

Package ‘bartcs’

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Title Bayesian Additive Regression Trees for Confounder Selection

Version 0.0.0.9000

Description Fit Bayesian Additive Regression Trees (BART) models to select confounders and estimate treatment effect.

License GPL (>= 3)

URL <https://github.com/yooyh/bartcs>

BugReports <https://github.com/yooyh/bartcs/issues>

Depends R (>= 2.10)

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bartcs-package

bartcs: Bayesian Nonparametric Adjustment of Confounding

Description

Functions in bartcs serve one of three purposes.

1. Functions for fitting: `sbart()`, `mbart()`.
2. Functions for summary: `summary()`, `gelman_rubin()`, `plot()`
3. Util function for openMP: `count_omp_thread()`

bart

Fit BART models to select confounders and estimate treatment effect

Description

Fit Bayesian Regression Additive Trees (BART) models to select relevant confounders among a large set of potential confounders and to estimate average treatment effect ($Y(1) - Y(0)$).

Usage

```
sbart(
  Y, trt, X,
  trt_treated      = 1,
  trt_control      = 0,
  num_tree         = 50,
  num_chain        = 4,
  num_burn_in      = 100,
  num_thin         = 0,
  num_post_sample  = 100,
  step_prob        = c(0.28, 0.28, 0.44),
  alpha            = 0.95,
  beta             = 2,
  nu               = 3,
  q                = 0.95,
  dir_alpha        = 5,
  boot_size        = NULL,
  parallel         = NULL,
  verbose          = TRUE
)
```

```
mbart(
  Y, trt, X,
  trt_treated      = 1,
  trt_control      = 0,
  num_tree         = 50,
  num_chain        = 4,
  num_burn_in      = 100,
  num_thin         = 0,
```

```

num_post_sample = 100,
step_prob       = c(0.28, 0.28, 0.44),
alpha          = 0.95,
beta           = 2,
nu             = 3,
q              = 0.95,
dir_alpha      = 5,
boot_size      = NULL,
parallel       = NULL,
verbose        = TRUE
)

```

Arguments

Y	Outcome variable.
trt	Treatment variable.
X	Potential confounders.
trt_treated	Value of trt for treated group.
trt_control	Value of trt for control group.
num_tree	Number of trees in BART model.
num_chain	Number of MCMC chains. Need to set num_chain > 1 for Gelman-Rubin diagnostic.
num_burn_in	Number of MCMC samples to be discarded per chain as initial burn-in periods.
num_thin	Number of thinning per chain. One in every num_thin samples are selected.
num_post_sample	Final number of posterior samples per chain. Number of MCMC iterations per chain is burn_in + num_thin * num_post_sample.
step_prob	A vector of tree alteration probabilities (GROW, PRUNE, CHANGE). Each alteration is proposed to change the tree structure. Default setting is (0.28, 0.28, 0.44).
alpha, beta	Hyperparameters for tree regularization prior. A terminal node of depth d will split with probability of $\alpha * (1 + d)^{-\beta}$.
nu, q	Values to calibrate hyperparameter of sigma prior. Default setting is (nu, q) = (3, 0.95) from Chipman et al. 2010
dir_alpha	Hyperparameter of Dirichlet prior for selection probabilities.
boot_size	Number of bootstrap sample size. Bootstrap samples will be used to compute potential outcomes $Y(1)$ and $Y(0)$.
parallel	If TRUE, model fitting will be parallelized with respect to $n = \text{nrow}(X)$. Parallelization is recommended for very high n only.
verbose	If TRUE, message will be printed during training. If FALSE, message will be suppressed.

Details

`sbart()` and `mbart()` fit an exposure model and outcome model(s) for estimating treatment effect with adjustment of confounders in the presence of a large set of potential confounders (Kim et al. 2022).

The exposure model $E[A|X]$ and the outcome model(s) $E[Y|A, X]$ are linked together with a common Dirichlet prior accrues posterior selection probability to confounders (X) on the basis of association with both the exposure (A) and the outcome (Y).

There is a distinction between fitting each outcome model for the treated and control groups and fitting a single outcome model for the entire sample.

- `sbart()` specifies two **"separate"** outcome models for two binary treatment levels. Thus, it fits three models: one exposure model and two separate outcomes for $A = 0, 1$.
- `mbart()` specifies a single **"marginal"** outcome models. Thus, it fits two models: one exposure model and one outcome model for the entire sample.

All inferences are made with outcome models.

Value

`bartcs` object is a list with following components.

ATE	Posterior samples of average treatment effect ($Y(1) - Y(0)$).
Y1	Posterior samples of potential outcome $Y(1)$.
Y0	Posterior samples of potential outcome $Y(0)$.
var_prob	Posterior inclusion probability of each variable.
chains	Result of each MCMC chain. Each list element consists of followings. <ul style="list-style-type: none"> • ATE Posterior sample of average treatment effect ($Y(1) - Y(0)$). • Y1 Posterior sample of potential outcome $Y(1)$. • Y0 Posterior sample of potential outcome $Y(0)$. • var_prob Posterior inclusion probability of each variable. • var_count Number of selection of each variable in each MCMC iteration. Its dimension is <code>num_post_sample * ncol(X)</code>. • sigma2_out Posterior samples of sigma2 in the outcome model. • dir_alpha Posterior samples of dir_alpha.
model	<code>sbart</code> or <code>mbart</code>
label	Column names of X .
params	Parameters used in the model.

References

- Chipman, H. A., George, E. I., & McCulloch, R. E. (2010). BART: Bayesian additive regression trees. *The Annals of Applied Statistics*, 4(1), 266-298. doi:10.1214/09AOAS285
- Kim, C., Tec, M., & Zigler, C. M. (2022). Bayesian Nonparametric Adjustment of Confounding. *arXiv preprint arXiv:2203.11798*. doi:10.48550/arXiv.2203.11798

count_omp_thread	<i>Count number of threads for parallel computation</i>
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Description

`count_omp_thread` counts the number of threads for parallel computation using openMP. If it returns 1, openMP is not viable.

Usage

```
count_omp_thread()
```

gelman_rubin	<i>Gelman-Rubin diagnostic for bartcs objects.</i>
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Description

gelman_rubin() computes Gelman-Rubin diagnostic for bartcs objects.

Usage

```
gelman_rubin(x)
```

Arguments

x bartcs object

Value

Gelman-Rubin diagnostic value

ihdp	<i>Infant Health and Development Program Data</i>
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Description

Infant Health and Development Program (IHDP) is a randomized experiment from 1985 to 1988 which study the effect of home visits on cognitive test scores for infants.

Usage

```
ihdp
```

Format

An object of class `data.frame` with 747 rows and 30 columns.

Details

This dataset was first used by Hill (2011), then used by others researchers like Shilita et al (2016) and Louizos et al. (2017).

Our version of dataset is a the dataset used by Louizos et al. (2017). This is the first realization of 10 generated datasets and you can find other realizations at from [here](#).

References

- Hill, J. L. (2011). Bayesian nonparametric modeling for causal inference. *Journal of Computational and Graphical Statistics*, 20(1), 217-240. doi:10.1198/jcgs.2010.08162
- Louizos, C., Shalit, U., Mooij, J. M., Sontag, D., Zemel, R., & Welling, M. (2017). Causal effect inference with deep latent-variable models. *Advances in neural information processing systems*, 30. doi:10.48550/arXiv.1705.08821 <https://github.com/AMLab-Amsterdam/CEVAE>
- Shalit, U., Johansson, F. D., & Sontag, D. (2017, July). Estimating individual treatment effect: generalization bounds and algorithms. In *International Conference on Machine Learning* (pp. 3076-3085). PMLR. doi:10.48550/arXiv.1606.03976

plot.bartcs	<i>Draw plot for bartcs object</i>
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Description

Two options are available: posterior inclusion probability (pip) plot and trace plot.

Usage

```
## S3 method for class 'bartcs'
plot(x, method = NULL, parameter = NULL, ...)
```

Arguments

x	bartcs object
method	"pip" for posterior inclusion probability plot or "trace" for trace plot.
parameter	Target of parameter for traceplot.
...	Additional arguments for pip plot. Check ?ggcharts::bar_chart for possible arguments.

Details

PIP plot:

When a posterior sample is sampled during training, sbart() or mbart() also count which variable is included in the model and compute pip for each variable. For bartcs object x, this is stored in x\$var_count and x\$var_prob respectively. plot(method = "pip") uses this information and draw plot using ggcharts::bar_chart().

Traceplot:

Parameters are recorded for each MCMC iterations. Parameters include "ATE", "Y1", "Y0", "dir_alpha", and either "sigma2_out" from mbart() or "sigma2_out1" and "sigma2_out0" from sbart(). Vertical line indicates burn-in.

Examples

```
# `x` is a bartcs object

# # pip plot
# plot(x, method = "pip")
# plot(x, method = "pip", top_n = 10)
# plot(x, method = "pip", threshold = 0.5)
# Check `?ggcharts::bar_chart` for other possible arguments.

# # trace plot
# plot(x, method = "trace")
# plot(x, method = "trace", "Y1")
# plot(x, method = "trace", "dir_alpha")
```

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