Package ‘psrwe’

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Title  PS-Integrated Methods for Incorporating RWE in Clinical Studies

Version  3.1

Description  High-quality real-world data can be transformed into scientific real-world evidence (RWE) for regulatory and healthcare decision-making using proven analytical methods and techniques. For example, propensity score (PS) methodology can be applied to pre-select a subset of real-world data containing patients that are similar to those in the current clinical study in terms of covariates, and to stratify the selected patients together with those in the current study into more homogeneous strata. Then, methods such as the power prior approach or composite likelihood approach can be applied in each stratum to draw inference for the parameters of interest. This package provides functions that implement the PS-integrated RWE analysis methods proposed in Wang et al. (2019) <doi:10.1080/10543406.2019.1657133>, Wang et al. (2020) <doi:10.1080/10543406.2019.1684309> and Chen et al. (2020) <doi:10.1080/10543406.2020.1730877>.

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License  GPL (>= 3)

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**Description**

This package provides R functions for conducting clinical studies with real-world evidence (RWE) incorporated in the study design and analysis.

**PS-integrated power prior**

We extend the Bayesian power prior approach for a single-arm study (the current study) to leverage external real-world data (RWD). We use propensity score methodology to pre-select a subset of real-world data containing patients that are similar to those in the current study in terms of covariates, and to stratify the selected patients together with those in the current study into more homogeneous strata. The power prior approach is then applied in each stratum to obtain stratum-specific posterior distributions, which are combined to complete the Bayesian inference for the parameters of interest.

**PS-integrated composite likelihood**

A propensity score-integrated composite likelihood (PSCL) approach is developed for cases in which the control arm of a two-arm randomized controlled trial (RCT) (treated vs. control) is augmented with patients from real-world data (RWD) containing both clinical outcomes and covariates at the patient-level. The PSCL approach first estimates the propensity score for every patient as the probability of the patient being in the RCT rather than the RWD, and then stratifies all patients into strata based on the estimated propensity scores. Within each propensity score stratum, a composite likelihood function is specified and utilized to down-weight the information contributed by the RWD source. Estimates of the stratum-specific parameters are obtained by maximizing the composite likelihood function. These stratum-specific estimates are then combined to obtain an overall population-level estimate of the parameter of interest.

**References**


**ex_dta**

*Example dataset Example dataset of a single arm study.*

**Description**

Example dataset
Example dataset of a single arm study.

**Usage**

`data(ex_dta)`

**Format**

A data frame with the following variables:

- Groupcurrent, rwd
- Y_BinBinary outcome
- Y_ConContinuous outcome
- Y_SurvSurvival outcome in days
- StatusEvent status (0=alive, 1=dead)
- V1-V7Covariates

---

**ex_dta_rct**

*Example dataset Example dataset of a randomized study.*

**Description**

Example dataset
Example dataset of a randomized study.

**Usage**

`data(ex_dta_rct)`

**Format**

A data frame with the following variables:

- Groupcurrent, rwd
- Armcontrol, treatment
- Y_ConContinuous outcome
- V1-V7Covariates
get_distance

Distance between two distributions

Description

Calculate difference measures using different metrics.

Usage

get_distance(
  cov0,
  cov1,
  metric = c("ovl", "ksd", "astd", "std", "abd", "ley", "mhb", "omkss")
)

Arguments

cov0 Vector (or matrix for metric = "mhb") of samples from the first distribution.
cov1 Vector (or matrix for metric = "mhb") of samples from the second distribution.
metric Metric to use for calculating the distance with options:
  ovl Overlapping area (default)
  ksd Kullback-Leibler distance
  astd Standardized absolute mean difference
  std Standardized mean difference
  abd Absolute difference in means
  ley Levy distance
  mhb Mahalanobis distance
  omkss One minus Kolmogorov-Smirnov statistic

Value

A real value of the distance.

Examples

x <- rnorm(100, mean = 0, sd = 1)
y <- rnorm(1000, mean = 1, sd = 2)
get_distance(x, y, "ovl")
get_distance(x, y, "abd")
plot.PSRWE_DTA  

Plot PS distributions

Description

S3 method for visualizing PS adjustment

Usage

```r
## S3 method for class 'PSRWE_DTA'
plot(x, plot_type = c("ps", "balance", "diff"), ...)
```

Arguments

- `x`: Class RWE_DWITHPS created by psrwe_* functions
- `plot_type`: Types of plots.
  - `ps`: PS density plot
  - `balance`: Covariate balance plot
  - `diff`: Standardized mean differences, metric = std or astd
- `...`: Additional parameter for the plot

plot.PSRWE_DTA_MAT  

Plot PS distributions

Description

S3 method for visualizing PS adjustment based on matching.

Usage

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

Arguments

- `x`: A list of class PSRWE_DTA_MAT that is generated using the psrwe_match function.
- `...`: Parameters for plot.PSRWE_DTA

See Also

plot.PSRWE_DTA
**plot.PSRWE_RST**

*Plot estimation results for power prior approach*

**Description**

S3 method plotting estimation results

**Usage**

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

**Arguments**

- `x` A list of class PSRWE_RST that is generated using the `psrwe_powerp`, `psrwe_compl`, or `psrwe_survkm` function.
- `...` Additional parameters.

**print.PSRWE_BOR**

*Print borrow information*

**Description**

Print summary information of borrowing

**Usage**

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

**Arguments**

- `x` A list of class PSRWE_BOR that is generated using the `psrwe_borrow` function.
- `...` Additional parameters

**See Also**

`psrwe_borrow`
print.PSRWE_DTA  

*Print PS estimation results*

**Description**

Print summary information of PS estimation results

**Usage**

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

**Arguments**

- `x`: A list of class `PSRWE_DTA` that is generated using the `psrwe_est` function.
- `...`: Parameters for `summary.PSRWE_DTA`

**See Also**

`summary.PSRWE_DTA`

---

print.PSRWE_DTA_MAT  

*Print PS estimation results*

**Description**

Print summary information of PS estimation results

**Usage**

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

**Arguments**

- `x`: A list of class `PSRWE_DTA_MAT` that is generated using the `psrwe_match` function.
- `...`: Additional parameters

**See Also**

`summary.PSRWE_DTA_MAT`
**print.PSRWE_RST**

*Print estimation results*

---

**Description**

Print summary information of outcome mean estimation results

**Usage**

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

**Arguments**

- `x`: A list of class PSRWE_RST that is generated using the `psrwe_powerp, psrwe_compl`, or `psrwe_survkm` function.
- `...`: Additional parameters

**See Also**

- `summary.PSRWE_RST`

---

**print.PSRWE_RST.OUTANA**

*Print outcome analysis results*

---

**Description**

Print summary information of outcome analysis results

**Usage**

```r
## S3 method for class 'PSRWE_RST_OUTANA'
print(x, show_details = FALSE, show_rct = FALSE, ...) # S3 method for class 'PSRWE_RST_OUTANA'
```

**Arguments**

- `x`: A list of class PSRWE_RST_OUTANA that is generated using the `psrwe_outana` function.
- `show_details`: print out more observed summary
- `show_rct`: print out more analysis summary for RCT arms
- `...`: Additional parameters
psrwe_borrow Get number of subjects borrowed from each statum

Description

Based on PS distances or number of current control subjects, split the total number of subjects to be borrowed from the external data source to each stratum.

Usage

```r
psrwe_borrow(
  dtaps,
  total_borrow,
  method = c("distance", "inverse_distance"),
  ...
)
```

Arguments

dtaps A class PSRWE_DTA or PSRWE_DTA_MAT object.
total_borrow Total number of subjects to be borrowed.
method Method to split total_borrow for a class PSRWE_DTA object, which can be based on distance (method = "distance") or inverse distance (method = "inverse_distance"). Ignored for class PSRWE_DTA_MAT object.
... Additional parameters for summary.PSRWE_DTA.

Value

A class PSRWE_BORR list. It appends the following items to the dtaps:

- Proportion: Proportion splitting the number of total borrow among strata.
- N_Borrow: The number of to be borrowed subjects in each stratum.
- Alpha: Weight parameter value in each stratum.

Examples

```r
data(ex_dta)
dta_ps <- psrwe_est(ex_dta,
  v_covs = paste("V", 1:7, sep = ""),
  v_grp = "Group",
  cur_grp_level = "current")
ps_borrow <- psrwe_borrow(total_borrow = 20, dta_ps)
ps_borrow

## Use different similarity metric
ps_borrow_omkss <- psrwe_borrow(total_borrow = 20, dta_ps,
```
psrwe_ci

Confidence/Credible Interval for PS-Integrated Estimation Estimate the confidence/credible interval for the PS-integrated approach.

Description

Confidence/Credible Interval for PS-Integrated Estimation

Estimate the confidence/credible interval for the PS-integrated approach.

Usage

psrwe_ci(
  dta_psrst,
  method_ci = c("wald", "wilson"),
  conf_type = c("log_log", "plain"),
  conf_int = 0.95,
  ...
)

Arguments

dta_psrst a returned object with class PSRWE_EST
method_ci a method name for confidence interval (default Wald)
conf_type a type name of transformation for the confidence interval of PSKM approach (default log_log)
conf_int a two-sided level of confidence/credible limits (default 0.95)
... other options

Details

method_ci = "wilson" is for binary outcomes only.

Value

A list with class name PSRWE_EST.
Examples

```r
data(ex_dta)
dta_ps <- psrwe_est(ex_dta, 
v_covs = paste("V", 1:7, sep = ""), 
v_grp = "Group", 
cur_grp_level = "current")
ps_borrow <- psrwe_borrow(total_borrow = 30, dta_ps)
ps_rst <- psrwe_compl(ps_borrow, v_outcome = "Y_Con")
rst <- psrwe_ci(ps_rst)
rst
```

---

**psrwe_compl**

**PS-Integrated Composite Likelihood Estimation**

---

**Description**

Estimate the mean of the outcome based on PS-integrated composite likelihood approach. Variance is estimated by Jack-Knife method. Applies to the case when there is only one external data source.

**Usage**

```r
psrwe_compl(
  dta_psbor, 
  v_outcome = "y", 
  outcome_type = c("continuous", "binary"), 
  ... 
)
```

**Arguments**

- `dta_psbor` A class PSRWE_BOR object generated by `psrwe_borrow`.
- `v_outcome` Column name corresponding to the outcome.
- `outcome_type` Type of outcomes: continuous or binary.
- `...` Parameters for `rwe_cl`

**Value**

A data frame with class name PSRWE_RST. It contains the composite estimation of the mean for each stratum as well as the jackknife estimation for each subject. The results should be further summarized by its S3 method `summary`. 
Examples

data(ex_dta)
data_ps <- psrwe_est(ex_dta,
v_covs = paste("V", 1:7, sep = ""),
v_grp = "Group",
cur.grp_level = "current")
ps_borrow <- psrwe_borrow(total_borrow = 30, dta_ps)
rst <- psrwe_compl(ps_borrow, v_outcome = "Y_Con")
rst

---

psrwe_est

Estimate propensity scores

Description

Estimate propensity scores using logistic regression or random forest model.

Usage

psrwe_est(
data,
ps_fml = NULL,
ps_method = c("logistic", "randomforest"),
v_covs = "V1",
v_grp = "Group",
cur.grp_level = 1,
v_arm = NULL,
ctl_arm_level = NULL,
stra_ctl_only = TRUE,
nstrata = 5,
...)

Arguments

data
ps_fml
ps_method
v_covs
v_grp
cur.grp_level
v_arm

Data frame with group assignment and covariates.
Propensity score (PS) formula. If NULL, all covariates will be included in the PS model in a linear form.
Method to calculate propensity scores. Can be set to logistic for logistic regression or randomforest for a random forest approach.
Column names corresponding to covariates.
Column name corresponding to group assignment.
Group level for the current study. Default is cur.grp_level = 1. Ignored for single arm studies.
Column name corresponding to arm assignment.
ctl_arm_level  Arm level for the control arm. Ignored for single-arm studies.
stra_ctl_only Create strata by control arm patients only. Default TRUE. Ignored by single arm studies. For randomized studies, when stra_ctl_only is FALSE, strata are created based on the PS scores of the entire current study patients.
nstrata  Number of PS strata to be created.
...  Additional parameters for calculating the propensity score to be used in randomForest or glm.

Value
A list of class PSRWE_DAT with items:

- dataOriginal data with column _ps_ for estimated PS scores and _strata_ for PS stratum added.
- ps.fmlPS formula for estimated PS scores.
- is_rctWhether the current study is a randomized study.
- nstrataNumber of strata.

Examples

data(ex_dta)
psrwe_est(ex_dta,
  v_covs = paste("V", 1:7, sep = ""),
  v_grp = "Group",
  cur_grp_level = "current")

__psrwe_infer__

Inference for the PS-Integrated Estimation Inference for the PS-integrated approach.

Description
Inference for the PS-Integrated Estimation
Inference for the PS-integrated approach.

Usage

psrwe_infer(dta_psrst, alternative = c("less", "greater"), mu = 0)

Arguments

dta_psrst  a returned object with class PSRWE_EST
alternative  a character string for the alternative hypothesis that must be one of "less" (default) or "greater"
mu  a number indicating the true value of the parameter of interest (or the difference in means for two arms)
**psrwe_match**

**Value**

A list with class name PSRWE_EST.

**Examples**

```r
data(ex_dta)
dta_ps <- psrwe_est(ex_dta,
                   v_covs = paste("V", 1:7, sep = ""),
                   v_grp = "Group",
                   cur_grp_level = "current")
ps_borrow <- psrwe_borrow(total_borrow = 30, dta_ps)
ps_rst <- psrwe_compl(ps_borrow, v_outcome = "Y_Con")
rst <- psrwe_infer(ps_rst)
rst
```

**Description**

Match patients in external data source with patients in current study based on PS using nearest neighbor method.

**Usage**

```r
psrwe_match(
  dta_ps,
  ratio = 3,
  strata_covs = NULL,
  caliper = 1,
  seed = NULL,
  method = c("nnwor", "optm"),
  ...
)
```

**Arguments**

- `dta_ps`: A list of class PSRWE_DAT that is generated using the `psrwe_est` function.
- `ratio`: Matching ratio (RWD : Current) with default value 3 meaning 3:1 matching.
- `strata_covs`: Stratification covariates for matching.
- `caliper`: PS matching caliper width. Default 1. This specifies a width (euclidean distance) on the probability scale.
- `seed`: Random seed.
- `method`: matching algorithm for PS matching.
- `...`: Additional parameters for matching.
Value

A list of class `PSRWE_DTA_MAT` with items:

- `data`: Original data with column `_ps_` for estimated PS scores, `match_id` for matched current study subject ID, and `_strata_` for PS stratum added.
- `ps_fml`: PS formula for estimated PS scores.
- `nstrata`: Number of strata.
- `ratio`: Matching ratio.

Examples

data(ex_dta)
dta_ps <- psrwe_est(ex_dta,  
v_covs = paste("V", 1:7, sep = ""),  
v_grp = "Group",  
cur_grp_level = "current")
dta_ps_mat <- psrwe_match(dta_ps, ratio = 2, strata_covs = "V1",  
seed = 123)
dta_ps_mat

## With optmatch
.remark_optmatch <- function() {  
warning("The optmatch package may restrict use (academic license).")  
dta_ps_opt <- psrwe_match(dta_ps, ratio = 2,  
strata_covs = "V1",  
method = "optm", seed = 123)  
dta_ps_opt
}

## Unmark below to run if optmatch is available.
# .remark_optmatch()
```r
conf_int = 0.95,
alternative = c("less", "greater"),
mu = 0,
...
)

Arguments

dta_psrst  a returned object with class PSRWE_EST
method_ci  a method name for confidence interval (default Wald)
conf_type  a type name of transformation for the confidence interval of PSKM approach
           (default log_log)
conf_int   a two-sided level of confidence/credible limits (default 0.95)
alternative a character string for the alternative hypothesis that must be one of "less" (default) or "greater"
mu        a number indicating the true value of the parameter of interest (or the difference
           in means for two arms)
...        other options

Details

This function is mainly for summarizing and reporting the outcome analysis for the PS-integrated
estimation. The input dta_psrst can be generated from the functions psrwe_powerp, psrwe_compl,
and psrwe_survkm. See the functions psrwe_ci and psrwe_infer for the options of outcome
analyses.

Value

A list with class name PSRWE_EST_OUTANA.

Examples

data(ex_dta)
dta_ps <- psrwe_est(ex_dta,
   v_covs = paste("V", 1:7, sep = ""),
   v_grp = "Group",
   cur_grp_level = "current")
ps_borrow <- psrwe_borrow(total_borrow = 30, dta_ps)
ps_rst <- psrwe_compl(ps_borrow, v_outcome = "Y_Con")
rst <- psrwe_outana(ps_rst)
rst
```
psrwe_powerp

Get posterior samples based on PS-power prior approach

Description

Draw posterior samples of the parameters of interest for the PS-power prior approach

Usage

psrwe_powerp(
  dta_psbor,
  v_outcome = "Y",
  outcome_type = c("continuous", "binary"),
  prior_type = c("fixed", "random"),
  ...
  seed = NULL
)

Arguments

dta_psbor A class PSRWE_BOR object generated by psrwe_borrow.
v_outcome Column name corresponding to the outcome.
outcome_type Type of outcomes: continuous or binary.
prior_type Whether treat power parameter as fixed (fixed) or fully Bayesian (random).
... extra parameters for calling function rwe_stan.
seed Random seed.

Value

A class PSRWE_RST list with the following objects

**Observed**  Observed mean and SD of the outcome by group, arm and stratum

**Control**  A list of estimated mean and SD of the outcome by stratum in the control arm

**Treatment**  A list of estimated mean and SD of the outcome by stratum in the treatment arm for RCT

**Effect**  A list of estimated mean and SD of the treatment effect by stratum for RCT

**Borrow**  Borrowing information from dta_psbor

**stan_rst**  Result from STAN sampling
Examples

```r
data(ex_dta)
dta_ps <- psrwe_est(ex_dta,
  v_covs = paste("V", 1:7, sep = ""),
  v_grp = "Group",
  cur_grp_level = "current")
ps_borrow <- psrwe_borrow(total_borrow = 30, dta_ps)
rst <- psrwe_powerp(ps_borrow, v_outcome = "Y_Con", seed = 123)
```

---

**psrwe_survkm**  
*PS-Integrated Kaplan-Meier Estimation*

**Description**

Estimate the mean of a survival outcome at a given time point based on PS-integrated Kaplan-Meier approach. Variance is estimated by Jack-Knife method. Applies to the case when there is only one external data source.

**Usage**

```r
psrwe_survkm(dta_psbor, v_time = "time", v_event = "event", pred_tp = 1, ...)
```

**Arguments**

- `dta_psbor`  
  A class PSRWE_BOR object generated by `psrwe_borrow`.

- `v_time`  
  Column name corresponding to event time

- `v_event`  
  Column name corresponding to event status

- `pred_tp`  
  Time of interest (e.g., 1 year)

- `...`  
  Additional Parameters.

**Value**

A data frame with class name PSRWE_RST. It contains the composite estimation of the mean for each stratum as well as the jackknife estimation. The results should be further summarized by its S3 method summary.

**Examples**

```r
data(ex_dta)
dta_ps <- psrwe_est(ex_dta,
  v_covs = paste("V", 1:7, sep = ""),
  v_grp = "Group",
  cur_grp_level = "current")
ps_borrow <- psrwe_borrow(total_borrow = 30, dta_ps)
```
```r
rst <- psrwe_survkm(ps_borrow,
  v_time = "Y_Surv",
  v_event = "Status")
rst
```

---

**rwe_cl**  
*Composite Likelihood Estimation*

**Description**

Estimate parameter of interest based composite likelihood for a single PS stratum

**Usage**

```r
rwe_cl(
  dta_cur,
  dta_ext,
  n_borrow = 0,
  outcome_type = c("continuous", "binary"),
  equal_sd = TRUE
)
```

**Arguments**

- `dta_cur` Vector of outcome from a PS stratum in current study
- `dta_ext` Vector of outcome from a PS stratum in external data source
- `n_borrow` Number of subjects to be borrowed
- `outcome_type` Type of outcomes: continuous or binary.
- `equal_sd` Boolean. whether sd is the same between the current study and external data source

**Value**

Maximum composite likelihood estimator of the mean

**Examples**

```r
x <- rnorm(100, mean = 0, sd = 1)
y <- rnorm(1000, mean = 1, sd = 2)
rwe_cl(x, y, n_borrow = 20, equal_sd = FALSE)
```
**rwe_cut**

*Create strata*

**Description**

Cut a sequence of numbers into bins.

The cut points are chosen such that there will with equal numbers in each bin for \( x \). By default, values of \( y \) that are outside the range of \( x \) will be excluded from the bins, unless they are in the `keep_inx`.

**Usage**

```r
rwe_cut(x, y = x, breaks = 5, keep_inx = NULL)
```

**Arguments**

- `x`: Vector of values based on which cut points will be determined
- `y`: Vector of values to be cut, default to be the same as `x`
- `breaks`: Number of cut points
- `keep_inx`: Indices of `y` that will be categorized as 1 or the largest bin even if their values are out of range of `x`, i.e. the `y`'s that will not be trimmed

**Value**

A vector of stratum assignment for `y`. The `y`'s that are outside the range of `x` and not in `keep_inx` are assigned `NA` in the result.

**Examples**

```r
x <- rnorm(100, mean = 0, sd = 1)
y <- rnorm(1000, mean = 1, sd = 2)
rwe_cut(x, y, breaks = 5)
```

---

**rwe_km**

*Kaplan-Meier Estimation*

**Description**

Estimate survival probability based on Kaplan-Meier estimator for a single PS stratum

**Usage**

```r
rwe_km(dta_cur, dta_ext = NULL, n_borrow = 0, pred_tp = 1)
```
Arguments

dta_cur  Matrix of time and event from a PS stratum in current study
dta_ext  Matrix of time and event from a PS stratum in external data source
n_borrow Number of subjects to be borrowed
pred_tp  Time points to be estimated

Value

Estimation of survival probabilities at time pred_tps

---

rwe_stan  

Call STAN models

Description

Call STAN models. Called by psrwe_powerp.

Usage

rwe_stan(
  lst_data,
  stan_mdl = c("powerps", "powerpsbinary", "powerp"),
  chains = 4,
  iter = 2000,
  warmup = 1000,
  control = list(adapt_delta = 0.95),
  ...
)

Arguments

lst_data  List of study data to be passed to STAN
stan_mdl  STAN model including
  powerps  PS-power prior model for continuous outcomes
  powerpsbinary  PS-power prior model for binary outcomes
  powerp  Power prior model
chains  STAN parameter. Number of Markov chains
iter  STAN parameter. Number of iterations
warmup  STAN parameter. Number of burnin.
control  STAN parameter. See rstan::stan for details.
  ...  other options to call STAN sampling such as thin, algorithm. See rstan::sampling for details.

Value

Result from STAN sampling
Summary PS estimation and stratification results

Description

Get number of subjects and the distances of PS distributions for each PS stratum.

Usage

```r
## S3 method for class 'PSRWE_DTA'
summary(object, metric = c("ovl", "ksd", "std", "abd", "ley", "mhb", "omkss"),
      min_n0 = 10,
      ...)
```

Arguments

- `object`: A list of class PSRWE_DTA that is generated using the `psrwe_est` function.
- `metric`: Metric to use for calculating the distance with options:
  - `ovl`: Overlapping area (default)
  - `ksd`: Kullback-Leibler distance
  - `astd`: Standardized absolute mean difference
  - `std`: Standardized mean difference
  - `abd`: Absolute difference in means
  - `ley`: Levy distance
  - `mhb`: Mahalanobis distance
  - `omkss`: One minus Kolmogorov-Smirnov statistic
- `min_n0`: Threshold for number of external subjects, below which the external data in the current stratum will be ignored by setting the PS distance to 0. Default value 10.
- `...`: Additional parameters.

Value

A list with columns:

- **Summary**: A data frame with Stratum, number of subjects in RWD, current study, number of subjects in control and treatment arms for RCT studies, and distance in PS distributions.
- **Overall**: A data frame with overall number of not-trimmed subjects in RWD, number of patients in current study, number of subjects in control and treatment arms for RCT studies, and distance in PS distributions.
- **N**: Vector of total number of total RWD patients, number of trimmed RWD patients, and total number of current study patients.
- **ps_fml**: PS model.
- **Distance_metric**: Metric used for calculating the distance.
Examples

```r
data(ex_dta)
dta_ps <- psrwe_est(ex_dta,
v_covs = paste("V", 1:7, sep = ""),
v_grp = "Group",
cur_grp_level = "current")
dta_ps

## With different similarity metric
print(dta_ps, metric = "omkss")
dta_ps_sum <- summary(dta_ps, metric = "omkss")
```

---

**summary.PSRWE_DTA_MAT**  
*Summarize PS estimation and matching results*

**Description**

Get number of subjects for each PS stratum.

**Usage**

```r
## S3 method for class 'PSRWE_DTA_MAT'
summary(object, ...)
```

**Arguments**

- `object`: A list of class `PSRWE_DTA_MAT` that is generated using the `psrwe_match` function.
- `...`: Additional parameters.

**Value**

A list with columns:

- **Summary**: A data frame with Stratum (defined by covariates), number of subjects in RWD, current study, number of subjects in control and treatment arms for RCT studies.
- **Overall**: A data frame with overall number of not-trimmed subjects in RWD, number of patients in current study, number of subjects in control and treatment arms for RCT studies.
- **N**: Vector of total number of total RWD patients, number of trimmed RWD patients, total number of current study patients, number of current control patients with less than `ratio` matched RWD subjects.
- **ps_fml**: PS model.
- **N_Match**: Number of current control subjects matched with `ratio`, 0 and other number of RWD subjects.
- **ratio**: Matching ratio.
summary.PSRWE_RST

Summarize overall estimation results

Description

S3 method summarizing overall estimation results

Usage

```r
## S3 method for class 'PSRWE_RST'
summary(object, ...)
```

Arguments

- `object`: A list of class `PSRWE_RST` that is generated using the `psrwe_powerp`, `psrwe_compl`, or `psrwe_survkm` function.
- `...`: Additional parameters.

Value

A list with data frames for the borrowing and estimation results.
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