Package ‘MAICtools’

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Type Package

Title Performing Matched-Adjusted Indirect Comparisons (MAIC)

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Description A generalised workflow for Matching-Adjusted Indirect Comparison (MAIC) analysis, which supports both anchored and non-anchored MAIC methods. In MAIC, unbiased trial outcome comparison is achieved by weighting the subject-level outcomes of the intervention trial so that the weighted aggregate measures of prognostic or effect-modifying variables match those of the comparator trial. Measurements supported include time-to-event (e.g., overall survival) and binary (e.g., objective tumor response). The method is described in Signorovitch et al. (2010) <doi:10.2165/11538370-000000000-00000> and Signorovitch et al. (2012) <doi:10.1016/j.jval.2012.05.004>.

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Contents

`AgD_bl` *Description of AgD_bl dataset*

Description

An example data frame containing aggregate summary data from the comparator study.

Usage

```
data(AgD_bl)
```

Format

A data frame with X rows and Y variables:

STUDY Label of the comparator study, e.g., "Study XX-1".

TRT Grouping variable, e.g., "active" or "control".

N Number of subjects in each group.

AGEGR Baseline characteristics variables for matching.

SEX Baseline characteristics variables for matching.

ECOG Baseline characteristics variables for matching.

SMK Baseline characteristics variables for matching.

METBRAIN Baseline characteristics variables for matching.

METLIVER Baseline characteristics variables for matching.

BMI.mean Baseline characteristics variables for matching.

BMI.sd Baseline characteristics variables for matching.

DIAG.mean Baseline characteristics variables for matching.

DIAG.sd Baseline characteristics variables for matching.

Examples

```
data(AgD_bl)
head(AgD_bl)
```

`AgD_eff` *Description of AgD_eff dataset*

Description

An example data frame containing aggregate results data from the comparator study.

Usage

```
data(AgD_eff)
```

Format

A data frame with X rows and Y variables:

STUDY Label of the comparator study, e.g., "Study XX-1".

PARAM Subsets to be analyzed, e.g., "PFSINV", "OS".

EST Point estimate of the effect size.

CIL The lower confidence limit of the point estimate of the effect size.

CIU The upper confidence limit of the point estimate of the effect size.

Examples

```
data(AgD_eff)
head(AgD_eff)
```

`anchored_maic` *Conduct Anchored Matching-Adjusted Indirect Comparison (MAIC).*

Description

The endpoint of interest is either time-to-event (e.g., overall survival) or binary (e.g., objective tumor response). The methods described in this documentation are based on those originally outlined by Signorovitch et al., 2012, and further detailed in the National Institute for Health and Care Excellence (NICE) Decision Support Unit (DSU) Technical Support Document (TSD) 18.

Arguments

`ipds_wts`	A data frame containing individual patient data from the intervention study, with a column containing the estimated weights (derived using `estimate_weights`).
`intervention.arm`	The name of the grouping column in the data frame specified by `ipds_wts`, e.g., intervention.arm = TRT. The default is `TRT`.
`agds_eff`	A data frame containing aggregate efficacy results from the comparator study.
`comparator`	The name of the study column in the data frame specified by `agds_eff`, e.g., `comparator` = `STUDY`. The default is `STUDY`.
`comparator.study`	A character specifying the comparator study, which must be quoted and cannot be empty (e.g., `comparator.study` = `"Study XX-1"`). This is the value of the study column in `agds_eff` set by the `comparator` parameter.
`ipds.param.var`	The name of the column that specifies only a subset of the `ipds_wts` to be used.
`ipds.param`	A character specifying the subset of the rows to be used. This is the value of the column set by the `ipds.param.var`.
`agds.param.var`	The name of the column that specifies only a specific result of the `agds_eff` to be used.
`agds.param`	A character specifying the subset of the rows to be used. This is the value of the column set by the `agds.param.var`.
`agds.estimate`	The column name of the point estimate of the effect size.
`agds.ci.lower`	The column name for the lower confidence limit of the point estimate of the effect size.
`agds.ci.upper`	The column name for the upper confidence limit of the point estimate of the effect size.
`time`	The name of the survival or follow-up time column in the `ipds_wts`.
`status`	The status indicator, normally 0 = event, 1 = censored. Can be reset using the `event` parameter.
`event`	A numeric value that represents the survival status, 0 = event, 1 = censored.
`response`	The name of the response status column in the `ipds_wts`.

`stralist`	A string specifying the stratification factors in a stratified analysis, e.g., `stralist = "BPDL1, CNSBRAIN, AGEGR"`.
`dtype`	Two options are available: "HR" and "OR". The default is "HR".
`wt.col`	The name of the estimated weights column in the data frame specified by `ipds_wts`. The default is `wt`.
`CIw`	The numeric value specifying the width of the confidence interval, with a default of 0.95.
`digits`	Specify the number of decimal places for the output results.

Value

A data frame containing the anchored matching-adjusted indirect comparison results.

Examples

```
results1 <- anchored_maic(
  ipds_wts = pts, intervention.arm = TRT,
  agds_eff = AgD_eff, comparator = STUDY,
  comparator.study = "Study XX-1",
  ipds.param.var = PARAMCD, ipds.param = "OS",
  agds.param.var = PARAM, agds.param = "OS",
  agds.estimate = EST, agds.ci.lower = CIL, agds.ci.upper = CIU,
  time = AVAL, status = CNSR, event = 0,
  stralist = "BPDL1, CNSBRAIN, AGEGR", dtype = "HR",
  wt.col = wt, CIw = 0.95, digits = 2)

results1

results2 <- anchored_maic(
  ipds_wts = pts, intervention.arm = TRT,
  agds_eff = AgD_eff, comparator = STUDY,
  comparator.study = "Study XX-1",
  agds.param.var = PARAM, agds.param = "ORR",
  agds.estimate = EST, agds.ci.lower = CIL, agds.ci.upper = CIU,
  response = RESP,
  stralist = "BPDL1, CNSBRAIN, AGEGR", dtype = "OR",
  wt.col = wt, CIw = 0.95, digits = 2)

results2
```

`check_matching` *Check Whether the Variables are Balanced After Weighting*

Description

Check Whether the Variables are Balanced After Weighting

Arguments

`ipds_wts`	A data frame containing individual patient data from the intervention study, with a column containing the estimated weights (derived using `estimate_weights`).
`agds`	A data frame containing aggregate summary data from the comparator study.
`summary.list`	A character list with two elements giving the names of variables for summarizing: the first is a vector of binary variables, and the second is a vector of continuous variables. The variable names must match the column names in *ipds* and do not need to be the same as those in *matching.list*. Use c() if a type is absent.
`matching.list`	A character list with two elements giving the names of variables for matching: the first is a vector of binary variables, and the second is a vector of continuous variables. The variable names must match the column names in *ipds* and *agds*. Use c() if a type is absent.
`intervention.arm`	The name of the grouping column in the data frame specified by *ipds*, e.g., `intervention.arm = TRT`. The default is `TRT`.
`comparator`	The name of the study column in the data frame specified by *agds*, e.g., `comparator = STUDY`. The default is `STUDY`.
`comparator.study`	A character specifying the comparator study, which must be quoted and cannot be empty (e.g., `comparator.study = "Study XX-1"`). This is the value of the study column in *agds* set by the *comparator* parameter.
`comparator.arm`	The name of the grouping column in the data frame specified by *agds*, e.g., `comparator.arm = TRT`. The default is `TRT`.
`comparator.n`	The name of the subjects number column in the data frame specified by *agds*, e.g., `comparator.n = N`. The default is `N`.
`wt.col`	The name of the estimated weights column in the data frame specified by *ipds_wts*. The default is `wt`.

Value

A data frame containing all specified variables summarised before and after weighting.

Examples

```
cov <- list(
  binary = c("ECOG", "SMK", "METBRAIN"),
  continuous = c("BMI", "DIAG")
)

cov_all <- list(
  binary = c("SEX", "ECOG", "SMK", "METBRAIN", "METLIVER"),
  continuous = c("BMI", "DIAG", "WEIGHT", "HEIGHT")
)

baseline <- check_matching(
  ipds_wts = pts, agds = AgD_bl,
```

```
  summary.list = cov_all, matching.list = cov,
  intervention.arm = TRT,
  comparator = STUDY, comparator.study = "Study XX-1",
  comparator.n = N, comparator.arm = TRT)

baseline
```

`check_matching2wider` *Convert a Longer Table Generated by check_matching() Into a Wider Table*

Description

Convert a Longer Table Generated by check_matching() Into a Wider Table

Arguments

`baseline.longer`	A data frame containing the summarised results generated by *check_matching()*.
`intervention.arm`	The name of the grouping column in the data frame specified by *ipds*, e.g., intervention.arm = TRT. The default is TRT.
`digits`	Specify the number of decimal places for the output results.

Value

A data frame containing the summarized results in a wider format.

Examples

```
cov <- list(
  binary = c("ECOG", "SMK", "METBRAIN"),
  continuous = c("BMI", "DIAG")
)

cov_all <- list(
  binary = c("SEX", "ECOG", "SMK", "METBRAIN", "METLIVER"),
  continuous = c("BMI", "DIAG", "WEIGHT", "HEIGHT")
)

baseline <- check_matching(
  ipds_wts = pts, agds = AgD_bl,
  summary.list = cov_all, matching.list = cov,
  intervention.arm = TRT,
  comparator = STUDY, comparator.study = "Study XX-1",
  comparator.n = N, comparator.arm = TRT)
```

```
baseline_summary <- check_matching2wider(
  baseline.longer = baseline,
  intervention.arm = TRT)

baseline_summary
```

`estimate_ess` *Estimate Effective Sample Size (ESS)*

Description

Estimate Effective Sample Size (ESS)

Arguments

`ipds_wts`	A data frame containing individual patient data from the intervention study, with a column containing the estimated weights (derived using `estimate_weights`).
`agds`	A data frame containing aggregate summary data from the comparator study.
`intervention.arm`	The name of the grouping column in the data frame specified by *ipds*, e.g., intervention.arm = TRT. The default is TRT.
`comparator`	The name of the study column in the data frame specified by *agds*, e.g., comparator = STUDY. The default is STUDY.
`comparator.study`	A character specifying the comparator study, which must be quoted and cannot be empty (e.g., comparator.study = "Study XX-1"). This is the value of the study column in *agds* set by the *comparator* parameter.
`comparator.arm`	The name of the grouping column in the data frame specified by *agds*, e.g., comparator.arm = TRT. The default is TRT.
`comparator.n`	A The name of the subjects number column in the data frame specified by *agds*, e.g., comparator.n = N. The default is N.
`wt.col`	The name of the estimated weights column in the data frame specified by *ipds_wts*. The default is wt.
`digits`	Specify the number of decimal places for the output results.

Value

A data frame containing effective sample size (ESS) after weighting.

Examples

```
ess <- estimate_ess(
  ipds_wts = pts, agds = AgD_bl,
  intervention.arm = TRT,
  comparator = STUDY, comparator.study = "Study XX-1", comparator.arm = TRT,
  comparator.n = N)
ess
```

`estimate_weights` *Functions for the Estimation of Propensity Weights*

Description

Functions for the Estimation of Propensity Weights

Arguments

`ipds`	A data frame containing individual patient data from the intervention study, with baseline characteristic variables for matching.
`agds`	A data frame containing aggregate summary data from the comparator study.
`matching.list`	A character list with two elements giving the names of variables for matching: the first is a vector of binary variables, and the second is a vector of continuous variables. The variable names must match the column names in *ipds* and *agds*. Use c() if a type is absent.
`intervention.arm`	The name of the grouping column in the data frame specified by *ipds*, e.g., intervention.arm = TRT. The default is TRT.
`comparator`	The name of the study column in the data frame specified by *agds*, e.g., comparator = STUDY. The default is STUDY.
`comparator.study`	A character specifying the comparator study, which must be quoted and cannot be empty (e.g., comparator.study = "Study XX-1"). This is the value of the study column in *agds* set by the *comparator* parameter.
`comparator.arm`	The name of the grouping column in the data frame specified by *agds*, e.g., comparator.arm = TRT. The default is TRT.
`opt.method`	The optim method to be used. The default is "BFGS".
`seed`	The seed for centralized variable missing value imputation (KNN method).
`...`	Refer to optim for additional parameters.

Value

A data frame containing individual patient data, calculated weights, and rescaled weights.

Examples

```
cov <- list(
  c("ECOG", "SMK", "METBRAIN"),
  c("BMI", "DIAG")
)

pts <- estimate_weights(
  ipds = IPD,
  agds = AgD_bl,
  matching.list = cov,
  intervention.arm = TRT,
  comparator = STUDY,
  comparator.study = "Study XX-1",
  comparator.arm = TRT
)
```

`hist_weights` *Histograms of Weights and Rescaled Weights Distributions*

Description

Histograms of Weights and Rescaled Weights Distributions

Arguments

`ipds_wts`	A data frame containing individual patient data from the intervention study, with a column containing the estimated weights (derived using `estimate_weights`).
`intervention.arm`	The name of the grouping column in the data frame specified by *ipds*, e.g., `intervention.arm` = `TRT`. The default is `TRT`.
`wt.col`	The name of the estimated weights column in the data frame specified by *ipds_wts*. The default is `wt`.
`rswt.col`	The name of the estimated rescaled weights column in the data frame specified by *ipds_wts*. The default is `wt_rs`.
`bin`	The number of bins or bars of the histogram.
`xstepby`	An integer guiding the breaks on the X-axis.
`ystepby`	An integer guiding the breaks on the Y-axis.
`...`	Refer to geom_histogram for additional parameters.

Value

Histograms of weights and rescaled weights distributions.

Examples

```
hist_weights(pts, intervention.arm = TRT, xstepby = 2, ystepby = 50)
```

`IPD` *Description of IPD dataset*

Description

An example data frame containing individual patient data from the intervention study, with baseline characteristic variables for matching.

Usage

```
data(IPD)
```

Format

A data frame with X rows and Y variables:

SUBJID Subject Unique Identifier.

TRT Grouping variable, e.g., "active" or "control".

BPDL1 Stratification factors for stratified analysis.

CNSBRAIN Stratification factors for stratified analysis.

AGEGR Stratification factors for stratified analysis.

WEIGHT Baseline characteristic variables for matching or summarizing.

HEIGHT Baseline characteristic variables for matching or summarizing.

BMI Baseline characteristic variables for matching or summarizing.

DIAG Baseline characteristic variables for matching or summarizing.

SEX Baseline characteristic variables for matching or summarizing.

ECOG Baseline characteristic variables for matching or summarizing.

SMK Baseline characteristics variables for matching.

METBRAIN Baseline characteristics variables for matching.

METLIVER Baseline characteristics variables for matching.

PARAMCD Subsets to be analyzed, e.g., "PFSINV", "OS".

AVAL Survival or follow up time.

CNSR The status indicator, 0 = event, 1 = censored.

RESP Response status, 1 = responder, 0 = non-responder.

Examples

```
data(IPD)
head(IPD)
```

`pseudo` *Description of pseudo dataset*

Description

An example data frame containing pseudo patient data from the comparator study

Usage

```
data(pseudo)
```

Format

A data frame with X rows and Y variables:

SUBJID Subject Unique Identifier.

PARAMCD Subsets to be analyzed, e.g., "PFSINV", "OS".

ARM Label of the comparator study, = "Comparator".

AVAL Survival or follow up time.

CNSR The status indicator, 0 = event, 1 = censored.

wt Weights, = 1.

Examples

```
data(pseudo)
head(pseudo)
```

`pts` *Description of pts dataset*

Description

An example data frame containing individual patient data and estimated weights.

Usage

```
data(pts)
```

Format

A data frame with X rows and Y variables:

SUBJID Subject Unique Identifier.

TRT Grouping variable, e.g., "active" or "control".

BPDL1 Stratification factors for stratified analysis.

CNSBRAIN Stratification factors for stratified analysis.

AGEGR Stratification factors for stratified analysis.

WEIGHT Baseline characteristic variables for matching or summarizing.

HEIGHT Baseline characteristic variables for matching or summarizing.

BMI Baseline characteristic variables for matching or summarizing.

DIAG Baseline characteristic variables for matching or summarizing.

SEX Baseline characteristic variables for matching or summarizing.

ECOG Baseline characteristic variables for matching or summarizing.

SMK Baseline characteristics variables for matching.

METBRAIN Baseline characteristics variables for matching.

METLIVER Baseline characteristics variables for matching.

PARAMCD Subsets to be analyzed, e.g., "PFSINV", "OS".

AVAL Survival or follow up time.

CNSR The status indicator, 0 = event, 1 = censored.

RESP Response status, 1 = responder, 0 = non-responder.

wt Estimated propensity weights.

wt_rs Estimated rescaled propensity weights.

Examples

```
data(pts)
head(pts)
```

`summarize_weights` *Summarize the Distribution of Weight Values*

Description

Summarize the Distribution of Weight Values

Arguments

`ipds_wts`	A data frame containing individual patient data from the intervention study, with a column containing the estimated weights (derived using `estimate_weights`).
`intervention.arm`	The name of the grouping column in the data frame specified by *ipds*, e.g., intervention.arm = TRT. The default is TRT.
`wt.col`	The name of the estimated weights column in the data frame specified by *ipds_wts*. The default is wt.
`rswt.col`	The name of the estimated rescaled weights column in the data frame specified by *ipds_wts*. The default is wt_rs.
`digits`	Specify the number of decimal places for the output results.

Value

A data frame containing a summary table of weights and rescaled weights.

Examples

```
summarize_weights(ipds_wts = pts, intervention.arm = TRT)
```

`unanchored_kmplot` *Generate a Kaplan-Meier Plot with Individual Efficacy Data and Pseudo Efficacy Data.*

Description

Generate a Kaplan-Meier Plot with Individual Efficacy Data and Pseudo Efficacy Data.

Arguments

`unds_wts`	A combined data frame containing individual efficacy data from the intervention study and pseudo efficacy data from the comparator study.
`unds.arm`	The name of the grouping column in the combined data frame specified by *unds_wts*, e.g., comparator.arm = TRT. The default is TRT.
`unds.param.var`	The name of the column that specifies only a subset of the rows of the data to be used.
`unds.param`	A character specifying the subset of the rows to be used. This is the value of the column set by the *unds.param.var*.
`time`	The name of the survival or follow up time column in the combined data frame.
`status`	The status indicator, normally 0 = event, 1 = censored. Can be reseted using the *event* parameter.
`event`	A numeric value that represents the survival status, 0 = event, 1 = censored.

`wt.col`	The name of the estimated weights column in the data frame specified by *unds_wts*. The default is wt.
`km.xlim`	A numeric value specifying the right limit of the scale on the X-axis.
`xstepby`	An integer guiding the breaks on the X-axis.
`km.ylim`	A numeric value specifying the upper limit of the scale on the Y-axis.
`ystepby`	An integer guiding the breaks on the Y-axis.
`xlab`	A character giving label of the X-axis. The default is "Time (Months)".
`ylab`	A character giving label of the Y-axis. The default is "Survival probability".
`km.legend`	A character vector of length >=1 to appear in the legend.
`km.title`	A character used to set the main title at the top.
`...`	Refer to ggsurvplot for additional parameters..

Value

A Kaplan-Meier plot object that contains individual efficacy data from the intervention study and pseudo efficacy data from the comparator study.

Examples

```
unanchored_kmplot(
  unds_wts = unpts, unds.arm = ARM,
  unds.param.var = PARAMCD, unds.param = "OS",
  time = AVAL, status = CNSR, event = 0,
  wt.col = wt, km.xlim = 35, xstepby = 3,
  km.legend = c("Arm A", "ARM B"),
  km.title = "AAAA")
```

`unanchored_maic` *Conduct non-Anchored Matching-Adjusted Indirect Comparison (MAIC).*

Description

Conduct non-Anchored Matching-Adjusted Indirect Comparison (MAIC).

Arguments

`unds_wts`	A combined data frame containing individual efficacy data from the intervention study and pseudo efficacy data from the comparator study.
`unds.arm`	The name of the grouping column in the combined data frame specified by *unds_wts*, e.g., comparator.arm = TRT. The default is TRT.
`comparator.study`	A character specifying or presenting the comparator study, e.g., comparator.study = "Study XX-1".

`unds.param.var`	The name of the column that specifies only a subset of the rows of the data to be used.
`unds.param`	A character specifying the subset of the rows to be used. This is the value of the column set by the *unds.param.var*.
`time`	The name of the survival or follow up time column in the combined data frame.
`status`	The status indicator, normally 0 = event, 1 = censored. Can be reseted using the *event* parameter.
`event`	A numeric value that represents the survival status, 0 = event, 1 = censored.
`response`	The name of the response status column in the *unds_wts*.
`dtype`	Two options are available: "HR" and "OR". The default is "HR".
`wt.col`	The name of the estimated weights column in the data frame specified by *unds_wts*. The default is wt.
`CIw`	The numeric value specifying the width of the confidence interval, with a default of 0.95.
`digits`	Specify the number of decimal places for the output results.

Value

A data frame containing the non-anchored matching-adjusted indirect comparison results.

Examples

```
results3 <- unanchored_maic(
  unds_wts = unpts, unds.arm = ARM,
  comparator.study = "Study XX-1",
  unds.param.var = PARAMCD, unds.param = "OS",
  time = AVAL, status = CNSR, event = 0,
  dtype = "HR")

results3

results4 <- unanchored_maic(
  unds_wts = unpts, unds.arm = ARM,
  #' unds.param = "ORR",
  #' comparator.study = "Study XX-1",
  response = CNSR,
  dtype = "OR")

results4
```

`unanchored_maic_bootstrap`

Conduct non-Anchored Matching-Adjusted Indirect Comparison (MAIC) and Calculate Confidence Intervals (CIs) Using Bootstrap.

Description

```
Two different methods for estimating a 95% confidence interval (CI) from
the bootstrap samples were explored:
* Percentile CIs
* Bias-corrected and accelerated (BCa) CIs
```

Arguments

`ipds`	A data frame containing individual patient data from the intervention study, with baseline characteristic variables for matching.
`psds`	A data frame containing pseudo data from the comparator study.
`agds`	A data frame containing aggregate summary data from the comparator study.
`matching.list`	A character list with two elements giving the names of variables for matching: the first is a vector of binary variables, and the second is a vector of continuous variables. The variable names must match the column names in *ipds* and *agds*. Use c() if a type is absent.
`intervention.arm`	The name of the grouping column in the data frame specified by *ipds*, e.g., intervention.arm = TRT. The default is TRT.
`comparator`	The name of the study column in the data frame specified by *agds*, e.g., comparator = STUDY. The default is STUDY.
`comparator.study`	A character specifying the comparator study, which must be quoted and cannot be empty (e.g., comparator.study = "Study XX-1"). This is the value of the study column in *agds* set by the *comparator* parameter.
`comparator.arm`	The name of the grouping column in the data frame specified by *agds*, e.g., comparator.arm = TRT. The default is TRT.
`ipds.param.var`	The name of the column that specifies only a subset of the *ipds* to be used.
`ipds.param`	A character specifying the subset of the rows to be used. This is the value of the column set by the *ipds.param.var*.
`psds.param.var`	The name of the column that specifies only a specifyed result of the *psds* to be used.
`psds.param`	A character specifying the subset of the rows to be used. This is the value of the column set by the *psds.param.var*.
`time`	The name of the survival or follow up time column.
`status`	The status indicator, normally 0 = event, 1 = censored. Can be reseted using the *event* parameter.

`event`	A numeric value that represents the survival status, 0 = event, 1 = censored.
`response`	The name of the response status column.
`dtype`	Two options are available: "HR" and "OR". The default is "HR".
`n.samples`	The number of bootstrap replicates.
`CIw`	The numeric value specifying the width of the confidence interval, with a default of 0.95.
`digits`	Specify the number of decimal places for the output results.
`...`	Refer to boot for additional parameters.

Value

A list containing 2 objects. First, a data frame containing the non-anchored matching-adjusted indirect comparison results. Second, a bootstrapping diagnostics histogram.

Examples

```
cov <- list(
  c("ECOG", "SMK", "METBRAIN"),
  c("BMI", "DIAG")
)

results5 <- unanchored_maic_bootstrap(
  ipds = IPD,
  agds = AgD_bl,
  psds = pseudo,
  matching.list = cov,
  intervention.arm = TRT,
  comparator = STUDY,
  comparator.study = "Study XX-1",
  comparator.arm = TRT,
  time = AVAL, status = CNSR, event = 0,
  dtype = "HR",
  ipds.param.var = PARAMCD, ipds.param = "OS",
  psds.param.var = NULL, psds.param = NULL,
  n.samples = 1000
)

results5$results
results5$plot
```

`unpts` *Description of unpts dataset*

Description

A combined data frame containing individual efficacy data from the intervention study and pseudo efficacy data from the comparator study.

Usage

```
data(unpts)
```

Format

A data frame with X rows and Y variables:

SUBJID Subject Unique Identifier.

PARAMCD Subsets to be analyzed, e.g., "PFSINV", "OS".

ARM Label of the study, "Intervention" for the intervention study and "Cmparator" for the comparator study.

AVAL Survival or follow up time.

CNSR The status indicator, 0 = event, 1 = censored.

wt Weights to be used.

Examples

```
data(unpts)
head(unpts)
```

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