

# Package ‘RobinCar’

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**Type** Package

**Title** Robust Inference for Covariate Adjustment in Randomized Clinical Trials

**Version** 1.2.0

## Description

Performs robust estimation and inference when using covariate adjustment and/or covariate-adaptive randomization in randomized clinical trials.

Ting Ye, Jun Shao, Yanyao Yi, Qinyuan Zhao (2023) <[doi:10.1080/01621459.2022.2049278](https://doi.org/10.1080/01621459.2022.2049278)>.

Ting Ye, Marlena Bannick, Yanyao Yi, Jun Shao (2023) <[doi:10.1080/24754269.2023.2205802](https://doi.org/10.1080/24754269.2023.2205802)>.

Ting Ye, Jun Shao, Yanyao Yi (2023) <[doi:10.1093/biomet/asad045](https://doi.org/10.1093/biomet/asad045)>.

Marlena Ban-

nick, Jun Shao, Jingyi Liu, Yu Du, Yanyao Yi, Ting Ye (2024) <[doi:10.1093/biomet/asaf029](https://doi.org/10.1093/biomet/asaf029)>.

Xiaoyu Qiu, Yuhan Qian, Jaehwan Yi, Jin-

qiu Wang, Yu Du, Yanyao Yi, Ting Ye (2025) <[doi:10.48550/arXiv.2408.12541](https://doi.org/10.48550/arXiv.2408.12541)>.

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**Imports** dplyr, magrittr, tidyr, emulator, numDeriv, tidyverse, stats, rlang, survival, fastDummies, data.table, broom, SuperLearner, AIPW, MASS, Rdpack (>= 0.7)

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**Author** Marlena Bannick [cre, aut] (ORCID:

<<https://orcid.org/0000-0001-6279-5978>>),

Yuhan Qian [aut],

Ting Ye [aut],

Yanyao Yi [aut],

Faith Bian [aut]

**Maintainer** Marlena Bannick <marlena.bannick@outlook.com>

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car_pb	<i>Generate permuted block treatment assignments</i>
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---

### Description

Generate permuted block treatment assignments

### Usage

```
car_pb(z, trt_label, trt_alc, blocksize = 4L)
```

**Arguments**

z	The car_strata design matrix, as a data frame with factor variables
trt_label	Treatment label
trt_alc	Treatment allocation vector
blocksize	Permuted block blocksize

**Value**

A vector of treatment assignments with labels from the 'trt\_label' argument, based on stratified permuted block randomization.

**Examples**

```
# Create car_strata variables
library(fastDummies)
library(dplyr)

x <- runif(100)
z <- cut(x, breaks=c(0, 0.25, 0.5, 0.75, 1.0))
z <- dummy_cols(z) %>%
  mutate(across(where(is.numeric), as.factor))

car_pb(z[, 2:5], c(0, 1, 2), trt_alc=c(1/4, 1/2, 1/4), blocksize=4L)
```

---

car\_ps

*Generate Pocock-Simon minimization treatment assignments*


---

**Description**

Generate Pocock-Simon minimization treatment assignments

**Usage**

```
car_ps(z, treat, ratio, imb_measure, p_bc = 0.8)
```

**Arguments**

z	The car_strata design matrix
treat	A vector of length k (the number of treatment arms), which labels the treatment arms being compared.
ratio	A vector of length k (the number of treatment arms), which indicates the allocation ratio, e.g., c(1,1,1) for equal allocation with three treatment arms.
imb_measure	What measure of imbalance should be minimized during randomization – either "Range" or "SD"
p_bc	The biased probability, i.e., the probability of assigning each patient to the arm that minimizes the imbalance. Default is 0.8

**Value**

**res** treatment assignment vector

A vector of treatment assignments with labels from the ‘treat’ argument, based on Pocock-Simon’s minimization.

**Author(s)**

Ting Ye Yanyao Yi

**Examples**

```
# Create car_strata variables
library(fastDummies)
library(dplyr)

x <- runif(100)
z <- cut(x, breaks=c(0, 0.25, 0.5, 0.75, 1.0))
z <- dummy_cols(z)
A <- car_ps(
  z=z[, 2:5],
  treat=c(0, 1, 2),
  ratio=c(1, 1, 1),
  imb_measure="Range"
)
```

---

car\_sr

*Generate simple randomization treatment assignments*

---

**Description**

Generate simple randomization treatment assignments

**Usage**

```
car_sr(n, p_trt)
```

**Arguments**

n	Number of observations
p_trt	Proportion allotted to treatment

**Value**

A vector of treatment assignments as 0’s and 1’s based on simple randomization.

**Examples**

```
car_sr(10, p_trt=0.4)
```

---

`data_gen`*Data generation function from JRSS-B paper*

---

**Description**

Data generation function from JRSS-B paper

**Usage**

```
data_gen(  
  n,  
  theta,  
  randomization,  
  p_trt,  
  case = c("case1", "case2", "case3", "case4", "case5")  
)
```

**Arguments**

<code>n</code>	total number of subjects to be generated
<code>theta</code>	true treatment effect
<code>randomization</code>	randomization method in c("SR","CABC","permuted_block","minimization","urn")
<code>p_trt</code>	proportion of treatment arm
<code>case</code>	simulation case in the paper

**Value**

A data frame with the following columns:

<code>t</code>	event time
<code>delta</code>	event indicator
<code>I1</code>	assignment to treatment group 1
<code>I0</code>	assignment to treatment group 0
<code>model_z1, model_z2</code>	covariates
<code>car_strata1, ...</code>	strata variables

---

 data\_gen2

*Data generation function from covariate adjusted log-rank paper*


---

### Description

Data generation function from covariate adjusted log-rank paper

### Usage

```
data_gen2(
  n,
  theta,
  randomization,
  p_trt,
  case = c("case1", "case2", "case3", "case4"),
  blocksize = 4
)
```

### Arguments

n	total number of subjects to be generated
theta	true treatment effect
randomization	randomization method in c("SR","CABC","permuted_block","minimization","urn")
p_trt	proportion of treatment arm
case	simulation case in the paper
blocksize	block size for permuted block design

### Value

A data frame with the following columns:

t	event time
delta	event indicator
I1	assignment to treatment group 1
I0	assignment to treatment group 0
model_w3	covariates
car_strata1, ...	strata variables

---

```
print.CalibrationResult  
    Print calibration result
```

---

**Description**

Print calibration result

**Usage**

```
## S3 method for class 'CalibrationResult'  
print(x, ...)
```

**Arguments**

x	A GLMModel result. If you'd like to calibrate a linear adjustment, use 'robin-car_glm' instead of 'robin-car_linear'.
...	Additional arguments

**Value**

Prints the treatment mean estimates (and variances) based on a calibration on top of a GLM working model, along with the settings used. See [RobinCar::robin-car\\_calibrate\(\)](#).

---

```
print.ContrastResult    Print contrast result
```

---

**Description**

Print contrast result

**Usage**

```
## S3 method for class 'ContrastResult'  
print(x, ...)
```

**Arguments**

x	A ContrastResult object
...	Additional arguments

**Value**

Prints estimates (and variances) of treatment contrasts based on a linear or GLM working model, along with the settings used. See [RobinCar::robin-car\\_contrast\(\)](#)

---

`print.GLMModelResult` *Print glm model result*

---

**Description**

Print glm model result

**Usage**

```
## S3 method for class 'GLMModelResult'  
print(x, ...)
```

**Arguments**

<code>x</code>	A GLMModelResult object
<code>...</code>	Additional arguments

**Value**

Prints the treatment mean estimates (and variances) based on a GLM working model, along with the settings used. See [RobinCar::robincar\\_glm\(\)](#).

---

`print.LinModelResult` *Print linear model result*

---

**Description**

Print linear model result

**Usage**

```
## S3 method for class 'LinModelResult'  
print(x, ...)
```

**Arguments**

<code>x</code>	A LinModelResult object
<code>...</code>	Additional arguments

**Value**

Prints the treatment mean estimates (and variances) based on a linear working model, along with the settings used. See [RobinCar::robincar\\_linear\(\)](#).

---

print.MHResult	<i>Print MH result</i>
----------------	------------------------

---

**Description**

Print MH result

**Usage**

```
## S3 method for class 'MHResult'  
print(x, ...)
```

**Arguments**

x	A ContrastResult object
...	Additional arguments

**Value**

Prints estimates (and variances) of treatment contrasts based on MH risk difference or ATE

---

print.TTResult	<i>Print TTE result</i>
----------------	-------------------------

---

**Description**

Print TTE result

**Usage**

```
## S3 method for class 'TTResult'  
print(x, ...)
```

**Arguments**

x	A TTResult object
...	Additional arguments

**Value**

Prints results of time-to-event covariate adjusted analyses including covariate-adjusted (stratified) logrank, robust Cox score, and covariate-adjusted hazard ratio. Prints summary statistics about number of observations and events, possibly by strata, and the test statistics and/or estimates, and p-values. See [RobinCar::robincar\\_tte\(\)](#) and [RobinCar::robincar\\_covhr\(\)](#).

---

robincar\_calibrate      *Perform linear or joint calibration*

---

### Description

Uses linear or joint calibration to "calibrate" the estimates from a linear or GLM-type adjustment. Linear calibration fits a linear model with treatment (and treatment-by-covariate interactions) and with the predicted  $\hat{\mu}(X_i) = (\hat{\mu}_1(X_i), \dots, \hat{\mu}_K(X_i))$  as constructed covariates where  $K$  is the number of treatment groups; joint calibration also includes  $Z_i$  the strata variables as covariates.

### Usage

```
robincar_calibrate(result, joint = FALSE, add_x = NULL)
```

### Arguments

result	A GLMModelResult
joint	If true, then performs joint calibration with the $\hat{\mu}(X_i)$ and strata $Z_i$ to achieve universality and efficiency gain rather than just linear calibration that uses $\hat{\mu}(X_i)$ .
add_x	Additional x to use in the calibration. Must have been in the original dataset that robincar_glm was called on.

### Value

A result object that has the same structure as [RobinCar::robincar\\_glm\(\)](#), with the argument 'result' included as "original" in the list.

---

robincar\_contrast      *Estimate a treatment contrast*

---

### Description

Estimate a treatment contrast using the result of [RobinCar::robincar\\_linear\(\)](#), [RobinCar::robincar\\_glm\(\)](#), or [RobinCar::robincar\\_SL\(\)](#) using the delta method.

### Usage

```
robincar_contrast(result, contrast_h, contrast_dh = NULL)
```

### Arguments

result	A LinModelResult or GLMModelResult
contrast_h	An optional function to specify a desired contrast
contrast_dh	An optional jacobian function for the contrast

**Value**

A contrast object which has the following attributes:

result	A <code>dplyr::tibble()</code> with the label of the treatment contrast (e.g., 1 vs. 0), the estimate of the treatment contrast, estimated SE, and p-value based on a z-test with estimate and SE.
varcov	The variance-covariance matrix for the treatment contrast estimates.
settings	List of model settings used for the contrast.

---

robincar_covhr	<i>Covariate-adjusted estimators for time to event data</i>
----------------	---

---

**Description**

Estimate a covariate-adjusted hazard ratio (`'adj_method="CL"'`), or a covariate-adjusted stratified hazard ratio (`'adj_method="CSL"'`).

**Usage**

```
robincar_covhr(
  df,
  treat_col,
  response_col,
  event_col,
  car_strata_cols = NULL,
  covariate_cols = NULL,
  p_trt = 0.5,
  ref_arm = NULL,
  car_scheme = "simple",
  adj_method = "CL",
  interval = c(-10, 10)
)
```

**Arguments**

df	A data.frame with the required columns
treat_col	Name of column in df with treatment variable
response_col	Name of the column in df with response variable
event_col	Name of column in df with event indicator (0/FALSE=no event, 1/TRUE=event)
car_strata_cols	Names of columns in df with car_strata variables
covariate_cols	Names of columns in df with covariate variables
p_trt	Treatment allocation ratio for the reference arm.

ref_arm	Reference arm of the treatment group, defaults to NULL, which results in using the first element of 'unique(data[, treat_col])'.
car_scheme	Name of the type of covariate-adaptive randomization scheme. One of: "simple", "pocock-simon", "biased-coin", "permuted-block".
adj_method	Adjustment method (one of "CL", "CSL")
interval	Interval for uniroot function

**Value**

An object with attribute named "result", which lists:

theta_L	estimate of the hazard ratio
se_theta_L	SE estimate of the hazard ratio
theta_CL	estimate of the covariate-adjusted hazard ratio
se_theta_CL	SE estimate of the covariate-adjusted hazard ratio

Other attributes are the settings used, data attributes, and the original data frame supplied by the user.

---

robincar_coxscore	<i>Robust cox score adjustment</i>
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---

**Description**

Robust cox score adjustment

**Usage**

```
robincar_coxscore(...)
```

**Arguments**

... Arguments to robincar\_tte, other than 'adj\_method'

**Value**

A result object with the following attributes:

result	A list: "statistic" is the robust Cox score test statistic which can be used to obtain p-values; "U" and "se" are the numerator and denominator of the test statistic, respectively.
settings	The covariate adjustment settings used.
original_df	The dataset supplied by the user.

robincar\_glm

*Covariate adjustment using generalized linear working model***Description**

Estimate treatment-group-specific response means and (optionally) treatment group contrasts using a generalized linear working model.

**Usage**

```
robincar_glm(
  df,
  treat_col,
  response_col,
  formula = NULL,
  car_strata_cols = NULL,
  car_scheme = "simple",
  g_family = stats::gaussian,
  g_accuracy = 7,
  contrast_h = NULL,
  contrast_dh = NULL,
  variance_type = 1
)
```

**Arguments**

df	A data.frame with the required columns
treat_col	Name of column in df with treatment variable
response_col	Name of the column in df with response variable
formula	The formula to use for adjustment specified using as.formula("..."). This overrides car_strata_cols and covariate_cols.
car_strata_cols	Names of columns in df with car_strata variables
car_scheme	Name of the type of covariate-adaptive randomization scheme. One of: "simple", "pocock-simon", "biased-coin", "permuted-block".
g_family	Family that would be supplied to glm(...), e.g., binomial. If no link specified, will use default link, like behavior in glm. If you wish to use a negative binomial working model with an unknown dispersion parameter, then use 'g_family="nb"'.
g_accuracy	Level of accuracy to check prediction un-biasedness.
contrast_h	An optional function to specify a desired contrast
contrast_dh	An optional jacobian function for the contrast (otherwise use numerical derivative)
variance_type	The type of variance estimator to use, type 1, 2, or 3. All three are asymptotically equivalent. See details for more.

## Details

The output is the AIPW estimator given by (for each treatment group  $a$ ):

$$\frac{1}{n} \sum_{i=1}^n \hat{\mu}_a(X_i) + \frac{1}{n_a} \sum_{i:A_i=a} \{Y_i - \hat{\mu}(X_i)\}$$

where  $Y_i$  is the outcome,  $A_i$  is the treatment assignment,  $X_i$  are the covariates,  $n_a = \sum_{i=1}^n A_i = a$ , and  $\hat{\mu}_a$  is the estimated conditional mean function based on the GLM working model. This working model has treatment  $a$ -specific coefficients if 'adj\_method' is "heterogeneous". Otherwise, they are shared across the treatment arms. Alternatively, if 'formula' is used, the working model can be specified according to the user.

Importantly, the estimated variance accounts for misspecification of the working model, and for covariate-adaptive randomization. The variance estimator is given by

$$\hat{V} = \hat{V}_{\text{SR}} - \hat{V}_{\Omega}$$

where  $\hat{V}_{\text{SR}}$  is the contribution to the variance under simple randomization, and  $\hat{V}_{\Omega}$  is a term that only appears when a covariate-adaptive randomization scheme is used. The  $\hat{V}_{\Omega}$  is the second line of  $\hat{V}$  in (Bannick et al. 2025).

There are three different estimators available for  $\hat{V}_{\text{SR}}$ , which the user can choose with the argument `variance_type`. We describe these here.

The three variance types are given as follows:

- Type 1 (default):

$$\text{diag} \left[ \hat{\pi}_a^{-1} (\text{Var}_a(Y_i) - 2\hat{Q}_{a,a} + \hat{\Sigma}_{a,a}), a = 1, \dots, K \right] + \hat{Q} + \hat{Q}^T - \hat{\Sigma}$$

- Type 2:

$$\text{diag} \left[ \hat{\pi}_a^{-1} (\text{Var}_a(Y_i - \hat{\mu}_a(X_i)) - 2\hat{Q}_{a,a} + \hat{\Sigma}_{a,a}), a = 1, \dots, K \right] + \hat{Q} + \hat{Q}^T - \hat{\Sigma}$$

- Type 3:

$$\text{diag} \left[ \hat{\pi}_a^{-1} E_a([Y_i - \hat{\mu}_a(X_i)]^2), a = 1, \dots, K \right] + \hat{A}$$

where  $\hat{\pi}_a$  is the treatment proportion for group  $a$ ,  $\hat{Q}_{a,b} = \text{Cov}_a(Y_i, \hat{\mu}_b(X_i))$ ,  $\hat{\Sigma}_{a,b} = \text{Cov}(\hat{\mu}_a(X_i), \hat{\mu}_b(X_i))$ , and the matrix  $\hat{A}$  has diagonal entries for  $(a, a)$  given by

$$2\text{Cov}_a(Y_i - \hat{\mu}_a(X_i), \hat{\mu}_a(X_i)) + \text{Var}_a(\hat{\mu}_a(X_i))$$

and off-diagonal entries for  $(a, b)$  given by

$$\text{Cov}_a(Y_i, \hat{\mu}_b(X_i)) + \text{Cov}_b(Y_i, \hat{\mu}_a(X_i)) - (1/2) [\text{Cov}_a(\hat{\mu}_a(X_i), \hat{\mu}_b(X_i)) + \text{Cov}_b(\hat{\mu}_a(X_i), \hat{\mu}_b(X_i))].$$

We use  $E_a$ ,  $\text{Var}_a$ , and  $\text{Cov}_a$  to refer to the empirical expectation, variance, and covariance among observations in group  $a$  only, and  $\text{Cov}$  is the covariance within the entire sample.

Please see the Supplemental Material Sect. H of (Bannick et al. 2025) for a discussion of the merits of each type of variance estimator. Briefly, we recommend variance types 1 generally, and variance type 3 if it is anticipated that the distribution of  $X$  varies substantially over treatment groups.

**Value**

If ‘contrast\_h’ argument is used, outputs a ‘main’ and a ‘contrast’ object. The ‘main’ object has the following structure:

result	A <code>dplyr::tibble()</code> with the treatment label, treatment mean estimate using AIPW, estimated SE, and p-value based on a z-test with estimate and SE.
varcov	The variance-covariance matrix for the treatment mean estimates.
settings	List of model settings used in covariate adjustment.
original_df	The original dataset provided by the user.
mod	The fit from the <code>glm()</code> working model used for covariate adjustment.
mu_a	Predicted potential outcomes for each treatment category (columns) and individual (rows). These are the $\hat{\mu}_a$
.	
g.estimate	The G-computation estimate based only on $\frac{1}{n} \sum_{i=1}^n \hat{\mu}_a(X_i)$ . This is equivalent to the AIPW estimate when a canonical link function is used.
data	Attributes about the dataset.

The ‘contrast’ object has a structure that is documented in `RobinCar::robincar_contrast()`.

**References**

Bannick MS, Shao J, Liu J, Du Y, Yi Y, Ye T (2025). “A General Form of Covariate Adjustment in Clinical Trials under Covariate-Adaptive Randomization.” *Biometrika*, asaf029. ISSN 1464-3510, [doi:10.1093/biomet/asaf029](https://doi.org/10.1093/biomet/asaf029).

---

robincar_linear	<i>Covariate adjustment using linear working model</i>
-----------------	--

---

**Description**

Estimate treatment-group-specific response means and (optionally) treatment group contrasts using a linear working model for continuous outcomes.

**Usage**

```
robincar_linear(
  df,
  treat_col,
  response_col,
  car_strata_cols = NULL,
  covariate_cols = NULL,
  car_scheme = "simple",
  adj_method = "ANOVA",
  contrast_h = NULL,
  contrast_dh = NULL
)
```

**Arguments**

df	A data.frame with the required columns
treat_col	Name of column in df with treatment variable
response_col	Name of the column in df with response variable
car_strata_cols	Names of columns in df with car_strata variables
covariate_cols	Names of columns in df with covariate variables. <b>**If you want to include the strata variables as covariates also, add them here.**</b>
car_scheme	Name of the type of covariate-adaptive randomization scheme. One of: "simple", "pocock-simon", "biased-coin", "permuted-block".
adj_method	Name of linear adjustment method to use. One of: "ANOVA", "ANCOVA", "ANHECOVA".
contrast_h	An optional function to specify a desired contrast
contrast_dh	An optional jacobian function for the contrast (otherwise use numerical derivative)

**Details**

\* Adjustment method "ANOVA" fits a linear model with formula  $Y \sim A$  where  $A$  is the treatment group indicator and  $Y$  is the response. \* "ANCOVA" fits a linear model with  $Y \sim A + X$  where  $X$  are the variables specified in the 'covariate\_cols' argument. \* "ANHECOVA" fits a linear model with  $Y \sim A * X$ , the main effects and treatment-by-covariate interactions.

**Value**

See value of [RobinCar::robincar\\_glm\(\)](#), this function is a wrapper using a linear link function.

---

robincar_logrank	<i>Robust (potentially stratified) logrank adjustment</i>
------------------	---

---

**Description**

Perform a robust covariate-adjusted logrank test ("CL") that can be stratified ("CSL") if desired.

**Usage**

```
robincar_logrank(adj_method, ...)
```

**Arguments**

adj_method	Adjustment method, one of "CL", "CSL"
...	Additional arguments to 'robincar_tte'

## Details

Note: Since RobinCar version 0.4.0, the variance of the test statistic has changed to better accommodate tied event times.

$\hat{\sigma}_{CL}^2$  and  $\hat{\sigma}_{CSL}^2$  for the covariate-adjusted stratified log-rank test are given by Ye, Shao, and Yi (2024) after equation (8) on page 700, with  $\hat{\sigma}_{SL}^2$  replaced by the following estimator, which is the standard denominator of the logrank test:

$$\frac{1}{n} \sum_j \sum_i v_j(t_i)$$

$$v_j(t_i) = \frac{Y_{0,j}(t)Y_{1,j}(t)d_j(t) [Y_j(t) - d_j(t)]}{Y_j(t)^2 [Y_j(t) - 1]}$$

where  $t_i$  are strata-specific unique failure times,  $d_j(t)$  is the number of events at time  $t$  in strata  $j$ ,  $Y_j(t)$  is the number at risk within strata  $j$  at time  $t$ , and  $Y_{a,j}(t)$  is the number at risk within strata  $j$  and treatment  $a$  at time  $t$ .

Please see Ye, Shao, and Yi (2024)'s "Covariate-adjusted log-rank test: guaranteed efficiency gain and universal applicability" in *Biometrika* for more details about  $\hat{\sigma}_{CSL}^2$ .

## Value

A result object with the following attributes:

result	A list: "statistic" is the adjusted logrank test statistic which can be used to obtain p-values; "U" and "se" are the numerator and denominator of the test statistic, respectively; if the input parameter "return_influence" is set to TRUE, the list will contain an element called "inf_func", which is a data.frame with columns "id" and "inf_func", which is the influence function for each subject for the covariate-adjusted log-rank test (stratified or unstratified). This influence function can be used, e.g., to calculate the correlation between interim and final test statistics in a group sequential design.
settings	The covariate adjustment settings used.
original_df	The dataset supplied by the user.

## Examples

```
library(magrittr)
library(dplyr)
library(forcats)
set.seed(0)
n=100
data.simu0=data_gen(n=n,
                    theta=0,
                    randomization="permuted_block",
                    p_trt=0.5,
                    case="case2") %>% mutate(strata1=sample(letters[1:3],n,replace=TRUE),
                                             strata2=sample(LETTERS[4:5],n,replace=TRUE))

out <- robincar_logrank(df=data.simu0,
```

```

      treat_col="I1",
      p_trt=0.5,
      ref_arm=0,
      response_col="t",
      event_col="delta",
      covariate_cols=c("model_z1", "model_z2"),
      car_scheme="simple",
      adj_method=c("CL"))

set.seed(0)
n=100
data.simu0=data_gen(n=n,
                    theta=0,
                    randomization="permuted_block",
                    p_trt=0.5,
                    case="case1")

data.simu <- data.simu0 %>%
  tidyr::pivot_longer(cols=starts_with("car_strata"),
                      names_prefix="car_strata",
                      names_to="strt") %>%
  filter(value==1) %>% select(-value) %>%
  mutate(strt=forcats::as_factor(strt)) %>%
  select(t,strt) %>%
  left_join(data.simu0, .)

out1 <- robincar_logrank(df=data.simu,
                        treat_col="I1",
                        p_trt=0.5,
                        ref_arm=0,
                        response_col="t",
                        event_col="delta",
                        car_strata_cols="strt",
                        covariate_cols=NULL,
                        car_scheme=c("permuted-block"),
                        adj_method=c("CSL")
)

```

---

robincar\_mh

*Estimate Mantel-Haenszel Risk Difference*


---

## Description

This function estimates Mantel-Haenszel risk difference and average treatment effect.

## Usage

```
robincar_mh(
  df,
```

```

    treat_col,
    response_col,
    strata_cols,
    estimand = "ATE",
    ci_type = "mGR"
  )

```

### Arguments

<code>df</code>	A data.frame with the required columns
<code>treat_col</code>	Name of column in df with treatment variable. Must be binary
<code>response_col</code>	Name of the column in df with response variable
<code>strata_cols</code>	Names of columns in df with strata variables
<code>estimand</code>	A character string specifying the estimand. One of "MH" or "ATE" (default). See Details
<code>ci_type</code>	A character string specifying the type of confidence interval. One of "GR", "mGR" (default), "Sato"

### Details

The estimand of interest can be either Mantel-Haenszel risk difference or Average Treatment Effect (ATE). The latter is the default option of ‘estimand’. When ‘estimand="ATE"’, ‘ci\_type’ is limited to the modified Greenland variance estimator (mGR). Otherwise, Greenland’s variance estimator (GR) and Sato’s variance estimator are optional.

### Examples

```

df <- RobinCar:::data_sim
df$y_bin = ifelse(df$y>2.5, 1, 0)
robincar_mh(df = df[df$A!=2,],
            treat_col = "A",
            response_col = "y_bin",
            strata_cols = c("z1", "z2"),
            estimand = "MH",
            ci_type = "mGR")

```

---

robincar\_SL

*BETA: Covariate adjustment using working models from the super learner libraries through the AIPW package with cross-fitting.*

---

### Description

Estimate treatment-group-specific response means and (optionally) treatment group contrasts using a generalized linear working model.

**Usage**

```
robincar_SL(
  df,
  treat_col,
  response_col,
  car_strata_cols = NULL,
  covariate_cols = NULL,
  car_scheme = "simple",
  covariate_to_include_strata = NULL,
  SL_libraries = c(),
  SL_learners = c(),
  k_split = 2,
  g_accuracy = 7,
  contrast_h = NULL,
  contrast_dh = NULL,
  variance_type = 1
)
```

**Arguments**

<code>df</code>	A data.frame with the required columns
<code>treat_col</code>	Name of column in df with treatment variable
<code>response_col</code>	Name of the column in df with response variable
<code>car_strata_cols</code>	Names of columns in df with car_strata variables
<code>covariate_cols</code>	Names of columns in df with covariate variables
<code>car_scheme</code>	Name of the type of covariate-adaptive randomization scheme. One of: "simple", "pocock-simon", "biased-coin", "permuted-block".
<code>covariate_to_include_strata</code>	Whether to include car_strata variables in covariate adjustment. Defaults to F for ANOVA and ANCOVA; defaults to T for ANHECOVA. User may override by passing in this argument.
<code>SL_libraries</code>	Vector of super-learner libraries to use for the covariate adjustment (see <a href="#">SuperLearner::listWrappers</a> )
<code>SL_learners</code>	Optional list of super-learner "learners" to use for the covariate adjustment (see <a href="#">SuperLearner::create.Learner()</a> )
<code>k_split</code>	Number of splits to use in cross-fitting
<code>g_accuracy</code>	Level of accuracy to check prediction un-biasedness (in digits).
<code>contrast_h</code>	An optional function to specify a desired contrast
<code>contrast_dh</code>	An optional jacobian function for the contrast (otherwise use numerical derivative)
<code>variance_type</code>	The type of variance estimator to use, type 1, 2, or 3. All three are asymptotically equivalent. See details of <a href="#">RobinCar::robincar_glm</a> for more.

## Details

\*WARNING: This function is still under development and has not been extensively tested.\* This function currently only works for two treatment groups. Before using this function, you must load the [SuperLearner](#) library with 'library(SuperLearner)', otherwise the function call will fail.

## Value

See value of [RobinCar::robincar\\_glm](#), but the working model for  $\hat{\mu}(X_i)$  is based on the [AIPW::AIPW](#) package that uses specified SuperLearner libraries and cross-fitting. Also, 'mod' attribute is an object of class [AIPW::AIPW](#).

## Examples

```
library(SuperLearner)
library(ranger)
n <- 1000
set.seed(10)
DATA2 <- data.frame(A=rbinom(n, size=1, prob=0.5),
                    y=rbinom(n, size=1, prob=0.2),
                    x1=rnorm(n),
                    x2=rnorm(n),
                    x3=as.factor(rbinom(n, size=1, prob=0.5)),
                    z1=rbinom(n, size=1, prob=0.5),
                    z2=rbinom(n, size=1, prob=0.5))

DATA2[, "y"] <- NA
As <- DATA2$A == 1
DATA2[DATA2$A == 1, "y"] <- rbinom(
  sum(As),
  size=1,
  prob=exp(DATA2[As,]$x1)/(1+exp(DATA2[As,]$x1)))
DATA2[DATA2$A == 0, "y"] <- rbinom(
  n-sum(As),
  size=1,
  prob=exp(1 +
    5*DATA2[!As,]$x1 + DATA2[!As,]$x2)/
    (1+exp(1 + 5*DATA2[!As,]$x1 + DATA2[!As,]$x2)))
DATA2$A <- as.factor(DATA2$A)

sl.mod <- robincar_SL(
  df=DATA2,
  response_col="y",
  treat_col="A",
  car_strata_cols=c("z1"),
  covariate_cols=c("x1"),
  SL_libraries=c("SL.ranger"),
  car_scheme="permuted-block",
  covariate_to_include_strata=TRUE
)

sl.mod$result
```

---

robincar_SL_median	<i>BETA: Covariate adjustment using working models from the super learner libraries through the AIPW package with cross-fitting, with median adjustment.</i>
--------------------	--

---

## Description

Estimate treatment-group-specific response means and (optionally) treatment group contrasts using a generalized linear working model. Perform median adjustment to limit randomness induced from cross-fitting.

## Usage

```
robincar_SL_median(
  n_times,
  seed,
  df,
  treat_col,
  response_col,
  car_strata_cols = NULL,
  covariate_cols = NULL,
  car_scheme = "simple",
  covariate_to_include_strata = NULL,
  SL_libraries = c(),
  SL_learners = c(),
  k_split = 2,
  g_accuracy = 7,
  contrast_h = NULL,
  contrast_dh = NULL
)
```

## Arguments

n_times	Number of times to run the robincar_SL function
seed	Seed to set before running the set of functions
df	A data.frame with the required columns
treat_col	Name of column in df with treatment variable
response_col	Name of the column in df with response variable
car_strata_cols	Names of columns in df with car_strata variables
covariate_cols	Names of columns in df with covariate variables
car_scheme	Name of the type of covariate-adaptive randomization scheme. One of: "simple", "pocock-simon", "biased-coin", "permuted-block".

covariate_to_include_strata	Whether to include car_strata variables in covariate adjustment. Defaults to F for ANOVA and ANCOVA; defaults to T for ANHECOVA. User may override by passing in this argument.
SL_libraries	Vector of super-learner libraries to use for the covariate adjustment (see <a href="#">SuperLearner::listWrappers</a> )
SL_learners	Optional list of super-learner "learners" to use for the covariate adjustment (see <a href="#">SuperLearner::create.Learner()</a> )
k_split	Number of splits to use in cross-fitting
g_accuracy	Level of accuracy to check prediction un-biasedness (in digits).
contrast_h	An optional function to specify a desired contrast
contrast_dh	An optional jacobian function for the contrast (otherwise use numerical derivative)

### Details

\*WARNING: This function is still under development and has not been extensively tested.\* This function currently only works for two treatment groups. Before using this function, you must load the SuperLearner library with 'library(SuperLearner)', otherwise the function call will fail.

### Value

See value of [RobinCar::robincar\\_SL](#). Attributes 'mods' and 'mu\_as' are lists of 'mod' and 'mu\_a' attributes, respectively, for each replicate of 'robincar\_SL' used in the median.

---

robincar_tte	<i>Covariate adjustment for time to event data</i>
--------------	--

---

### Description

Perform a covariate-adjusted logrank test ('adj\_method="CL"'), covariate-adjusted stratified logrank test ('adj\_method="CSL"'), or a covariate-adjusted robust Cox score test ('adj\_method="coxscore").

### Usage

```
robincar_tte(
  df,
  treat_col,
  response_col,
  event_col,
  adj_method,
  car_strata_cols = NULL,
  covariate_cols = NULL,
  p_trt = 0.5,
  ref_arm = NULL,
  sparse_remove = TRUE,
```

```

    car_scheme = "simple",
    return_influence = FALSE,
    id_col = NULL
  )

```

### Arguments

<code>df</code>	A data.frame with the required columns
<code>treat_col</code>	Name of column in df with treatment variable
<code>response_col</code>	Name of the column in df with response variable
<code>event_col</code>	Name of column in df with event indicator (0/FALSE=no event, 1/TRUE=event)
<code>adj_method</code>	Adjustment method (one of "CL", "CSL", or "coxscore")
<code>car_strata_cols</code>	Names of columns in df with car_strata variables
<code>covariate_cols</code>	Names of columns in df with covariate variables
<code>p_trt</code>	Treatment allocation ratio for the treatment arm.
<code>ref_arm</code>	Reference arm of the treatment group, defaults to NULL, which results in using the first element of <code>'unique(data[, treat_col])'</code> .
<code>sparse_remove</code>	Remove sparse car_strata from calculation
<code>car_scheme</code>	Name of the type of covariate-adaptive randomization scheme. One of: "simple", "pocock-simon", "biased-coin", "permuted-block".
<code>return_influence</code>	Return the influence function for the covariate-adjusted log-rank test for each individual
<code>id_col</code>	Name of the column in df indicating individual ids

### Details

`'robincar_coxscore'` and `'robincar_logrank'` are wrapper functions around `'robincar_tte'`.

### Value

For adjustment method "CL" or "CSL", see value of [RobinCar::robincar\\_logrank\(\)](#); for adjustment method "coxscore" see value of [RobinCar::robincar\\_coxscore\(\)](#).

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