

CRE: A R package for interpretable inference of heterogeneous treatment effects

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Summary

In health and social sciences, it is critically important to identify subgroups of the study population where a treatment has notable heterogeneity in the causal effects with respect to the average treatment effect. The bulk of heterogeneous treatment effect (HTE) literature focuses on two major tasks (Dwivedi et al., 2020): (i) estimating HTEs by examining the conditional average treatment effect (CATE); (ii) discovering subgroups of a population characterized by HTE. Several methodologies have been proposed for both tasks, but providing interpretability in the results is still an open challenge. Interpretability is a non-mathematical concept, yet it is often defined as the degree to which a human can understand the cause of a decision (Kim et al., 2016), (Miller, 2019), (Lakkaraju et al., 2016), (Wang & Rudin, 2022). Honest Causal Tree (Athey & Imbens, 2016) fits this definition perfectly, but despite its high interpretability, it tends to be highly unstable and to find an oversimplified representation of treatment heterogeneity. To accommodate these shortcomings, Bargagli-Stoffi et al. (2023) proposed Causal Rule Ensemble, a new method for HTE characterization in terms of decision rules, via an extensive exploration of heterogeneity patterns by an ensemble-of-trees approach, enforcing high stability in the discovery. CRE is an R Package providing a flexible implementation of the Causal Rule Ensemble algorithm.

Algorithm

Causal Rule Ensemble relies on the Treatment Effect linear decomposition assumption, characterizing the Conditional Average Treatment Effect (CATE) by $M + 1$ distinct contributions:

$$\tau(x) = \mathbb{E}[\tau_i | X_i = x] = \bar{\tau} + \sum_{m=1}^M \alpha_m \cdot r_m(x)$$

where $\bar{\tau}$ is the Average Treatment Effect (ATE), and for each m in $\{1, \dots, M\}$, r_m is an interpretable decision rule characterizing a specific subset of the covariate space, and α_m is the corresponding Additive Average Treatment Effect. CRE procedure is divided into two steps, discovery and estimation, and each observation is used for only one of the two steps (honest splitting). During the discovery step, CRE retrieves the M decision rules characterizing the heterogeneity in the treatment effect. A set of candidate decision rules is extracted by an ensemble of trees trained by a fit-the-fit procedure to model some Individual Treatment Effect (ITE) estimates, and among these, only a simple and robust subset of rules is selected for the linear decomposition by the Stability Selection algorithm via LASSO. During the estimation step, CRE estimates the ATE and AATEs, by the normal equations to model some ITE estimates. In both steps, CRE is agnostic concerning the method used for ITE estimation.

Usage

CRE is available both on [CRAN](#) and [GitHub](#) and can be installed and loaded into the R session using:

```
install.packages("CRE")
library("CRE")
```

`generate_cre_dataset()` is a flexible synthetic dataset generator, which can be used for simulations before applying CRE to real-world observational data sets.

```
dataset <- generate_cre_dataset(n = 2000,
                                rho = 0,
                                n_rules = 4,
                                p = 10,
                                effect_size = 2,
                                binary_covariates = TRUE,
                                binary_outcome = FALSE,
                                confounding = "no")
```

```
y <- dataset$y
z <- dataset$z
X <- dataset$X
```

We propose here three examples of how to run the Causal Rule Ensemble algorithm by the CRE package.

Example 1. Running Causal Rule Ensemble with default parameters described in Bargagli-Stoffi et al. (2023).

```
cre_results <- cre(y, z, X)
```

Example 2. Running Causal Rule Ensemble with customized ITE estimator.

```
ite_pred <- ... # personalized ite estimation
cre_results <- cre(y, z, X, ite = ite_pred)
```

Example 3. Running Causal Rule Ensemble with customized parameters.

```
method_params <- list(ratio_dis = 0.25,
                      ite_method_dis = "aipw",
                      ps_method_dis = "SL.xgboost",
                      oreg_method_dis = "SL.xgboost",
                      ite_method_inf = "aipw",
                      ps_method_inf = "SL.xgboost",
                      oreg_method_inf = "SL.xgboost")

hyper_params <- list(intervention_vars = c("x1", "x2", "x3", "x4"),
                    offset = NULL,
                    ntrees_rf = 20,
                    ntrees_gbm = 20,
                    node_size = 20,
                    max_nodes = 5,
                    max_depth = 3,
                    t_decay = 0.025,
                    t_ext = 0.025,
                    t_corr = 1,
                    t_pvalue = 0.05,
                    replace = FALSE,
                    stability_selection = TRUE,
                    cutoff = 0.8,
```

```
pfer = 0.1,  
penalty_rl = 1)
```

```
cre_results <- cre(y, z, X, method_params, hyper_params)
```

49 The results are collected in an S3 object containing: the number of decision rules extracted
50 at each step (M), the data.frame of the CATE decomposition estimates with correspond-
51 ing uncertainty quantification (CATE), the list of selected parameters (method_params and
52 hyper_params), and the predicted ITEs (ite_pred).

53 summarize() and print() display a summary of these results, and plot() visualizes the CATE
54 decomposition estimates in a range bar plot. Figure 1 reports an example of the proposed
55 results visualization for Example 1.

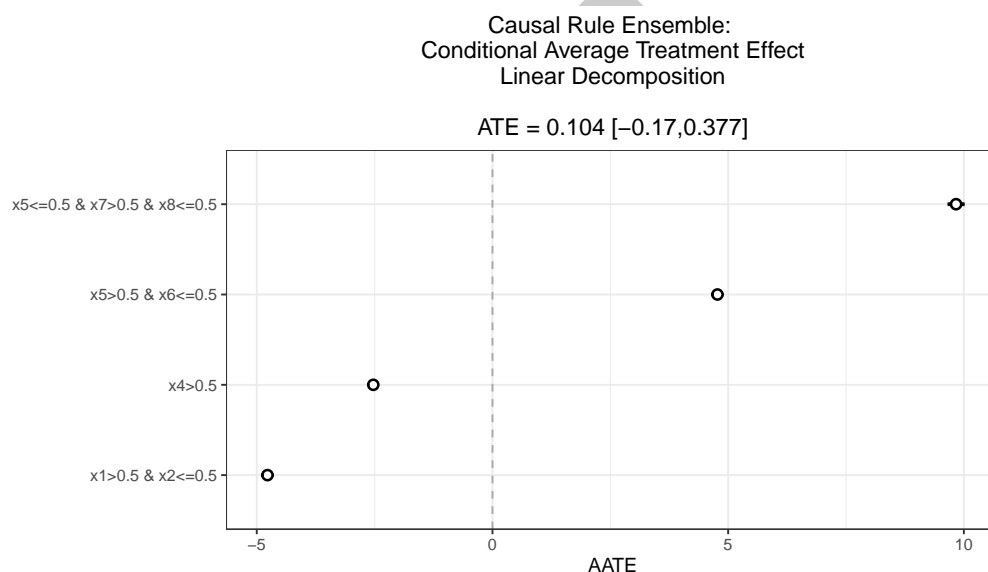


Figure 1: Visualization of Causal Rule Ensemble HTE linear decomposition for Example 1. For each decision rule discovered, the corresponding AATE estimate with 95% confidence interval is reported in a range bar plot. The decision rules are ordered from the most vulnerable (high AATE) to the least, and the ATE is reported on top of the plot.

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