Package 'CRE'

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Type Package

Title Interpretable Subgroups Identification Through Ensemble Learning of Causal Rules

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Description Provides an interpretable identification of subgroups with heterogeneous causal effect. The heterogeneous subgroups are discovered through ensemble learning of causal rules. Causal rules are highly interpretable if-then statement that recursively partition the features space into heterogeneous subgroups. A small number of significant causal rules are selected through Stability Selection to control for family-wise error rate in the finite sample setting. It proposes various estimation methods for the conditional causal effects for each discovered causal rule. It is highly flexible and multiple causal estimands and imputation methods are implemented. Lee, K., Bargagli-Stoffi, F. J., & Dominici, F. (2020). Causal rule ensemble: Interpretable inference of heterogeneous treatment effects. arXiv preprint <arXiv:2009.09036>.

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URL https://github.com/NSAPH-Software/CRE

BugReports https://github.com/NSAPH-Software/CRE/issues

Depends R (>= 3.5.0)

Imports MASS, stats, logger, gbm, randomForest, methods, xgboost, RRF, data.table, xtable, glmnet, bartCause, stabs, stringr, SuperLearner, dplyr, magrittr, ggplot2, bcf, inTrees

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R topics documented:

CRE-package 2
cre 3
generate_cre_dataset 5
get_logger 7
plot.cre 7
print.cre 8
set_logger 8
summary.cre 9

Index **10**

`CRE-package` *The 'CRE' package*

Description

Provides an interpretable identification of subgroups with heterogeneous causal effect. The heterogeneous subgroups are discovered through ensemble learning of causal rules. Causal rules are highly interpretable if-then statement that recursively partition the features space into heterogeneous subgroups. A small number of significant causal rules are selected through Stability Selection to control for family-wise error rate in the finite sample setting. It proposes various estimation methods for the conditional causal effects for each discovered causal rule. It is highly flexible and multiple causal estimands and imputation methods are implemented.

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References

Lee, K., Bargagli-Stoffi, F. J., & Dominici, F. (2020). Causal rule ensemble: Interpretable inference of heterogeneous treatment effects. arXiv preprint arXiv:2009.09036.

`cre` *Causal rule ensemble*

Description

Performs the Causal Rule Ensemble on a data set with a response variable, a treatment variable, and various features.

Usage

```
cre(y, z, X, method_params = NULL, hyper_params = NULL, ite = NULL)
```

Arguments

`y`	An observed response vector.
`z`	A treatment vector.
`X`	A covariate matrix (or a data frame).
`method_params`	The list of parameters to define the models used, including: • *Parameters for Honest Splitting* – *ratio_dis*: The ratio of data delegated to rules discovery (default: 0.5). • *Parameters for Discovery* – *ite_method_dis*: The method to estimate the discovery sample ITE (default: 'aipw'). – *ps_method_dis*: The estimation model for the propensity score on the discovery subsample (default: 'SL.xgboost'). – *or_method_dis*: The estimation model for the outcome regressions estimate_ite_aipw on the discovery subsample (default: 'SL.xgboost'). • *Parameters for Inference* – *ite_method_inf*: The method to estimate the inference sample ITE (default: 'aipw'). – *ps_method_inf*: The estimation model for the propensity score on the inference subsample (default: 'SL.xgboost'). – *or_method_inf*: The estimation model for the outcome regressions in estimate_ite_aipw on the inference subsample (default: 'SL.xgboost').
`hyper_params`	The list of hyper parameters to finetune the method, including: • *intervention_vars*: Intervention-able variables used for Rules Generation (default: NULL). • *offset*: Name of the covariate to use as offset (i.e. 'x1') for T-Poisson ITE Estimation. NULL if offset is not used (default: NULL).

- *ntrees_rf*: A number of decision trees for random forest (default: 20).
- *ntrees_gbm*: A number of decision trees for the generalized boosted regression modeling algorithm. (default: 20).
- *node_size*: Minimum size of the trees' terminal nodes (default: 20).
- *max_nodes*: Maximum number of terminal nodes per tree (default: 5).
- *max_depth*: Maximum rules length (default: 3).
- *replace*: Boolean variable for replacement in bootstrapping for rules generation by random forest (default: TRUE).
- *t_decay*: The decay threshold for rules pruning (default: 0.025).
- *t_ext*: The threshold to define too generic or too specific (extreme) rules (default: 0.01, range: (0,0.5)).
- *t_corr*: The threshold to define correlated rules (default: 1, range: (0,+inf)).
- *t_pvalue*: the threshold to define statistically significant rules (default: 0.05, range: (0,1)).
- *stability_selection*: Whether or not using stability selection for selecting the rules (default: TRUE).
- *cutoff*: Threshold (percentage) defining the minimum cutoff value for the stability scores (default: 0.9).
- *pfer*: Upper bound for the per-family error rate (tolerated amount of falsely selected rules) (default: 1).
- *penalty_rl*: Order of penalty for rules length during LASSO regularization (i.e. 0: no penalty, 1: rules_length, 2: rules_length^2) (default: 1).

`ite` The estimated ITE vector. If given both the ITE estimation steps in Discovery and Inference are skipped (default: NULL).

Value

An S3 object containing:

- A number of Decision Rules extracted at each step (`M`).
- A data.frame of Conditional Average Treatment Effect decomposition estimates with corresponding uncertainty quantification (`CATE`).
- A list of Method Parameters (`method_params`).
- A list of Hyper Parameters (`hyper_params`).
- An Individual Treatment Effect predicted (`ite_pred`).

Examples

```
set.seed(2021)
dataset <- generate_cre_dataset(n = 400, rho = 0, n_rules = 2, p = 10,
                                effect_size = 2, binary_covariates = TRUE,
                                binary_outcome = FALSE, confounding = "no")
y <- dataset[["y"]]
z <- dataset[["z"]]
```

```
X <- dataset[["X"]]

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 = NULL,
                     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 = 0.6,
                     pfer = 0.1,
                     penalty_rl = 1)

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

`generate_cre_dataset` *Generate CRE synthetic data*

Description

Generates synthetic data with continues or binary outcome.

Usage

```
generate_cre_dataset(
  n = 1000,
  rho = 0,
  n_rules = 2,
  p = 10,
  effect_size = 2,
  binary_covariates = TRUE,
  binary_outcome = TRUE,
  confounding = "no"
)
```

Arguments

n	An integer number that represents the number of observations. Non-integer values will be converted into an integer number.
rho	A positive double number that represents the correlation within the covariates (default: 0, range: (0,1)).
n_rules	The number of causal rules. (default: 2, range: 1,2,3,4).
p	The number of covariates (default: 10).
effect_size	The effect size magnitude in (default: 2, range: >=0).
binary_covariates	Whether to use binary or continuous covariates (default: TRUE).
binary_outcome	Whether to use binary or continuous outcomes (default: TRUE).
confounding	Only for continuous outcome, add confounding variables: • Linear confounding "lin". • Non-linear confounding "nonlin". • No confounding "no" (default).

Value

A list of synthetic data containing:

- An outcome vector (y),
- A treatment vector (z),
- A covariates matrix (X) and
- An individual treatment vector (ite)

Note

Set (binary/continuous) covariates domain (binary_covariates). Set (binary/continuous) outcome domain (binary_outcome). Increase complexity in heterogeneity discovery:

- Decreasing the sample size (n),
- adding correlation among variables (rho),
- increasing the number of rules (n_rules),
- increasing the number of covariates (p),
- decreasing the absolute value of the causal effect (effect_size),
- adding linear or not-linear confounders (confounding).

Examples

```
set.seed(123)
dataset <- generate_cre_dataset(n = 1000, rho = 0, n_rules = 2, p = 10,
                                effect_size = 2, binary_covariates = TRUE,
                                binary_outcome = TRUE, confounding = "no")
```

get_logger *Get Logger settings*

Description

Returns current logger settings.

Usage

```
get_logger()
```

Value

Returns a list that includes **logger_file_path** and **logger_level**.

Examples

```
set_logger("mylogger.log", "INFO")
log_meta <- get_logger()
```

plot.cre *Extend generic plot functions for CRE class*

Description

A wrapper function to extend generic plot functions for CRE class.

Usage

```
## S3 method for class 'cre'
plot(x, ...)
```

Arguments

x	A CRE object.
...	Additional arguments passed to customize the plot.

Value

Returns a ggplot2 object, invisibly. This function is called for side effects.

print.cre *Extend print function for the CRE object*

Description

Prints a brief summary of the CRE object

Usage

```
## S3 method for class 'cre'
print(x, verbose = 2, ...)
```

Arguments

x	A cre object from running the CRE function.
verbose	Set level of results description details: only results summary 0, results+parameters summary 1, results+parameters+rules summary (default 2).
...	Additional arguments passed to customize the results description.

Value

No return value. This function is called for side effects.

set_logger *Set Logger settings*

Description

Updates logger settings, including log level and location of the file.

Usage

```
set_logger(logger_file_path = "CRE.log", logger_level = "INFO")
```

Arguments

logger_file_path	A path (including file name) to log the messages. (Default: CRE.log)
logger_level	The log level. Available levels include: • TRACE • DEBUG • INFO (Default) • SUCCESS • WARN • ERROR • FATAL

Value

No return value. This function is called for side effects.

Examples

```
set_logger("Debug")
```

`summary.cre` *Print summary of CRE object*

Description

Prints a brief summary of the CRE object

Usage

```
## S3 method for class 'cre'
summary(object, verbose = 2, ...)
```

Arguments

`object`	A cre object from running the CRE function.
`verbose`	Set level of results description details: only results summary 0, results+parameters summary 1, results+parameters+rules summary (default 2).
`...`	Additional arguments passed to customize the results description.

Value

A summary of the CRE object

Index

CRE *(*CRE-package*)*, 2
cre, 3
CRE-package, 2

generate_cre_dataset, 5
get_logger, 7

plot.cre, 7
print.cre, 8

set_logger, 8
summary.cre, 9