variable.

\textbf{treatment} \hspace{1em} the name of the treatment variable.

\section*{References}


\section*{Examples}

See example in the help page for ‘bpsa’ using ‘?bpsa’.

\begin{verbatim}
bpsa.strat()
\end{verbatim}

\section*{Description}

Performs a stratified matching using a propensity score created by calling bpsa().

\section*{Usage}

\begin{verbatim}
bpsa.strat(x, prior.b0 = 0, prior.B0 = 0, mcmc.burnin = 1000, mcmc.iter = 1000, mcmc.thin = 1)
\end{verbatim}
Arguments

- a bpsa list created by calling the function ‘bpsa()’.

prior.b0 prior mean of beta under a multivariate normal prior. This can either be a scalar or a column vector with dimension equal to the number of betas. If this takes a scalar value, then that value will serve as the prior mean for all of the betas.

prior.B0 prior precision of beta under a multivariate normal prior. This can either be a scalar or a square matrix with dimensions equal to the number of betas. If this takes a scalar value, then that value times an identity matrix serves as the prior precision of beta. Default value of 0 is equivalent to an improper uniform prior for beta.

mcmc.burnin the number of iterations to throw away before sampling from the MCMC chain in the Bayesian outcome model. Default is set to 100.

mcmc.iter the number of iterations in the MCMC chain of the Bayesian outcome model. Default is set to 1,000.

mcmc.thin the thinning interval of the MCMC chain in the Bayesian outcome model. Default is set to 1.

Returned Values

MATCHING.METHOD a character string ‘strat’, indicating stratification method is utilized.

EFFECT the posterior mean and standard deviation of causal(treatment) effect.

INTERVAL the 95% posterior probability interval.

References


Examples

See example in the help page for ‘bpsa.strat’ using ‘?bpsa.strat’.
bpsa.opt.match()

Description
Performs an optimal full matching using a propensity score created by calling bpsa(). It can be quite time-consuming when sample size is large.

Usage
bpsa.opt.match(x, prior.b0 = 0, prior.B0 = 0, mcmc.burnin = 1000, mcmc.iter = 10000, mcmc.thin = 10)

Arguments
x a bpsa list created by calling the function ‘bpsa()’.

prior.b0 prior mean of beta under a multivariate normal prior. This can either be a scalar or a column vector with dimension equal to the number of betas. If this takes a scalar value, then that value will serve as the prior mean for all of the betas.

prior.B0 prior precision of beta under a multivariate normal prior. This can either be a scalar or a square matrix with dimensions equal to the number of betas. If this takes a scalar value, then that value times an identity matrix serves as the prior precision of beta. Default value of 0 is equivalent to an improper uniform prior for beta.

mcmc.burnin the number of iterations to throw away before sampling from the MCMC chain in the Bayesian outcome model. Default is set to 100.

mcmc.iter the number of iterations in the MCMC chain of the Bayesian outcome model. Default is set to 1,000.

mcmc.thin the thinning interval of the MCMC chain in the Bayesian outcome model. Default is set to 1.

Returned Values
MATCHING.METHOD a character string ‘optimal’, indicating optimal matching method is utilized.

MATCHES.MATRIX a N by M matrix showing the labels of matched groups, where N refers to number of subjects and M refers to number of posterior draws of the propensity score. In the example, N=200 and M=1000.
**EFFECT**  the posterior mean and standard deviation of causal(treatment) effect.

**INTERVAL**  the 95% posterior probability interval.

**References**

**Examples**
See example in the help page for ‘bpsa.opt.match’ using ‘?bpsa.opt.match’.

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### cov.balance()

**Description**
Checks the balance of independent variables (covariates) used in obtaining the propensity score.

**Usage**
cov.balance(x.bpsa, x.data = NULL, x.match, check.vars = x.bpsavarg.argsX.VARS, type.vars = NULL)

**Arguments**
- **x.bpsa**  the bpsa object used for covariate balance checking.
- **x.data**  user specified data to perform balance check upon. Default NULL is to use the dataset where the propensity score was created from.
- **x.match**  the type of matching that we want to check the covariate balance upon. Can be the output object of *bpsa.strat()* for Bayesian propensity score stratification or *bpsa.opt.match()* for Bayesian optimal matching.
**check.vars**  vector of the names of which covariates in x.data we want to check.

**type.vars**  vector of characters indicating whether variables in 'check.vars' are factors or not (TRUE, FALSE) respectively. Default NULL assumes all covariates are continuous variables. Must be the same length at check.vars.

**Returned Values**

**METHOD**  a character string ‘MCMC’ or ‘BMA’, indicating which estimation method is utilized.

**IMBALANCE**  a 7 by K matrix indicating covariate balance performance, including mean of each covariate in each of the two groups, mean difference of each covariate in two groups, covariate variance in each of the two groups, Cohen’s d/standardized mean difference (proportion difference for a binary variable) and variance ratio. The number of columns, K, refers to the number of covariates being checked.

**VAR.TYPE**  a character string indicating the covariate types, binary or continuous.

**INIT.COHEN.IMBALANCE**  initial Cohen’s d averaged over all the covariates.

**INIT.VARRATIO.IMBALANCE**  initial variance ratio averaged over all the covariates.

**COHEN.MCMC**  a M by K matrix showing Cohen’s d for each covariate based on each posterior draw of the propensity score. M refers to the number of posterior draws of the propensity score and K indicates the number of covariates.

**COHEN.MEANS**  Cohen’s d averaged over all the posterior draws of the propensity score and all the covariates.

**COHEN.QUANTILES**  95% posterior probability interval of Cohen’s d averaged over all the covariates.

**MEAN.DIFF.MCMC**  a M by K matrix of mean difference for each covariate based on each posterior draw of the propensity score.

**VAR.RATIO.MCMC**  a M by K matrix showing variance ratio for each covariate based on each posterior draw of the propensity score. For some matched groups with only one subject in the treatment or control group, the variances of the covariates will be 0 and in turn an infinite variance ratio will be obtained.
**VAR.RATIO.MEANS**  Variance ratio averaged over all the posterior draws of the propensity score and all the covariates. By default, the extreme variance ratios (if any, e.g., infinite) are included in the mean calculation. Users can calculate the average variance ratio in other ways based on the variance ratio matrix by calling ‘VAR.RATIO.MCMC’.

**VAR.RATIO.QUANTILE**  95% posterior probability interval of variance ratio averaged over all the covariates.

References


Examples

See examples for `bpsa.opt.match()`.

cov.bal.plot()

Description

Produce a plot for covariate balance checking using Cohen’s d and variance ratio of covariates in two different treatment conditions (e.g., treatment group and control group).

Usage

cov.bal.plot(bal.obj, show.var.names = FALSE, point.size = 3)

Arguments

- `bal.obj`  a covariance balance check object obtained by calling `cov.balance()`.
- `show.var.names`  set to TRUE to see variable names in plot.
- `point.size`  sets the size of the points in the `ggplot`.

Returned Values

Initial covariate balance plot and covariate balance plot after Bayesian propensity score adjustment in the pop-up plot windows.
References


Examples

See examples for bpsa.opt.match().