

Package ‘DeltaTools’

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Title DELTA Analytic Tools and Learning Curve Analysis

Version 0.1.4

Description A collection of tools for researchers interested in carrying out parametric estimation of learning curves and device effects based on the publication by Ssemaganda et al. (2025) <[doi:10.2147/MDER.S520191](https://doi.org/10.2147/MDER.S520191)> with modified versions of propensity score matching (PSM) and inverse probability of treatment weighting (IPTW).

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Imports broom (>= 1.0.12), caret (>= 7.0-1), data.table (>= 1.18.4), DescTools (>= 0.99.60), dplyr (>= 1.2.1), gbm (>= 2.2.3), ggplot2 (>= 4.0.3), glmnet (>= 5.0), ldbounds (>= 2.0.2), lmtree (>= 0.9-40), MatchIt (>= 4.7.2), methods, mgcv (>= 1.9-4), minpack.lm (>= 1.2-4), parameters (>= 0.28.3), plotly (>= 4.12.0), pROC (>= 1.19.0.1), ResourceSelection (>= 0.3-6), rms (>= 8.1-1), ROCR (>= 1.0-12), sjPlot (>= 2.9.0), stats, stringr (>= 1.6.0), tableone (>= 0.13.2), twang (>= 2.6.2)

Suggests kableExtra (>= 1.4.0), knitr (>= 1.51), rmarkdown (>= 2.31), testthat (>= 3.0.0)

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data.plc	<i>Parametric Learning Curve Analysis example data</i>
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Description

A synthetic patient population generated for learning effect and device signal detection using this function.

Usage

data.plc

Format

data.plc:
A data frame with 11,808 rows and 41 columns:
Patient Patient identifier
Operator Operator identifier
Institution Institution identifier
CaseOrder_All Case Order across all observations
CaseOrder_Inst Case Order across that institution
CaseOrder_Op Case Order across that operator
ProcDate Procedure date
CasePeriod Time period during which the case procedure occurred
OutcomePeriod Time period during which the case outcome occurred
CaseOrder_Inst_DevA Case Order across that institution and Device A
CaseOrder_Inst_DevB Case Order across that institution and Device B
CaseOrder_Op_DevA Case Order across that operator and Device A
CaseOrder_Op_DevB Case Order across that oepreator and Device B
Device Device placed during the procedure

Outcome_Final Outcome variable

Pt_F1 Patient factor 1

Pt_F2 Patient factor 2

Pt_F3 Patient factor 3

Pt_F4 Patient factor 4

Pt_F5 Patient factor 5

Pt_F6 Patient factor 6

Pt_F7 Patient factor 7

Pt_F8 Patient factor 8

Pt_F9 Patient factor 9

Pt_F10 Patient factor 10

Pt_F11 Patient factor 11

Pt_F12 Patient factor 12

Pt_F13 Patient factor 13

Pt_F14 Patient factor 14

Pt_F15 Patient factor 15

Pt_F16 Patient factor 16

Pt_F17 Patient factor 17

Pt_F18 Patient factor 18

Pt_F19 Patient factor 19

Pt_F20 Patient factor 20

Pt_F21 Patient factor 21

Op_F1 Operator factor 1

Op_F2 Operator factor 2

Inst_F1 Institution factor 1

Inst_F2 Institution factor 2

Inst_F3 Institution factor 3

data.ps

*Propensity Score Analysis and Inverse Probability of Treatment
Weighting example data*

Description

A synthetic patient population generated for use with the functions propensity score matching or inverse probability of treatment weighting.

Usage

data.ps

Format

`data.ps:`

A data frame with 29,778 rows and 24 columns:

Hypertension Hypertension indicator

Mortality30D 30-day mortality indicator

Aspirin Aspirin use indicator

Warfarin Warfarin use indicator

CreatPreProc_mgdl Pre-procedure serum creatinine level in mg/dL

FluoroMins Fluoroscopy time in minutes

NSTEMIatPresent Non-ST-Elevation Myocardial Infarction at presentation indicator

ProcDate Procedure date

NumVesselsIndexPCI Number of blocked vessels at index percutaneous coronary intervention

Patient Patient identifier

Readmission Hospital readmission indicator

PriorPCI History of percutaneous coronary intervention indicator

Emergent Emergent case indicator

TotalAdmitPCI Total admitted percutaneous coronary interventions

ChrLungDis Chronic lung disease indicator

Smoker Smoker indicator

Female Female sex

Dialysis Dialysis indicator

Diabetes Diabetes indicator

PeripheralArterialDis Peripheral arterial disease indicator

RepeatProc Repeat procedure indicator

DeviceB Device B indicator

Age Patient age in years

BMI Patient BMI in kg/m2

iptwDT

DeltaTools Function: iptwDT

Description

DeltaTools Function: iptwDT

Usage

```
iptwDT(
  data,
  outcomes,
  exposure,
  covariates.factor,
```

```

    covariates.continuous,
    identifier,
    link = "logit",
    avs = TRUE,
    lambda = "lambda.min",
    postmatch.adjusted.model = FALSE,
    allow.trimming = TRUE,
    allow.stabilization = TRUE,
    lower.cutoff = 5,
    upper.cutoff = 95,
    smd.t1 = 0.1,
    smd.t2 = 0.25
  )

```

Arguments

<code>data</code>	The data frame.
<code>outcomes</code>	A character vector of one or more outcomes.
<code>exposure</code>	A character string with the exposure.
<code>covariates.factor</code>	A character vector of factor covariates.
<code>covariates.continuous</code>	A character vector of continuous covariates.
<code>identifier</code>	A character string with the record identifier.
<code>link</code>	Specify the link function as "logit" or "probit".
<code>avs</code>	Set to TRUE to run automatic variable selection.
<code>lambda</code>	Specify lambda as "lambda.min" or "lambda.1se".
<code>postmatch.adjusted.model</code>	Set to TRUE to adjust for additional variables in a logistic regression model on the matched cohort.
<code>allow.trimming</code>	Set to TRUE to trim weights.
<code>allow.stabilization</code>	Set to TRUE to stabilize weights.
<code>lower.cutoff</code>	Quantile for lower cutoff to trim weights, only used if <code>allow.trimming = TRUE</code> . Otherwise, specify NULL.
<code>upper.cutoff</code>	Quantile for upper cutoff to trim weights, only used if <code>allow.trimming = TRUE</code> . Otherwise, specify NULL.
<code>smd.t1</code>	Standardized mean difference threshold 1 (more conservative).
<code>smd.t2</code>	Standardized mean difference threshold 2 (less conservative).

Value

A list containing relevant messages about the weighting and modeling process, descriptive statistics for the unweighted and weighted cohorts stratified by exposure variable, covariate balance assessment, and logistic regression modeling summaries.

Examples

```
# Inverse Probability of Treatment Weighting with automatic variable selection and
# trimmed, stabilized weights
wt <- iptwDT(data=data.ps,
             outcomes=c("Mortality30D", "Readmission", "RepeatProc"),
             exposure="DeviceB",
             covariates.factor=c("Aspirin", "ChrLungDis", "Diabetes", "Dialysis",
                                "Emergent", "Female", "Hypertension", "NSTEMIatPresent",
                                "PeripheralArterialDis", "PriorPCI", "Smoker", "Warfarin"),
             covariates.continuous=c("Age", "BMI", "CreatPreProc_mgdl", "FluoroMins",
                                     "NumVesselsIndexPCI", "TotalAdmitPCI"),
             identifier="Patient")
```

PLCAnalysis

DeltaTools Function: PLCAnalysis

Description

DeltaTools Function: PLCAnalysis

Usage

```
PLCAnalysis(
  data,
  datasetIdentifier = "Dataset1",
  caseIDFieldNM,
  caseDateFieldNM,
  outcomeFieldNM,
  orderFieldNM,
  operatorFieldNM,
  covariateFieldNMs,
  exposureFieldNM,
  exposureOfInterestNM,
  exposureOfInterestOperatorCaseSeriesFieldNM,
  allowIPTWWeighting = FALSE,
  normalizeIPTWWeights = FALSE,
  useGeneralCovariateFieldNMs = TRUE,
  iptwCovariateFieldNMs = c(),
  allowOperatorClustering = FALSE,
  allowGAMBasedAVS = FALSE,
  learningUnadjustedSignalRequired = TRUE,
  leDetectionAlpha = 0.05,
  lcEstimationAlpha = 0.05,
  bootstraps = 0,
  forceEstimationAsymptoteToZero = TRUE,
  deviceSignalEstimationAlpha = 0.05
)
```

Arguments

<code>data</code>	The data frame.
<code>datasetIdentifier</code>	A character string with the dataset identifier.
<code>caseIDFieldNM</code>	A character string with the case identifier.
<code>caseDateFieldNM</code>	A character string with the case date field.
<code>outcomeFieldNM</code>	A character string with the outcome.
<code>orderFieldNM</code>	A character string with the case order field.
<code>operatorFieldNM</code>	A character string with the operator field.
<code>covariateFieldNMs</code>	A character vector of covariates to adjust for in the model.
<code>exposureFieldNM</code>	A character string with the exposure.
<code>exposureOfInterestNM</code>	A character string with the exposure value of interest.
<code>exposureOfInterestOperatorCaseSeriesFieldNM</code>	A character string with the exposure of interest operator case series field.
<code>allowIPTWWeighting</code>	Set to TRUE to allow Inverse Probability of Treatment Weighting.
<code>normalizeIPTWWeights</code>	Set to TRUE to normalize IPTW weights.
<code>useGeneralCovariateFieldNMs</code>	Set to TRUE to use general covariate field names for IPTW.
<code>iptwCovariateFieldNMs</code>	A character vector of covariate field names for IPTW, used when <code>useGeneralCovariateFieldNMs=TRUE</code> .
<code>allowOperatorClustering</code>	Set to TRUE to allow operator clustering.
<code>allowGAMBasedAVS</code>	Set to TRUE to allow generalized additive model-based automatic variable selection.
<code>learningUnadjustedSignalRequired</code>	Set to TRUE to require a learning unadjusted signal be detected before attempting to detect the presence of a learning effect.
<code>leDetectionAlpha</code>	The alpha level for learning detection; the default value is 0.05.
<code>lcEstimationAlpha</code>	The alpha level for learning curve estimation; the default value is 0.05.
<code>bootstraps</code>	The default value for the number of bootstrapped samples is 0; may add other options in the future.
<code>forceEstimationAsymptoteToZero</code>	Defaults to TRUE to force the estimation asymptote to zero; may add other options in the future.

deviceSignalEstimationAlpha

The alpha level for device signal estimation; the default value is 0.05.

Value

A list containing relevant messages about detection of a learning effect and device signal, modeling summaries of the learning unadjusted signal, modeling summaries of the learning adjusted signal, learning detection summaries, and the GAM plot (if applicable).

Examples

```
# Retrospective Parametric Learning Curve Analysis
# Learning effect not detected, unadjusted device signal detected
plc <- PLCAAnalysis(data=data.plc,
  datasetIdentifier="Dataset1",
  caseIDFieldNM="Patient",
  caseDateFieldNM="ProcDate",
  outcomeFieldNM="Outcome_Final",
  orderFieldNM="CaseOrder_All",
  operatorFieldNM="Operator",
  covariateFieldNMs=c("Pt_F1", "Pt_F2", "Pt_F3", "Pt_F4", "Pt_F5",
    "Pt_F6", "Pt_F7", "Pt_F8", "Pt_F9", "Pt_F10",
    "Pt_F11", "Pt_F12", "Pt_F13", "Pt_F14", "Pt_F15",
    "Pt_F16", "Pt_F17", "Pt_F18", "Pt_F19", "Pt_F20",
    "Pt_F21", "Op_F1", "Op_F2", "Inst_F1", "Inst_F2",
    "Inst_F3"),
  exposureFieldNM="Device",
  exposureOfInterestNM="B",
  exposureOfInterestOperatorCaseSeriesFieldNM="CaseOrder_Op_DevB")
```

propensityScoreAnalysis

DeltaTools Function: propensityScoreAnalysis

Description

DeltaTools Function: propensityScoreAnalysis

Usage

```
propensityScoreAnalysis(
  data,
  outcomes,
  exposure,
  covariates.factor,
  covariates.continuous,
  identifier,
  datefield,
  link = "logit",
```

```

    avs = TRUE,
    period.type = "quarter",
    alpha = 0.05,
    m.days = 90,
    m.type = "closest",
    lambda = "lambda.min",
    match.date.range = FALSE,
    m.method = "nearest",
    m.dist = "glm",
    m.dist.opt = list(),
    m.est = "ATT",
    m.exact = NULL,
    m.mahvars = NULL,
    m.antiexact = NULL,
    m.discard = "none",
    m.reestimate = FALSE,
    m.s.weights = NULL,
    m.replace = FALSE,
    m.order = "largest",
    m.caliper = 0.01,
    m.ratio = 1,
    m.verbose = FALSE,
    m.include.obj = FALSE,
    postmatch.adjusted.model = FALSE
  )

```

Arguments

<code>data</code>	The data frame.
<code>outcomes</code>	A character vector of one or more outcomes.
<code>exposure</code>	A character string with the exposure.
<code>covariates.factor</code>	A character vector of factor covariates.
<code>covariates.continuous</code>	A character vector of continuous covariates.
<code>identifier</code>	A character string with the record identifier.
<code>datefield</code>	The observation date if matching within a date range.
<code>link</code>	Specify the link function as "logit" or "probit".
<code>avs</code>	Set to TRUE to run automatic variable selection.
<code>period.type</code>	Specifies time period as "week", "month", "quarter", "half-year", or "year"; specify "none" if not matching within a date range.
<code>alpha</code>	The probability of a Type I error.
<code>m.days</code>	Radius for time period, in days, if matching within a date range.
<code>m.type</code>	Specify matching type as "closest" or "random".
<code>lambda</code>	Specify lambda as "lambda.min" or "lambda.1se".

<code>match.date.range</code>	Set to TRUE to match within a date range.
<code>m.method</code>	Specify matching method as "nearest", "optimal", "full", "quick", "genetic", "cem", "exact", "cardinality", or "subclass".
<code>m.dist</code>	Specify the distance measure as "glm", "mahalanobis", a vector of distance measures, or a matrix of pairwise distances.
<code>m.dist.opt</code>	Specify a list of additional arguments for the function that estimates the distance measure. Otherwise, specify an empty list.
<code>m.est</code>	Specify the target estimand as "ATT" (Average Treatment Effect on the Treated), "ATC" (Average Treatment Effect on the Controls), or "ATE" (Average Treatment Effect).
<code>m.exact</code>	Specify a string with the variables for which exact matching should be used or specify a one-sided formula with the variables on the right-hand side. Otherwise, specify NULL.
<code>m.mahvars</code>	Specify a string with the variables on which Mahalanobis distance matching should be used or specify a one-sided formula with the variables on the right-hand side. Otherwise, specify NULL.
<code>m.antiexact</code>	Specify a string with the names of variables for which anti-exact matching should be used or specify a one-sided formula with the variables on the right-hand side. Otherwise, specify NULL.
<code>m.discard</code>	Specify whether "none", "treated", "control", or "both" units should be discarded when the propensity scores fall outside the common support region.
<code>m.reestimate</code>	Set to TRUE to re-estimate propensity scores in the sample that remains, only used if <code>m.discard</code> is not "none".
<code>m.s.weights</code>	Specify a numeric vector of sampling weights for the propensity score models and balance statistics, a string containing the variable to be used, or a one-sided formula with the variable on the right-hand side. Otherwise, specify NULL.
<code>m.replace</code>	Set to TRUE to match with replacement.
<code>m.order</code>	Specify matching order as "largest" or "data".
<code>m.caliper</code>	A numeric vector of caliper widths for each variable. Otherwise, NULL for no caliper.
<code>m.ratio</code>	Specify an integer for the number of control cases to match with each treated case in k:1 matching.
<code>m.verbose</code>	Set to TRUE to print information on the matching process to the console.
<code>m.include.obj</code>	Set to TRUE to include objects generated during the matching process in the output.
<code>postmatch.adjusted.model</code>	Set to TRUE to adjust for additional variables in a logistic regression model on the matched cohort.

Value

A list containing relevant messages about the matching process, summaries of unmatched and matched cohort variable balance assessment, descriptive statistics, logistic regression modeling summaries, proportional difference summaries, and observed vs expected summaries.

Examples

```
# Match within date range and without replacement using a standard caliper
ps <- propensityScoreAnalysis(data=data.ps,
                              outcomes=c("Mortality30D", "Readmission", "RepeatProc"),
                              exposure="DeviceB",
                              covariates.factor=c("Aspirin", "ChrLungDis", "Diabetes",
                                                    "Dialysis", "Emergent", "Female",
                                                    "Hypertension", "NSTEMIatPresent",
                                                    "PeripheralArterialDis", "PriorPCI",
                                                    "Smoker", "Warfarin"),
                              covariates.continuous=c("Age", "BMI", "CreatPreProc_mgdl",
                                                       "FluoroMins", "NumVesselsIndexPCI",
                                                       "TotalAdmitPCI"),
                              identifier="Patient",
                              datefield="ProcDate",
                              match.date.range=TRUE,
                              m.replace=FALSE,
                              m.caliper=0.2)
```

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