

Package ‘RobinCID’

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Title Robust Inference in Complex Innovative Trial Design

Version 1.0.0

Description Perform robust estimation and inference in platform trials and other master protocol trials.
Yuhan Qian, Yifan Yi, Jun Shao, Yanyao Yi, Gregory Levin, Nicole Mayer-Hamblert, Patrick J. Heagerty, Ting Ye (2025) <[doi:10.48550/arXiv.2411.12944](https://doi.org/10.48550/arXiv.2411.12944)>.

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URL <https://github.com/Eureeca/RobinCID>

BugReports <https://github.com/Eureeca/RobinCID/issues>

Suggests testthat (>= 3.0.0)

Config/testthat/edition 3

Imports checkmate, numDeriv, stats, MASS

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NeedsCompilation no

Author Yuhan Qian [aut, cre, cph],
Ting Ye [aut],
Yanyao Yi [aut],
Marlena Bannick [aut]

Maintainer Yuhan Qian <yhqian@uw.edu>

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RobinCID-package	RobinCID <i>Package</i>
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Description

RobinCID implements unbiased prediction and robust inference in R.

Author(s)

Maintainer: Yuhan Qian <yhqian@uw.edu> [copyright holder]

Authors:

- Ting Ye
- Yanyao Yi
- Marlena Bannick

See Also

Useful links:

- <https://github.com/Eureeca/RobinCID>
- Report bugs at <https://github.com/Eureeca/RobinCID/issues>

assign_prob_and_strata	<i>Assign Probability according to Design</i>
------------------------	---

Description

Assign Probability according to Design

Usage

```

assign_prob_and_strata(
  data,
  estimand,
  design = list(randomization_var_colnames = NULL, randomization_table = NULL),
  method,
  estimated_propensity = TRUE,
  stratify_by = NULL
)

```

Arguments

data (data.frame) Input data frame.
estimand (list) A list specifying the estimand.
design (list) A list describing the randomization design. See Details.
method estimation method.
estimated_propensity Whether to use estimated propensity score.
stratify_by The column name of stratification variable in data.

Details

design has two elements: randomization_var_colnames (vector) and randomization_table (data.frame)

Value

A new data with columns of the treatment assignment probability.

estimate_effect	<i>Compute Estimates and Covariance Matrix</i>
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Description

Compute Estimates and Covariance Matrix

Usage

```

estimate_effect(
  ret,
  y,
  treatment,
  treatments_for_compare,
  data,
  prob_mat,
  post_strata,
  stabilize
)

```

Arguments

ret	counterfactual prediction
y	Observed outcome
treatment	name of treatment
treatments_for_compare	description
data	(data.frame) data
prob_mat	(data.frame) treatment assignment probability
post_strata	(character) A string name of post-stratification variable
stabilize	(logical) whether to stabilize

Value

A list of "estimate_effect" object with following elements:

- estimate: estimate of the treatment effect.
- inner_variance: estimate of the covariance matrix.
- method: estimation method.

example

Trial Data

Description

This dataset is generated based on the first three enrollment windows outlined in Figure 1(a) in our paper.

Usage

example

Format

A data frame with 500 rows and 17 columns:

xc, xb, subtype The covariates.

t, substudy The enrollment window and substudy assignment

treatment The treatment assignment, "1", "2", "3" and "4"

y The continuous response.

y_b The binary response, $I(y>3)$.

s12, s12.2, s12.error, s13, s14 The stratification variables.

trt.1, trt.2, trt.3, trt.4 The assignment probabilities of trt 1, 2, 3, and 4.

Source

The data is generated by Yuhan.

find_data	<i>Find Data in a Fit</i>
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Description

Find Data in a Fit

Usage

```
find_data(fit, ...)
```

Arguments

fit	A fit object.
...	Additional arguments.

Value

A data frame used in the fit.

h_diff	<i>Contrast Functions and Jacobians</i>
--------	---

Description

Contrast Functions and Jacobians

Usage

```
h_diff(x)  
h_jac_diff(x)  
h_ratio(x)  
h_jac_ratio(x)  
h_odds_ratio(x)  
h_jac_odds_ratio(x)
```

Arguments

x	(numeric) Vector of values.
---	-----------------------------

Value

Vector of contrasts, or matrix of jacobians.

Examples

```
h_diff(1:3)
h_jac_ratio(1:3)
```

predict_counterfactual

Counterfactual Prediction

Description

Obtain counterfactual prediction of a fit.

Usage

```
predict_counterfactual(
  fit.j,
  fit.k,
  treatment,
  treatments_for_compare,
  prob_mat,
  post_strata,
  data,
  stabilize,
  settings
)
```

Arguments

fit.j	fitted object for trt j.
fit.k	fitted object for trt k.
treatment	name of treatment column
treatments_for_compare	(character) Treatments for comparison
prob_mat	(data.frame) treatment assignment probabilities
post_strata	(character) A string name of post-stratification variable.
data	(data.frame) raw dataset.
stabilize	stabilize
settings	estimation setting

Value

A list of prediction_cf object with following elements:

- estimation: = estimation,
- sample_size: sample size of ECE population.
- fit.j: fitted model for the treatment specified in tx_to_compare.
- fit.k: fitted model for the treatment specified in tx_to_compare.

robin_ps

*Post-Stratification Based Inference***Description**

Provides robust inference via post stratification.

Usage

```
robin_ps(
  data,
  estimand = list(tx_colname = NULL, tx_to_compare = NULL),
  design = list(randomization_var_colnames = NULL, randomization_table = NULL),
  stratify_by = NULL,
  outcome_model = list(formula = NULL, family = gaussian()),
  contrast_specs = list(contrast = "difference", contrast_jac = NULL),
  alpha = 0.05,
  ...
)
```

Arguments

data	(data.frame) A data frame containing the dataset.
estimand	(list) A list specifying the estimand, with two elements: <ul style="list-style-type: none"> • tx_colname (character): The column name of the treatment variable in data. • tx_to_compare (character vector): A vector specifying exactly two treatment levels to compare.
design	(list) A list specifying randomization information, with two elements: <ul style="list-style-type: none"> • randomization_var_colnames (character vector): Column names of randomization variables in data. • randomization_table (data.frame, default: NULL): A data frame containing treatment assignment probabilities for each level of the randomization variables. See <i>Details</i>.
stratify_by	(character, optional) The column name of the stratification variable in data. If provided, stratify_by overrides design.

`outcome_model` (list) A list specifying the outcome working model, with two elements:

- `formula` (formula): The regression formula for the analysis.
- `family` A description of the error distribution and link function for the model. Default: `gaussian()`.

`contrast_specs` (list) A list specifying the contrast function and its Jacobian:

- `contrast` (function or character): A function to compute the treatment effect, or one of "difference", "risk_ratio", or "odds_ratio" for default contrasts.
- `contrast_jac` (function, optional): A function to compute the Jacobian of the contrast function. Ignored if using default contrasts.

`alpha` (numeric) The nominal significance level. Default: 0.05.

... Additional arguments passed to `glm`.

Details

If family is `MASS::negative.binomial(NA)`, the function will use `MASS::glm.nb` instead of `glm`.

Value

A `treatment_effect` object.

Examples

```
data_sim <- RobinCID::example
tx_colname <- "treatment"
treatment_levels <- unique(data_sim[[tx_colname]])
tx_to_compare <- c("trt.1", "trt.3")
randomization_var_colnames <- c("t", "subtype")
df <- data_sim[c("xb", "xc", tx_colname, randomization_var_colnames, "y")]
randomization_table <- unique(data_sim[c(randomization_var_colnames, treatment_levels)])
robin_ps(
  data = df,
  estimand = list(tx_colname = tx_colname,
                 tx_to_compare = tx_to_compare),
  design = list(randomization_var_colnames = randomization_var_colnames,
               randomization_table = randomization_table),
  stratify_by = NULL,
  outcome_model = list(formula = y ~ 1,
                      family = gaussian())
)
```

robin_wt

Inverse Probability Weighting Based Inference

Description

Provides robust inference via inverse probability weighting.

Usage

```
robin_wt(
  data,
  estimand = list(tx_colname = NULL, tx_to_compare = NULL),
  design = list(randomization_var_colnames = NULL, randomization_table = NULL),
  estimated_propensity = TRUE,
  outcome_model = list(formula = NULL, family = gaussian()),
  contrast_specs = list(contrast = "difference", contrast_jac = NULL),
  alpha = 0.05,
  ...
)
```

Arguments

<code>data</code>	(<code>data.frame</code>) A data frame containing the dataset.
<code>estimand</code>	(<code>list</code>) A list specifying the estimand, with two elements: <ul style="list-style-type: none"> <code>tx_colname</code> (<code>character</code>): The column name of the treatment variable in <code>data</code>. <code>tx_to_compare</code> (<code>character</code> vector): A vector specifying exactly two treatment levels to compare.
<code>design</code>	(<code>list</code>) A list specifying randomization information, with two elements: <ul style="list-style-type: none"> <code>randomization_var_colnames</code> (<code>character</code> vector): Column names of randomization variables in <code>data</code>. <code>randomization_table</code> (<code>data.frame</code>, default: <code>NULL</code>): A data frame containing treatment assignment probabilities for each level of the randomization variables. See <i>Details</i>.
<code>estimated_propensity</code>	(<code>logical</code> , default: <code>TRUE</code>) Whether to use estimated propensity scores.
<code>outcome_model</code>	(<code>list</code>) A list specifying the outcome working model, with two elements: <ul style="list-style-type: none"> <code>formula</code> (<code>formula</code>): The regression formula for the analysis. <code>family</code> A description of the error distribution and link function for the model. Default: <code>gaussian()</code>.
<code>contrast_specs</code>	(<code>list</code>) A list specifying the contrast function and its Jacobian: <ul style="list-style-type: none"> <code>contrast</code> (<code>function</code> or <code>character</code>): A function to compute the treatment effect, or one of "difference", "risk_ratio", or "odds_ratio" for default contrasts. <code>contrast_jac</code> (<code>function</code>, optional): A function to compute the Jacobian of the contrast function. Ignored if using default contrasts.
<code>alpha</code>	(<code>numeric</code>) The nominal significance level. Default: <code>0.05</code> .
<code>...</code>	Additional arguments passed to <code>glm</code> .

Details

If `randomization_table` is provided, it must include columns corresponding to `randomization_var_colnames`, as well as treatment assignment probability columns named after the treatment levels in `tx_colname` from `data`.

If family is MASS::negative.binomial(NA), the function will use MASS::glm.nb instead of glm.

Value

A treatment_effect object.

Examples

```
data_sim <- RobinCID::example
tx_colname <- "treatment"
treatment_levels <- unique(data_sim[[tx_colname]])
tx_to_compare <- c("trt.1", "trt.3")
randomization_var_colnames <- c("t", "subtype")
df <- data_sim[c("xb", "xc", tx_colname, randomization_var_colnames, "y")]
randomization_table <- unique(data_sim[c(randomization_var_colnames, treatment_levels)])
robin_wt(
  data = df,
  estimand = list(tx_colname = tx_colname,
                  tx_to_compare = tx_to_compare),
  design = list(randomization_var_colnames = randomization_var_colnames,
                randomization_table = randomization_table),
  estimated_propensity = FALSE,
  outcome_model = list(formula = y ~ 1,
                       family = gaussian())
)
```

treatment_effect	<i>Treatment Effect</i>
------------------	-------------------------

Description

Obtain treatment effect and variance from counter-factual prediction

Usage

```
treatment_effect(object, pair, eff_measure, eff_jacobian, alpha, ...)
```

```
difference(object, ...)
```

```
risk_ratio(object, ...)
```

```
odds_ratio(object, ...)
```

Arguments

object	Object from which to obtain treatment effect. Must be obtained from estimate_effect().
pair	(integer or character) Names or index of the treatment levels.
eff_measure	(function) Treatment effect measurement function.

<code>eff_jacobian</code>	(function) Treatment effect jacobian function.
<code>alpha</code>	Nominal level
<code>...</code>	Additional arguments passed to <code>glm</code>

Value

A list of `treatment_effect` object with following elements:

- `mm_name`: name of the treatments to compare.
- `marginal_mean`: estimate of the treatment effect.
- `mmvariance`: estimate of the covariance matrix.
- `trt_effect`: estimate of the contrast.
- `variance`: estimate of the variance of contrast.
- `contrast`: name of the contrast function.
- `settings`: estimation settings.

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