

# Package ‘bartCause’

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**Title** Causal Inference using Bayesian Additive Regression Trees

**Depends** R (>= 3.1-0)

**Imports** dbarts (>= 0.9-16), methods, stats, graphics, parallel, utils,  
grDevices

**Suggests** testthat (>= 0.9-0), lme4, rpart, tmle, stan4bart

**Description** Contains a variety of methods to generate typical causal inference estimates using Bayesian Additive Regression Trees (BART) as the underlying regression model (Hill (2012) <[doi:10.1198/jcgs.2010.08162](https://doi.org/10.1198/jcgs.2010.08162)>).

**License** GPL (>= 2)

**NeedsCompilation** no

**URL** <https://github.com/vdorie/bartCause>

**BugReports** <https://github.com/vdorie/bartCause/issues>

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**Description**

Fits a collection of treatment and response models using the Bayesian Additive Regression Trees (BART) algorithm, producing estimates of treatment effects.

**Usage**

```
bartc(response, treatment, confounders, parametric, data, subset, weights,
      method.rsp = c("bart", "tmle", "p.weight"),
      method.trt = c("bart", "glm", "none"),
      estimand = c("ate", "att", "atc"),
      group.by = NULL,
      commonSup.rule = c("none", "sd", "chisq"),
      commonSup.cut = c(NA_real_, 1, 0.05),
      args.rsp = list(), args.trt = list(),
      p.scoreAsCovariate = TRUE, use.ranef = TRUE, group.effects = FALSE,
      crossvalidate = FALSE,
      keepCall = TRUE, verbose = TRUE,
      seed = NA_integer_,
      ...)
```

**Arguments**

response	A vector of the outcome variable, or a reference to such in the data argument. Can be continuous or binary.
treatment	A vector of the binary treatment variable, or a reference to data.
confounders	A matrix or data frame of covariates to be used in estimating the treatment and response model. Can also be the right-hand-side of a formula (e.g. $x_1 + x_2 + \dots$ ). The data argument will be searched if supplied.
parametric	The right-hand-side of a formula (e.g. $x_1 + x_2 + (1   g) \dots$ ) giving the equation of a parametric form to be used for estimating the mean structure. See the details section below.
data	An optional data frame or named list containing the response, treatment, and confounders.
subset	An optional vector using to subset the data. Can refer to data if provided.
weights	An optional vector of population weights used in model fitting and estimating the treatment effect. Can refer to data if provided.
method.rsp	A character string specifying which method to use when fitting the response surface and estimating the treatment effect. Options are: "bart" - fit the response surface with BART and take the average of the individual treatment effect estimates, "p.weight" - fit the response surface with BART but compute the treatment effect estimate by using a propensity score weighted sum of individual

effects, and "tmle" - as above, but further adjust the individual estimates using the Targeted Minimum Loss based Estimation (TMLE) adjustment.

method.trt	A character string specifying which method to use when fitting the treatment assignment mechanism, or a vector/matrix of propensity scores. Character string options are: "bart" - fit BART directly to the treatment variable, "glm" - fit a generalized linear model with a binomial response and all confounders added linearly, and "none" - do no propensity score estimation. Cannot be "none" if the response model requires propensity scores. When supplied as a matrix, it should be of dimensions equal to the number of observations times the number of samples used in any response model.
estimand	A character string specifying which causal effect to target. Options are "ate" - average treatment effect, "att" - average treatment effect on the treated, and "atc" - average treatment effect on the controls.
group.by	An optional factor that, when present, causes the treatment effect estimate to be calculated within each group.
commonSup.rule	Rule for exclusion of observations lacking in common support. Options are "none" - no suppression, "sd" - exclude units whose predicted counterfactual standard deviation is extreme compared to the maximum standard deviation under those units' observed treatment condition, where extreme refers to the distribution of all standard deviations of observed treatment conditions, "chisq" - exclude observations according to ratio of the variance of posterior predicted counterfactual to the posterior variance of the observed condition, having a Chi Squared distribution with one degree of freedom under the null hypothesis of have equal distributions.
commonSup.cut	Cutoffs for commonSup.rule. Ignored for "none", when commonSup.rule is "sd", refers to how many standard deviations of the distribution of posterior variance for counterfactuals an observation can be above the maximum of posterior variances for that treatment condition. When commonSup.rule is "chisq", is the $p$ value used for rejection of the hypothesis of equal variances.
p.scoreAsCovariate	A logical such that when TRUE, the propensity score is added to the response model as a covariate. When used, this is equivalent to the 'ps-BART' method described by described by Hahn, Murray, and Carvalho.
use.ranef	Logical specifying if group.by variable - when present - should be included as a "random" or "fixed" effect. If true, <code>rbart</code> will be used for BART models. Using random effects for treatment assignment mechanisms of type "glm" require that the <code>lme4</code> package be available.
group.effects	Logical specifying if effects should be calculated within groups if the group.by variable is provided. Response methods of "tmle" and "p.weight" are such that if group effects are calculated, then the population effect is not provided.
keepCall	A logical such that when FALSE, the call to <code>bartc</code> is not kept. This can reduce the amount of information printed by <code>summary</code> when passing in data as literals.
crossvalidate	One of TRUE, FALSE, "trt", or "rsp". Enables code to attempt to estimate the optimal end-node sensitivity parameter. This uses a rudimentary Bayesian optimization routine and can be extremely slow.

verbose	A logical that when TRUE prints information as the model is fit.
seed	Optional integer specifying the desired pRNG seed. It should not be needed when running single-threaded - <code>set.seed</code> will suffice, and can be used to obtain reproducible results when multi-threaded. See Reproducibility section of <code>bart2</code> .
args.rsp, args.trt, ...	Further arguments to the treatment and response model fitting algorithms. Arguments passed to the main function as ... will be used in both models. <code>args.rsp</code> and <code>args.trt</code> can be used to set parameters in a single fit, and will override other values. See <code>glm</code> and <code>bart2</code> for reference.

## Details

`bartc` represents a collection of methods that primarily use the Bayesian Additive Regression Trees (BART) algorithm to estimate causal treatment effects with binary treatment variables and continuous or binary outcomes. This requires models to be fit to the response surface (distribution of the response as a function of treatment and confounders,  $p(Y(1), Y(0)|X)$ ) and optionally for treatment assignment mechanism (probability of receiving treatment, i.e. propensity score,  $Pr(Z = 1|X)$ ). The response surface model is used to impute counterfactuals, which may then be adjusted together with the propensity score to produce estimates of effects.

Similar to `lm`, models can be specified symbolically. When the data term is present, it will be added to the search path for the response, treatment, and confounders variables. The confounders must be specified devoid of any "left hand side", as they appear in both of the models.

### Response Surface

The response surface methods included are:

- "bart" - use BART to fit the response surface and produce individual estimates  $\hat{Y}(1)_i$  and  $\hat{Y}(0)_i$ . Treatment effect estimates are obtained by averaging the difference of these across the population of interest.
- "p.weight" - individual effects are estimated as in "bart", but treatment effect estimates are obtained by using a propensity score weighted average. For the average treatment effect on the treated, these weights are  $p(z_i|x_i)/(\sum z/n)$ . For ATC, replace  $z$  with  $1 - z$ . For ATE, "p.weight" is equal to "bart".
- "tmle" - individual effects are estimated as in "bart" and a weighted average is taken as in "p.weight", however the response surface estimates and propensity scores are corrected by using the Targeted Minimum Loss based Estimation method.

### Treatment Assignment

The treatment assignment models are:

- "bart" - fit a binary BART directly to the treatment using all the confounders.
- "none" - no modeling is done. Only applies when using response method "bart" and `p.scoreAsCovariate` is FALSE.
- "glm" - fit a binomial generalized linear model with logistic link and confounders included as linear terms.
- Finally, a vector or matrix of propensity scores can be supplied. Propensity score matrices should have a number of rows equal to the number of observations in the data and a number of columns equal to the number of posterior samples.

### Parametrics

bartc uses the stan4bart package, when available, to fit semi-parametric surfaces. Equations can be given as to `lm`. Grouping structures are also permitted, and use the syntax of `lmer`.

### Generics

For a fitted model, the easiest way to analyze the resulting fit is to use the `generics` `fitted`, `extract`, and `predict` to analyze specific quantities and `summary` to aggregate those values into targets (e.g. ATE, ATT, or ATC).

### Common Support Rules

Common support, or that the probability of receiving all treatment conditions is non-zero within every area of the covariate space ( $P(Z = 1|X = x) > 0$  for all  $x$  in the inferential sample), can be enforced by excluding observations with high posterior uncertainty. bartc supports two common support rules through `commonSup.rule` argument:

- "sd" - observations are cut from the inferential sample if:  $s_i^{f(1-z)} > m_z + a \times sd(s_j^{f(z)})$ , where  $s_i^{f(1-z)}$  is the posteriors standard deviation of the predicted counterfactual for observation  $i$ ,  $s_j^{f(z)}$  is the posterior standard deviation of the prediction for the observed treatment condition of observation  $j$ ,  $sd(s_j^{f(z)})$  is the empirical standard deviation of those quantities, and  $m_z = \max_j \{s_j^{f(z)}\}$  for all  $j$  in the same treatment group, i.e.  $Z_j = z$ .  $a$  is a constant to be passed in using `commonSup.cut` and its default is 1.
- "chisq" - observations are cut from the inferential sample if:  $(s_i^{f(1-z)} / s_i^{f(z)})^2 > q_\alpha$ , where  $s_i$  are as above and  $q_\alpha$ , is the upper  $\alpha$  percentile of a  $\chi^2$  distribution with one degree of freedom, corresponding to a null hypothesis of equal variance. The default for  $\alpha$  is 0.05, and it is specified using the `commonSup.cut` parameter.

### Special Arguments

Some default arguments are unconventional or are passed in a unique fashion.

- If `n.chains` is missing, unlike in `bart2` a default of 10 is used.
- For `method.rsp == "tmle"`, a special arg. `trt` of `posteriorOfTMLE` determines if the TMLE correction should be applied to each posterior sample (TRUE), or just the posterior mean (FALSE).

### Missing Data

Missingness is allowed only in the response. If some response values are NA, the BART models will be trained just for where data are available and those values will be used to make predictions for the missing observations. Missing observations are not used when calculating statistics for assessing common support, although they may still be excluded on those grounds. Further, missing observations may not be compatible with response method "tmle".

### Value

bartc returns an object of class `bartcFit`. Information about the object can be derived by using methods `summary`, `plot_sigma`, `plot_est`, `plot_indiv`, and `plot_support`. Numerical quantities are recovered with the `fitted` and `extract` generics. Predictions for new observations are obtained with `predict`.

Objects of class `bartcFit` are lists containing items:

<code>method.rsp</code>	character string specifying the method used to fit the response surface
<code>method.trt</code>	character string specifying the method used to fit the treatment assignment mechanism
<code>estimand</code>	character string specifying the targeted causal effect
<code>fit.rsp</code>	object containing the fitted response model
<code>data.rsp</code>	<code>dbartsData</code> object used when fitting the response model
<code>fit.trt</code>	object containing the fitted treatment model
<code>group.by</code>	optional factor vector containing the groups in which treatment effects are estimated
<code>est</code>	matrix or array of posterior samples of the treatment effect estimate
<code>p.score</code>	the vector of propensity scores used as a covariate in the response model, when applicable
<code>samples.p.score</code>	matrix or array of posterior samples of the propensity score, when applicable
<code>mu.hat.obs</code>	samples from the posterior of the expected value for individual responses under the observed treatment regime
<code>mu.hat.cf</code>	samples from the posterior of the expected value for individual responses under the counterfactual treatment
<code>name.trt</code>	character string giving the name of the treatment variable in the data of <code>fit.rsp</code>
<code>trt</code>	vector of treatment assignments
<code>call</code>	how <code>bartc</code> was called
<code>n.chains</code>	number of independent posterior sampler chains in response model
<code>commonSup.rule</code>	common support rule used for suppressing observations
<code>commonSup.cut</code>	common support parameter used to set cutoff when suppressing observations
<code>sd.obs</code>	vector of standard deviations of individual posterior predictors for observed treatment conditions
<code>sd.cf</code>	vector of standard deviations of individual posterior predictors for counterfactuals
<code>commonSup.sub</code>	logical vector expressing which observations are used when estimating treatment effects
<code>use.ranef</code>	logical for whether ranef models were used; only added when true
<code>group.effects</code>	logical for whether group-level estimates are made; only added when true
<code>seed</code>	a random seed for use when drawing from the posterior predictive distribution

**Author(s)**

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## References

- Chipman, H., George, E. and McCulloch R. (2010) BART: Bayesian additive regression trees. *The Annals of Applied Statistics* **4**(1), 266–298. The Institute of Mathematical Statistics. doi:[10.1214/09AOAS285](https://doi.org/10.1214/09AOAS285).
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- Hill, J. L. and Su Y. S. (2013) Assessing Lack of Common Support in Causal Inference Using Bayesian Nonparametrics: Implications for Evaluating the Effect of Breastfeeding on Children’s Cognitive Outcomes *The Annals of Applied Statistics* **7**(3), 1386–1420. The Institute of Mathematical Statistics. doi:[10.1214/13AOAS630](https://doi.org/10.1214/13AOAS630).
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- Hahn, P. R., Murray, J. S., and Carvalho, C. M. (2020) Bayesian Regression Tree Models for Causal Inference: Regularization, Confounding, and Heterogeneous Effects (with Discussion). *Bayesian Analysis* **15**(3), 965–1056. International Society for Bayesian Analysis. doi:[10.1214/19BA1195](https://doi.org/10.1214/19BA1195).

## See Also

[bart2](#)

## Examples

```
## fit a simple linear model
n <- 100L
beta.z <- c(.75, -0.5, 0.25)
beta.y <- c(.5, 1.0, -1.5)
sigma <- 2

set.seed(725)
x <- matrix(rnorm(3 * n), n, 3)
tau <- rgamma(1L, 0.25 * 16 * rgamma(1L, 1 * 32, 32), 16)

p.score <- pnorm(x %*% beta.z)
z <- rbinom(n, 1, p.score)

mu.0 <- x %*% beta.y
mu.1 <- x %*% beta.y + tau

y <- mu.0 * (1 - z) + mu.1 * z + rnorm(n, 0, sigma)

# low parameters only for example
fit <- bartc(y, z, x, n.samples = 100L, n.burn = 15L, n.chains = 2L)
summary(fit)

## example to show refitting under the common support rule
fit2 <- refit(fit, commonSup.rule = "sd")
fit3 <- bartc(y, z, x, subset = fit2$commonSup.sub,
             n.samples = 100L, n.burn = 15L, n.chains = 2L)
```

**Description**

Visual exploratory data analysis and model fitting diagnostics for causal inference models fit using the `bartc` function.

**Usage**

```
## S3 method for class 'bartcFit'
fitted(object,
  type = c("pate", "sate", "cate", "mu.obs", "mu.cf", "mu.0",
           "mu.1", "y.cf", "y.0", "y.1", "icate", "ite",
           "p.score", "p.weights"),
  sample = c("inferential", "all"),
  ...)

extract(object, ...)

## S3 method for class 'bartcFit'
extract(object,
  type = c("pate", "sate", "cate", "mu.obs", "mu.cf", "mu.0",
           "mu.1", "y.cf", "y.0", "y.1", "icate", "ite",
           "p.score", "p.weights", "sigma"),
  sample = c("inferential", "all"),
  combineChains = TRUE,
  ...)

## S3 method for class 'bartcFit'
predict(object, newdata,
  group.by,
  type = c("mu", "y", "mu.0", "mu.1", "y.0", "y.1", "icate", "ite",
           "p.score"),
  combineChains = TRUE,
  ...)

refit(object, newresp, ...)

## S3 method for class 'bartcFit'
refit(object,
  newresp = NULL,
  commonSup.rule = c("none", "sd", "chisq"),
  commonSup.cut = c(NA_real_, 1, 0.05),
  ...)
```



**Arguments**

object	Object of class <code>bartcFit</code> .
type	Which quantity to return. See details for a description of possible values.
sample	Return information for either the "inferential" (e.g. treated observations when the estimand is <code>att</code> ) or "all" observations.
combineChains	If the models were fit with more than one chain, results retain the chain structure unless <code>combineChains</code> is <code>TRUE</code> .
newresp	Not presently used, but provided for compatibility with other definitions of the <code>refit</code> generic.
newdata	Data corresponding to the confounders in a <code>bartc</code> fit.
group.by	Optional grouping variable. See definition of <code>group.by</code> in <code>bartc</code> .
commonSup.rule, commonSup.cut	As in <code>bartc</code> .
...	Additional parameters passed up the generic method chain.

**Details**

`fitted` returns the values that would serve as predictions for an object returned by the `bartc` function, while `extract` instead returns the full matrix or array of posterior samples. The possible options are:

- "pate", "sate", "cate" - various target quantities; see [summary](#)
- "mu" - predict only: expected value; requires user-supplied treatment variable in `newdata`
- "y" - predict only: sample of the response; requires user-supplied treatment variable in `newdata`
- "mu.obs" - (samples from the posterior of) the expected value under the observed treatment condition, i.e.  $\hat{m}u_i(1) * z_i + \hat{m}u_i(0) * (1 - z_i)$
- "mu.cf" - the expected value under the counterfactual treatment condition, i.e.  $\hat{m}u_i(1) * (1 - z_i) + \hat{m}u_i(0) * z_i$
- "mu.0" - the expected value under the control condition
- "mu.1" - the expected value under the treated condition
- "y.cf" - samples of the response under the the counterfactual treatment condition, i.e.  $\hat{y}_i(1 - z_i)$ ; values are obtained by adding noise to `mu.cf` using the posterior predictive distribution
- "y.0" - observed responses under the control together with predicted under the treated, i.e.  $\hat{y}_i(1) * z_i + y(0) * (1 - z_i)$
- "y.1" - observed responses under the treatment together with predicted under the control, i.e.  $y_i(1) * z_i + \hat{y}(0) * (1 - z_i)$
- "ite" - (sample) individual treatment effect estimates, i.e.  $(y_i(z_i) - y_i(1 - z_i)) * (2z_i - 1)$ ; uses observed responses and posterior predicted counterfactuals
- "icate" - individual conditional average treatment effect estimates, i.e.  $\hat{m}u_i(1) - \hat{m}u_i(0)$
- "p.score" - probability that each observation is assigned to the treatment group
- "p.weights" - weights assigned to each individual difference if the response method is "p.weight"

- "sigma" - residual standard deviation from continuous response models

refit exists to allow the same regressions to be used to calculate estimates under different common support rules. To refit those models on a subset, see the examples in [bartc](#).

predict allows the fitted model to be used to make predictions on an out-of-sample set. Requires model to be fit with keepTrees equal to TRUE. As 'y' values are all considered out of sample, the posterior predictive distribution is always used when relevant.

### Value

For fitted, extract, and predict, a matrix, array, or vector depending on the dimensions of the result and the number of chains. For the following, when n.chains is one the dimension is dropped.

- "pate", "sate", or "cate" - with fitted, a scalar; with extract, n.chains x n.samples
- "p.score" - depending on the fitting method, samples may or not be present; when samples are absent, a vector is returned for both functions; when present, the same as "y".
- all other types - with fitted, a vector of length equal to the number of observations (n.obs); with extract or predict, a matrix or array of dimensions n.chains x n.samples x n.obs.

For refit, an object of class bartcFit.

### Author(s)

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### See Also

[bartc](#)

### Examples

```
## fit a simple linear model
n <- 100L
beta.z <- c(.75, -0.5, 0.25)
beta.y <- c(.5, 1.0, -1.5)
sigma <- 2

set.seed(725)
x <- matrix(rnorm(3 * n), n, 3)
tau <- rgamma(1L, 0.25 * 16 * rgamma(1L, 1 * 32, 32), 16)

p.score <- pnorm(x %*% beta.z)
z <- rbinom(n, 1, p.score)

mu.0 <- x %*% beta.y
mu.1 <- x %*% beta.y + tau

y <- mu.0 * (1 - z) + mu.1 * z + rnorm(n, 0, sigma)

# low parameters only for example
fit <- bartc(y, z, x, n.samples = 100L, n.burn = 15L, n.chains = 2L)
```

```

# compare fit to linear model
lm.fit <- lm(y ~ z + x)

plot(fitted(fit, type = "mu.obs"), fitted(lm.fit))

# rank order sample individual treatment effect estimates and plot
ites <- extract(fit, type = "ite")
ite.m <- apply(ites, 2, mean)
ite.sd <- apply(ites, 2, sd)
ite.lb <- ite.m - 2 * ite.sd
ite.ub <- ite.m + 2 * ite.sd

ite.o <- order(ite.m)

plot(NULL, type = "n",
      xlim = c(1, length(ite.m)), ylim = range(ite.lb, ite.ub),
      xlab = "effect order", ylab = "individual treatment effect")
lines(rbind(seq_along(ite.m), seq_along(ite.m), NA),
      rbind(ite.lb[ite.o], ite.ub[ite.o], NA), lwd = 0.5)
points(seq_along(ite.m), ite.m[ite.o], pch = 20)

```

---

bartc-plot

*Plot methods for bartc*


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## Description

Visual exploratory data analysis and model fitting diagnostics for causal inference models fit using the [bartc](#) function.

## Usage

```

plot_sigma(x, main = "Traceplot sigma",
           xlab = "iteration", ylab = "sigma",
           lty = 1:x$n.chains,
           ...)

plot_est(x, main = paste("Traceplot", x$estimand),
         xlab = "iteration", ylab = x$estimand,
         lty = 1:x$n.chains, col = NULL,
         ...)

plot_indiv(x, main = "Histogram Individual Quantities",
           type = c("icate", "mu.obs", "mu.cf", "mu.0",
                   "mu.1", "y.cf", "y.0", "y.1", "ite"),
           xlab = "treatment effect",
           breaks = 20,
           ...)

```

```
plot_support(x, main = "Common Support Scatterplot",
            xvar = "tree.1", yvar = "tree.2",
            sample = c("inferential", "all"),
            xlab = NULL, ylab = NULL,
            pch.trt = 21, bg.trt = "black",
            pch.ctl = pch.trt, bg.ctl = NA,
            pch.sup = pch.trt, bg.sup = NA, col.sup = "red", cex.sup = 1.5,
            legend.x = "topleft", legend.y = NULL,
            ...)
```

### Arguments

<code>x</code>	Object of class <code>bartcFit</code> .
<code>main</code>	Character title of plot.
<code>xlab</code>	Character label of $x$ axis. For <code>plot_support</code> , if <code>NULL</code> a default will be used.
<code>ylab</code>	Character label of $y$ axis. For <code>plot_support</code> , if <code>NULL</code> a default will be used.
<code>lty</code>	For line plots ( <code>plot_sigma</code> , <code>plot_est</code> ), models use the values of <code>lty</code> to visually distinguish each chain.
<code>col</code>	For line plots, use <code>col</code> vector to distinguish between groups (if any).
<code>breaks</code>	Argument to <code>hist</code> .
<code>type</code>	The individual quantity to be plotted. See <code>fitted</code> .
<code>xvar</code>	Variable for use on $x$ axis. Can be one of <code>"tree.XX"</code> , <code>"pca.XX"</code> , <code>"css"</code> , any individual level quantity accepted by <code>fitted</code> , the number or name of a column used to fit the response model, or a given vector. See below for details.
<code>sample</code>	Return information for either the <code>"inferential"</code> (e.g. treated observations when the estimand is <code>att</code> ) or <code>"all"</code> observations.
<code>yvar</code>	Variable for use on the $y$ axis, of the same form as <code>xvar</code> .
<code>pch.trt</code>	<code>pch</code> point value used when plotting treatment observations.
<code>bg.trt</code>	<code>bg</code> background value used when plotting treatment observations.
<code>pch.ctl</code>	<code>pch</code> point value used when plotting control observations.
<code>bg.ctl</code>	<code>bg</code> background value used when plotting treatment observations.
<code>pch.sup</code>	<code>pch</code> point value used when plotting suppressed observations.
<code>bg.sup</code>	<code>bg</code> background value used when plotting suppressed observations.
<code>col.sup</code>	<code>col</code> color value used when plotting suppressed observations.
<code>cex.sup</code>	<code>cex</code> size value used when plotting suppressed observations.
<code>legend.x</code>	<code>x</code> value passed to <code>legend</code> . If <code>NULL</code> , legend plotting is skipped.
<code>legend.y</code>	Optional <code>y</code> value passed to <code>legend</code>
<code>...</code>	Optional graphical parameters.

## Details

Produces various plots using objects fit by `bartc`. `plot_sigma` and `plot_est` are traditional parameter trace plots that can be used to diagnose the convergence of the posterior sampler. If the `bartc` model is fit with `n.chains` greater than one, by default each chain will be plotted with its own line type.

`plot_indiv` produces a simple histogram of the distribution of the estimates of the individual effects, taken as the average of their posterior samples.

`plot_support` is used to visualize the common support diagnostic in the form of a scatterplot. Points that the diagnostic excludes are outlined in red. The contents of the  $x$  and  $y$  axes are controlled by the `xvar` and `yvar` arguments respectively and can be of the form:

- "tree.XX" - Variable number "XX" as selected by variable importance in predicting individual treatment effects using a tree fit by `rpart`. "XX" must be a number not exceeding the number of continuous variables used to fit the response model.
- "pca.XX" - "XX"th principal component axis.
- "css" - The common support statistic.
- "y" - Observed response variable.
- "y0" - Predicted values for the response under the control as obtained by `fitted`.
- "y1" - Predicted values for the response under the treatment `fitted`.
- "indiv.diff" - Individual treatment effect estimates, or  $\hat{y}(1) - \hat{y}(0)$ .
- "p.score" - Propensity score used to fit the response model (if applicable).
- "p.weights" - Weights used when taking average of individual differences for response method "p.weight".
- predictor columns - Given by name or number.
- supplied vector - Any vector of length equal to the number of observations.

## Value

None, although plotting occurs as a side-effect.

## Author(s)

Vincent Dorie: <vdorie@gmail.com>.

## See Also

[bartc](#)

## Examples

```
# generate fake data using a simple linear model
n <- 100L
beta.z <- c(.75, -0.5, 0.25)
beta.y <- c(.5, 1.0, -1.5)
sigma <- 2
```

```

set.seed(725)
x <- matrix(rnorm(3 * n), n, 3)
tau <- rgamma(1L, 0.25 * 16 * rgamma(1L, 1 * 32, 32), 16)

p.score <- pnorm(x %*% beta.z)
z <- rbinom(n, 1, p.score)

mu.0 <- x %*% beta.y
mu.1 <- x %*% beta.y + tau

y <- mu.0 * (1 - z) + mu.1 * z + rnorm(n, 0, sigma)

# run with low parameters only for example
fit <- bartc(y, z, x, n.samples = 100L, n.burn = 15L, n.chains = 2L,
            n.threads = 1L,
            commonSup.rule = "sd")

## plot specific functions

# sigma plot can be used to access convergence of chains
plot_sigma(fit)

# show points lacking common support
plot_support(fit, xvar = "tree.1", yvar = "css", legend.x = NULL)

# see example in ?"bartc-generics" for rank-ordered individual effects plot

```

---

summary.bartcFit

*Summary for bartcFit Objects*


---

## Description

Summarizes bartc fits by calculating target quantities and uncertainty estimates.

## Usage

```

## S3 method for class 'bartcFit'
summary(object,
        target = c("pate", "sate", "cate"),
        ci.style = c("norm", "quant", "hpd"), ci.level = 0.95,
        pate.style = c("ppd", "var.exp"),
        ...)

```

## Arguments

object	Object of class bartcFit.
target	Treatment effect to calculate. One of "pate" - population average treatment effect, "sate" - sample average treatment effect, and "cate" - conditional average treatment effect.

ci.style	Means of calculating confidence intervals (posterior credible regions). Options include "norm" - use a normal approximation, "quant" - the empirical quantiles of the posterior samples, and "hpd" - region of highest posterior density.
ci.level	Level of confidence for intervals.
pate.style	For target "pate", calculate uncertainty by using "ppd" - the posterior predictive distribution or "var.exp" a variance expansion formula.
...	Not used at moment, but present to match summary generic signature.

## Details

summary produces a numeric and qualitative summary of a [bartc](#) fit.

### Target Types

The SATE and PATE involve calculating predicted response values under different treatment conditions. When using [extract](#) or [fitted](#), these values are simulated directly from the posterior predictive distribution. However, since these quantities all have the same expected value, in order to provide consistent results summary only uses those simulations to derive credible intervals. Thus the estimates for CATE, SATE, and PATE all should be reported as the same but with increasing degrees of uncertainty.

### Grouped Data

If a model is fit with a supplied grouping variable and `group.effects = TRUE`, the estimates will also be reported within groups. When possible, the last line corresponds to the population. Within group estimates for response methods such as "tmle" cannot easily be extrapolated to the population at large - the means will combine based on the sample sizes but the uncertainty estimates will lack correlations.

## Value

An object of class `bartcFit.summary` equivalent to a list with named items:

call	how <code>bartc</code> was called
method.rsp	character string specifying the method used to fit the response surface
method.trt	character string specifying the method used to fit the treatment assignment mechanism
ci.info	a named list with items <code>target</code> , <code>ci.style</code> , <code>ci.level</code> , and <code>pate.style</code> as passed to <code>summary</code>
n.obs	total number of observations
n.samples	number of samples within any one chain
n.chains	total number of chains
commonSup.rule	common support rule used when fitting object to produce estimates
estimates	a <code>data.frame</code> with columns "estimate" - the target, "sd" - standard deviation of posterior of estimate, "ci.lower" - lower bound of credible region, "ci.upper" - upper bound of credible region, and optionally "n.cut" - how many observations were dropped using common support rule

**Author(s)**

Vincent Dorie: <vdorie@gmail.com>.



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