Package ‘LocalControl’

November 26, 2020

Type Package

Title Nonparametric Methods for Generating High Quality Comparative Effectiveness Evidence

Version 1.1.2.2

Date 2020-11-24

Description Implements novel nonparametric approaches to address biases and confounding when comparing treatments or exposures in observational studies of outcomes. While designed and appropriate for use in studies involving medicine and the life sciences, the package can be used in other situations involving outcomes with multiple confounders. The package implements a family of methods for non-parametric bias correction when comparing treatments in observational studies, including survival analysis settings, where competing risks and/or censoring may be present. The approach extends to bias-corrected personalized predictions of treatment outcome differences, and analysis of heterogeneity of treatment effect-sizes across patient subgroups. For further details, please see: Lauve NR, Nelson SJ, Young SS, Obenchain RL, Lambert CG. LocalControl: An R Package for Comparative Safety and Effectiveness Research. Journal of Statistical Software. 2020. p. 1–32. Available from <doi:10.18637/jss.v096.i04>.

License Apache License 2.0 | file LICENSE

SystemRequirements C++11

LazyData TRUE

LinkingTo Rcpp

Imports Rcpp, gss, cluster, lattice, stats, graphics

Suggests colorspace, RColorBrewer, TeachingDemos, data.table, ggplot2, gridExtra, rpart, rpart.plot, xtable

RoxygenNote 7.1.1

Encoding UTF-8

NeedsCompilation yes

Depends R (>= 3.0.0)

Repository CRAN
Maintainer  Christophe G. Lambert <cglambert@unm.edu>

Author  Nicolas R. Lauve [aut] (<https://orcid.org/0000-0002-9348-0319>),
        Stuart J. Nelson [aut] (<https://orcid.org/0000-0002-8756-0179>),
        S. Stanley Young [aut] (<https://orcid.org/0000-0001-9449-5478>),
        Robert L. Obenchain [aut] (<https://orcid.org/0000-0002-8395-1666>),
        Melania Pintilie [ctb],
        Martin Kutz [ctb],
        Christophe G. Lambert [aut, cre]
        (<https://orcid.org/0000-0003-1994-2893>)

Date/Publication  2020-11-26 09:10:05 UTC

R topics documented:

cardSim ................................................................. 2
framingham ............................................................. 3
lindner ................................................................. 4
LocalControl ............................................................ 4
LocalControl-deprecated ............................................. 7
LocalControlClassic .................................................. 8
LocalControlCompetingRisksConfidence ............................. 11
LocalControlNearestNeighborsConfidence ......................... 12
plot.LocalControlCR ................................................. 14
plot.LocalControlCS ................................................ 16
SPSbalan .............................................................. 17
SPSloess ............................................................... 19
SPSlogit .............................................................. 21
SPSnbins ............................................................ 22
SPSoutco ............................................................. 23
UPSadcum ............................................................. 25
UPSaltdd ............................................................. 27
UPSboxplot ........................................................... 29
UPSgraph ............................................................. 30
UPShclus ............................................................. 31
UPSivadj ............................................................. 32
UPSLTDdist .......................................................... 34
UPSnltd .............................................................. 35

Index  38

cardSim  Simulated cardiac medication data for survival analysis

Description

This dataset was created to demonstrate the effects of Local Control on correcting bias within a set of data.
Format

A data frame with 1000 rows and 6 columns:

- **id** Unique identifier for each row.
- **time** Time in years to the outcome specified by status.
- **status** 1 if the patient experienced cardiac arrest. 0 if censored before that.
- **drug** Medication the patient received for cardiac health (drug 1 or drug 0).
- **age** Age of the patient, ranges from 18 to 65 years.
- **bmi** Patient body mass index. Majority of observations fall between 22 and 30.

Author(s)

Lauve NR, Lambert CG

---

**framingham**

"Framingham heart study data extract on smoking and hypertension."

Description

Data collected over a 24 year study suitable for competing risks survival analysis of hypertension and death as a function of smoking.

Format

A data frame with 2316 rows and 11 columns:

- **female** Sex of the patient. 1=female, 0=male.
- **totchol** Total cholesterol of patient at study entry.
- **age** Age of the patient at study entry.
- **bmi** Patient body mass index.
- **BPVar** Average units of systolic and diastolic blood pressure above normal: \(((\text{SystolicBP}-120)/2) + (\text{DiasystolicBP}-80)\)
- **hearrte** Patient heartrate taken at study entry.
- **glucose** Patient blood glucose level.
- **cursmoke** Whether or not the patient was a smoker at the time of study entry.
- **outcome** Did the patient die, experience hypertension, or leave the study without experiencing either event.
- **time_outcome** The time at which the patient experienced outcome.
- **cigpday** Number of cigarettes smoked per day at time of study entry.

References

LocalControl

Description

The effects of Abciximab use on both survival and cardiac billing.

Format

A data frame with 996 rows and 10 columns:

- lifepres  Life years preserved post treatment: 0 (died) vs. 11.6 (survived).
- cardbill  Cardiac related billing in dollars within 12 months.
- abcix     Indicates whether the patient received Abciximab treatment: 1=yes 0=no.
- stent     Was a stent deployed? 1=yes, 0=no.
- height    Patient height in centimeters.
- female    Patient sex: 1=female, 0=male.
- diabetic  Was the patient diabetic? 1=yes, 0=no.
- acutemi   Had the patient suffered an acute myocardial infarction within the last seven days? 1=yes, 0=no.
- ejecfrac  Left ventricular ejection fraction.
- ves1proc  Number of vessels involved in the first PCI procedure.

References


LocalControl

Description

Implements a non-parametric methodology for correcting biases when comparing the outcomes of two treatments in a cross-sectional or case control observational study. This implementation of Local Control uses nearest neighbors to each point within a given radius to compare treatment outcomes. Local Control matches along a continuum of similarity (radii), clustering the near neighbors to a given observation by variables thought to be sources of bias and confounding. This is analogous to combining a host of smaller studies that are each homogeneous within themselves, but represent the spectrum of variability of observations across diverse subpopulations. As the clusters
get smaller, some of them can become noninformative, whereby all cluster members contain only one treatment, and there is no basis for comparison. Each observation has a unique set of near-neighbors, and the approach becomes more akin to a non-parametric density estimate using similar observations within a covariate hypersphere of a given radius. The global treatment difference is taken as the average of the treatment differences of the neighborhood around each observation.

While `LocalControlClassic` uses the number of clusters as a varying parameter to visualize treatment differences as a function of similarity of observations, this function instead uses a varying radius. The maximum radius enclosing all observations corresponds to the biased estimate which compares the outcome of all those with treatment A versus all those with treatment B. An easily interpretable graph can be created to illustrate the change in estimated outcome difference between two treatments, on average, across all clusters, as a function of using smaller and more homogenous clusters. The `LocalControlNearestNeighborsConfidence` procedure statistically resamples this Local Control process to generate confidence estimates. It is also helpful to plot a box-plot of the local treatment difference at a radius of zero, requiring that every observation has at least one perfect match on the other treatment. When perfect matches exist, one can estimate the treatment difference without making assumptions about the relative importance of the clustering variables. The `plot.LocalControlCS` function will plot both visualizations in a single graph.

**Usage**

```r
LocalControl(
  data,
  modelForm = NULL,
  outcomeType = "default",
  treatmentColName,
  outcomeColName,
  cenCode = 0,
  clusterVars,
  timeColName = "",
  treatmentCode,
  labelColName = "",
  radStepType = "exp",
  radDecayRate = 0.8,
  radMinFract = 0.01,
  radiusLevels = numeric(),
  normalize = TRUE,
  verbose = FALSE,
  numThreads = 1
)
```

**Arguments**

- `data`: DataFrame containing all variables which will be used for the analysis.
- `modelForm`: A formula containing the necessary variables for Local Control analysis. This can be used as an alternative to the primary interface for cross-sectional studies. The formula should be in the following format: "outcome ~ treatment | clusterVar1 ... clusterVarN".
- `outcomeType`: Specifies the outcome type for the analysis.
treatmentColName
A string containing the name of a column in data. The column contains the treatment variable specifying the treatment groups.

outcomeColName
A string containing the name of a column in data. The column contains the outcome variable to be compared between the treatment groups.

cenCode
A value specifying which of the outcome values corresponds to a censored observation.

clusterVars
A character vector containing column names in data. Each column contains an X-variable, or covariate which will be used to form patient clusters.

timeColName
A string containing the name of a column in data. The column contains the time to outcome for each of the observations in data.

treatmentCode
(optional) A string containing one of the factor levels from the treatment column. If provided, the corresponding treatment will be considered "Treatment 1". Otherwise, the first "level" of the column will be considered the primary treatment.

labelColName
(optional) A string containing the name of a column from data. The column contains labels for each of the observations in data, defaults to the row indices.

radStepType
(optional) Used in the generation of correction radii. The step type used to generate each correction radius after the maximum. Currently accepts "unif" and "exp" (default). "unif" for uniform decay ex: (radDecayRate = 0.1) (1, 0.9, 0.8, 0.7, ..., ~minRadFract, 0) "exp" for exponential decay ex: (radDecayRate = 0.9) (1, 0.9, 0.81, 0.729, ..., ~minRadFract, 0)

radDecayRate
(optional) Used in the generation of correction radii. The size of the "step" between each of the generated correction radii. If radStepType == "exp", radDecayRate must be a value between (0,1). This value defaults to 0.8.

radMinFract
(optional) Used in the generation of correction radii. A floating point number representing the smallest fraction of the maximum radius to use as a correction radius.

radiusLevels
(optional) By default, Local Control builds a set of radii to fit data. The radiusLevels parameter allows users to override the construction by explicitly providing a set of radii.

normalize
(optional) Logical value. Tells local control if it should or should not normalize the covariates. Default is TRUE.

verbose
(optional) Logical value. Display or suppress the console output during the call to Local Control. Default is FALSE.

numThreads
(optional) An integer value specifying the number of threads which will be assigned to the analysis. The maximum number of threads varies depending on the system hardware. Defaults to 1 thread.

Value
A list containing the results from the call to LocalControl.

- outcomes List containing two dataframes for the average T1 and T0 outcomes within each cluster at each radius.
• counts List containing two dataframes which hold the number of T1 and T0 patients within each cluster at each radius.
• ltds Dataframe containing the average LTD within each cluster at each radius.
• summary Dataframe containing summary statistics about the analysis for each radius.
• params List containing the parameters used to call LocalControl.

References

• Martin Kutz, Kaspar Fischer, Bernd Gartner. miniball-1.0.3. https://github.com/hbf/miniball.

Examples

# cross-sectional
data(lindner)
linVars <- c("stent", "height", "female", "diabetic", "acutemi", "ejecfrac", "ves1proc")
csresults = LocalControl(data = lindner, 
    clusterVars = linVars, 
    treatmentColName = "abcix", 
    outcomeColName = "cardbill", 
    treatmentCode = 1)
plot(csresults)

# survival / competing risks example
data(cardSim)
crresults = LocalControl(data = cardSim, outcomeType = "survival", 
    outcomeColName = "status", 
    timeColName = "time", 
    treatmentColName = "drug", 
    treatmentCode = 1, 
    clusterVars = c("age", "bmi"))
plot(crresults)
Description

These functions are provided for compatibility with previous versions of LocalControl. They may eventually be completely removed.

Details

- `localControlNearestNeighbors` now called using `LocalControl` with the outcomeType = "cross-sectional".
- `localControlCompetingRisks` now called using `LocalControl` with the outcomeType = "survival".
- `plotLocalControlCIF` now called using `plot.LocalControlCR`.
- `plotLocalControlLTD` now called using `plot.LocalControlCS`.

LocalControlClassic  Local Control Classic

Description

LocalControlClassic was originally contained in the deprecated CRAN package USPS, this function is a combination of three of the original USPS functions, UPShclus, UPSaccum, and UPSnnltd. This replicates the original implementation of the Local Control functionality in Robert Obenchain’s USPS package. Some of the features have been removed due to deprecation of R packages distributed through CRAN. For a given number of patient clusters in baseline X-covariate space, LocalControlClassic() characterizes the distribution of Nearest Neighbor "Local Treatment Differences" (LTDs) on a specified Y-outcome variable.

Usage

```r
LocalControlClassic(
  data,
  clusterVars,
  treatmentColName, 
  outcomeColName, 
  faclev = 3, 
  scedas = "homo", 
  clusterMethod = "ward", 
  clusterDist = "euclidean", 
  clusterCounts = c(50, 100, 200) 
)
```

Arguments

data The data frame containing all baseline X covariates.
clusterVars List of names of X variable(s).
LocalControlClassic

treatmentColName
Name of treatment factor variable.

outcomeColName
Name of outcome Y variable.

faclev
Maximum number of different numerical values an outcome variable can assume without automatically being converted into a "factor" variable; faclev=1 causes a binary indicator to be treated as a continuous variable determining an average or proportion.

scedas
Scedasticity assumption: "homo" or "hete".

clusterMethod
Type of clustering method, defaults to "complete". Currently implemented methods: "ward", "single", "complete" or "average".

clusterDist
Distance type to use, defaults to "euclidean". Currently implemented: "euclidean", "manhattan", "maximum", or "minkowski".

clusterCounts
A vector containing different number of clusters in baseline X-covariate space which Local Control will iterate over.

Value

Returns a list containing several elements.

hiclus
Name of clustering object created by UPShclus().

dframe
Name of data.frame containing X, t & Y variables.

trtm
Name of treatment factor variable.

yvar
Name of outcome Y variable.

numclust
Number of clusters requested.

actclust
Number of clusters actually produced.

PStdif
Character string describing the treatment difference.

nnhbindf
Vector containing cluster number for each patient.

rawmean
Unadjusted outcome mean by treatment group.

rawvars
Unadjusted outcome variance by treatment group.

rawfreq
Number of patients by treatment group.

ratdif
Unadjusted mean outcome difference between treatments.

ratsde
Standard error of unadjusted mean treatment difference.

binmean
Unadjusted mean outcome by cluster and treatment.

binvars
Unadjusted variance by cluster and treatment.

binfreq
Number of patients by bin and treatment.

awbdif
Across cluster average difference with cluster size weights.

awbsde
Standard error of awbdif.

wwbdif
Across cluster average difference, inverse variance weights.

wwbsde
Standard error of wwbdf.
faclev  Maximum number of different numerical values an outcome variable can assume without automatically being converted into a “factor” variable; faclev=1 causes a binary indicator to be treated as a continuous variable determining an average or proportion.

youtype  "continuous" => only next eight outputs; "factor" => only last three outputs.

aovdiff  ANOVA summary for treatment main effect only.

form2  Formula for outcome differences due to bins and to treatment nested within bins.

bindiff  ANOVA summary for treatment nested within cluster.

sig2  Estimate of error mean square in nested model.

pbindif  Unadjusted treatment difference by cluster.

pbinsde  Standard error of the unadjusted difference by cluster.

pbinsiz  Cluster radii measure: square root of total number of patients.

symsiz  Symbol size of largest possible Snowball in a UPSnltd() plot with 1 cluster.

factab  Marginal table of counts by Y-factor level and treatment.

cumchi  Cumulative Chi-Square statistic for interaction in the three-way, nested table.

cumdf  Degrees of Freedom for the Cumulative Chi-Squared.

References


Examples

data(lindner)

cvars <- c("stent","height","female","diabetic","acutemi",
"ejecfrac","ves1proc")

numClusters <- c(1, 2, 10, 15, 20, 25, 30, 35, 40, 45, 50)

results <- LocalControlClassic( data = lindner,
    clusterVars = cvars,
    treatmentColName = "abcix",
    outcomeColName = "cardbill",
    clusterCounts = numClusters)

UPLTDist(results, ylim=c(-15000,15000))

LocalControlCompetingRisksConfidence

Calculate confidence intervals around the cumulative incidence functions (CIFs) generated by LocalControl when outcomeType = "survival".

Description

Given the output of LocalControl, this function produces pointwise standard error estimates for the cumulative incidence functions (CIFs) using a modified version of Choudhury’s approach (2002). This function currently supports the creation of 90%, 95%, 98%, and 99% confidence intervals with linear, log(-log), and arcsine transformations of the estimates.

Usage

LocalControlCompetingRisksConfidence(
    LCCompRisk,
    confLevel = "95%",
    confTransform = "asin"
)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>LCCompRisk</td>
<td>Output from a successful call to LocalControl with outcomeType = &quot;survival&quot;.</td>
</tr>
<tr>
<td>confLevel</td>
<td>Level of confidence with which the confidence intervals will be formed. Choices are: &quot;90%&quot;, &quot;95%&quot;, &quot;98%&quot;, &quot;99%&quot;.</td>
</tr>
<tr>
<td>confTransform</td>
<td>Transformation of the confidence intervals, defaults to arcsin (&quot;asin&quot;). &quot;log&quot; and &quot;linear&quot; are also implemented.</td>
</tr>
</tbody>
</table>
References


Examples

```r
data(cardSim)
results = LocalControl(data = cardSim,
                      outcomeType = "survival",
                      outcomeColName = "status",
                      timeColName = "time",
                      treatmentColName = "drug",
                      treatmentCode = 1,
                      clusterVars = c("age", "bmi"))

conf = LocalControlCompetingRisksConfidence(results)
```

Description

Given a number of bootstrap iterations and the params used to call `LocalControl` with outcomeType = "default", this function calls LocalControl nBootstrap times. The 50% and 95% quantiles are drawn from the distribution of results to produce the LTD confidence intervals.

Usage

```r
LocalControlNearestNeighborsConfidence(
  data,
  nBootstrap,
  randSeed,
  treatmentColName,
  treatmentCode = "",
  outcomeColName,
  clusterVars,
  labelColName = "",
  numThreads = 1,
  radiusLevels = numeric(),
  radStepType = "exp",
  radDecayRate = 0.8)
```
radMinFract = 0.01,
normalize = TRUE,
verbose = FALSE
)

Arguments

data
DataFrame containing all variables which will be used for the analysis.

nBootstrap
The number of times to resample and run LocalControl for the confidence intervals.

randSeed
The seed used to set random number generator state prior to resampling. No default value, provide one for reproducible results.

treatmentColName
A string containing the name of a column in data. The column contains the treatment variable specifying the treatment groups.

treatmentCode
(optional) A string containing one of the factor levels from the treatment column. If provided, the corresponding treatment will be considered "Treatment 1". Otherwise, the first "level" of the column will be considered the primary treatment.

outcomeColName
A string containing the name of a column in data. The column contains the outcome variable to be compared between the treatment groups. If outcomeType = "survival", the outcome column holds the failure/censor assignments.

clusterVars
A character vector containing column names in data. Each column contains an X-variable, or covariate which will be used to form patient clusters.

labelColName
(optional) A string containing the name of a column from data. The column contains labels for each of the observations in data, defaults to the row indices.

numThreads
(optional) An integer value specifying the number of threads which will be assigned to the analysis. The maximum number of threads varies depending on the system hardware. Defaults to 1 thread.

radiusLevels
(optional) By default, Local Control builds a set of radii to fit data. The radiusLevels parameter allows users to override the construction by explicitly providing a set of radii.

radStepType
(optional) Used in the generation of correction radii. The step type used to generate each correction radius after the maximum. Currently accepts "unif" and "exp" (default), "unif" for uniform decay ex: (radDecayRate = 0.1) (1, 0.9, 0.8, 0.7, ..., ~minRadFract, 0) "exp" for exponential decay ex: (radDecayRate = 0.9) (1, 0.9, 0.81, 0.729, ..., ~minRadFract, 0)

radDecayRate
(optional) Used in the generation of correction radii. The size of the "step" between each of the generated correction radii. If radStepType == "exp", radDecayRate must be a value between (0,1). This value defaults to 0.8.

radMinFract
(optional) Used in the generation of correction radii. A floating point number representing the smallest fraction of the maximum radius to use as a correction radius.

normalize
(optional) Logical value. Tells local control if it should or should not normalize the covariates. Default is TRUE.
verbose (optional) Logical value. Display or suppress the console output during the call to Local Control. Default is FALSE.

References


Examples

```r
## Not run:
#input the abciximab study data of Kereiakes et al. (2000).
data(lindner)

linVars <- c("stent", "height", "female", "diabetic", "acutemi",
            "ejectfrac", "ves1proc")

results <- LocalControl(data = lindner,
                        clusterVars = linVars,
                        treatmentColName = "abcix",
                        outcomeColName = "cardbill",
                        treatmentCode = 1)

#Calculate the confidence intervals via resampling.
confResults = LocalControlNearestNeighborsConfidence(
                        data = lindner,
                        clusterVars = linVars,
                        treatmentColName = "abcix",
                        outcomeColName = "cardbill",
                        treatmentCode = 1, nBootstrap = 20)

# Plot the local treatment difference with confidence intervals.
plot(results, confResults)
## End(Not run)
```

---

**plot.LocalControlCR**  
*Plot cumulative incidence functions (CIFs) from Local Control.*

**Description**

Given the results from LocalControl with `outcomeType = "survival"`, plot a corrected and uncorrected cumulative incidence function (CIF) for both groups.
Usage

```r
## S3 method for class 'LocalControlCR'
plot( 
  x, 
  ..., 
  rad2plot, 
  xlim, 
  ylim = c(0, 1), 
  col1 = "blue", 
  col0 = "red", 
  xlab = "Time", 
  ylab = "Cumulative incidence", 
  legendLocation = "topleft", 
  main = "", 
  group1 = "Treatment 1", 
  group0 = "Treatment 0"
)
```

Arguments

- `x` Return object from LocalControl with outcomeType = "survival".
- `...` Arguments passed on to `graphics::plot`
- `rad2plot` The index or name ("rad_#") of the radius to plot. By default, the radius with pct_informative closest to 0.8 will be selected.
- `xlim` The x axis bounds. Defaults to `c(0, max(lccrResults$Failtimes))`.
- `ylim` The y axis bounds. Defaults to `c(0,1)`.
- `col1` The plot color for group 1.
- `col0` The plot color for group 0.
- `xlab` The x axis label. Defaults to "Time".
- `ylab` The y axis label. Defaults to "Cumulative incidence".
- `legendLocation` The location to place the legend. Default "topleft".
- `main` The main plot title. Default is empty.
- `group1` The name of the primary group (Treatment 1).
- `group0` The name of the secondary group (Treatment 0).

References

**Examples**

```r
data("cardSim")
results = LocalControl(data = cardSim,
                       outcomeType = "survival",
                       outcomeColName = "status",
                       timeColName = "time",
                       treatmentColName = "drug",
                       treatmentCode = 1,
                       clusterVars = c("age", "bmi"))

plot(results)
```

**plot.LocalControlCS**  
Plots the local treatment difference as a function of radius for Local-Control.

**Description**

Creates a plot where the y axis represents the local treatment difference, while the x axis represents the percentage of the maximum radius. If the confidence summary (nnConfidence) is provided, the 50% and 95% confidence estimates are also plotted.

**Usage**

```r
## S3 method for class 'LocalControlCS'
plot(
  x,
  ..., 
  nnConfidence, 
  ylim, 
  legendLocation = "bottomleft", 
  ylab = "LTD", 
  xlab = "Fraction of maximum radius", 
  main = ""
)
```

**Arguments**

- `x`  
  Return object from LocalControl with "default" outcomeType.

- `...`  
  Arguments passed on to `graphics::plot`

- `nnConfidence`  
  Return object from LocalControlNearestNeighborsConfidence

- `ylim`  
  The y axis bounds. Defaults to c(0,1).

- `legendLocation`  
  The location to place the legend. Default "topleft".

- `ylab`  
  The y axis label. Defaults to "LTD".

- `xlab`  
  The x axis label. Defaults to "Fraction of maximum radius".

- `main`  
  The main plot title. Default is empty.
SPSbalan

Test for Within-Bin X-covariate Balance in Supervised Propensity Scoring

Description

Test for Conditional Independence of X-covariate Distributions from Treatment Selection within Given, Adjacent PS Bins. The second step in Supervised Propensity Scoring analyses is to verify that baseline X-covariates have the same distribution, regardless of treatment, within each fitted PS bin.

Usage

SPSbalan(envir, dframe, trtm, yvar, qbin, xvar, faclev = 3)
Arguments

- **envir**: The local control environment
- **dfname**: Name of augmented data.frame written to the appn="" argument of SPSlogit().
- **trtm**: Name of the two-level treatment factor variable.
- **yvar**: The outcome variable.
- **qbin**: Name of variable containing bin numbers.
- **xvar**: Name of one baseline covariate X variable used in the SPSlogit() PS model.
- **faclev**: Maximum number of different numerical values an X-covariate can assume without automatically being converted into a “factor” variable; faclev=1 causes a binary indicator to be treated as a continuous variable determining a proportion.

Value

An output list object of class SPSbalan. The first four are returned with a continuous x-variable. The next 4 are used if it is a factor variable.

- **aovdiffANOVA**: output for marginal test.
- **form2Formula**: for differences in X due to bins and to treatment nested within bins.
- **bindiffANOVA**: output for the nested within bin model.
- **df3Output**: data.frame containing 3 variables: X-covariate, treatment and bin.
- **factab**: Marginal table of counts by X-factor level and treatment.
- **tab**: Three-way table of counts by X-factor level, treatment and bin.
- **cumchi**: Cumulative Chi-Square statistic for interaction in the three-way, nested table.
- **cumdf**: Degrees of Freedom for the Cumulative Chi-Squared.

Author(s)

Bob Obenchain <wizbob@att.net>

References

**SPSloess**

**LOESS Smoothing of Outcome by Treatment in Supervised Propensity Scoring**

**Description**

Express Expected Outcome by Treatment as LOESS Smooths of Fitted Propensity Scores.

**Usage**

```r
SPSloess(
  envir,
  dframe,
  trtm,
  pscr,
  yvar,
  faclev = 3,
  deg = 2,
  span = 0.75,
  fam = "symmetric"
)
```

**Arguments**

- `envir` Local control classic environment.
- `dframe` data.frame of the form returned by SPSlogit().
- `trtm` the two-level factor on the left-hand-side in the formula argument to SPSlogit().
- `pscr` fitted propensity scores of the form returned by SPSlogit().
- `yvar` continuous outcome measure or result unknown at the time patient was assigned (possibly non-randomly) to treatment; "NA"s are allowed in yvar.
- `faclev` optional; maximum number of distinct numerical values a variable can assume and yet still be converted into a factor variable; faclev=1 causes a binary indicator to be treated as a continuous variable determining a proportion.
- `deg` optional; degree (1=linear or 2=quadratic) of the local fit.
- `span` optional; span (0 to 2) argument for the loess() function.
- `fam` optional; "gaussian" or "symmetric".

**Details**

Once one has fitted a somewhat smooth curve through scatters of observed outcomes, Y, versus the fitted propensity scores, X, for the patients in each of the two treatment groups, one can consider the question: “Over the range where both smooth curves are defined (i.e. their common support), what is the (weighted) average signed difference between these two curves?”
If the distribution of patients (either treated or untreated) were UNIFORM over this range, the (unweighted) average signed difference (treated minus untreated) would be an appropriate estimate of the overall difference in outcome due to choice of treatment.

Histogram patient counts within 100 cells of width 0.01 provide a naive "non-parametric density estimate" for the distribution of total patients (treated or untreated) along the propensity score axis. The weighted average difference (and standard error) displayed by SPSsmoot() are based on an R density() smooth of these counts.

In situations where the propensity scoring distribution for all patients in a therapeutic class is known to differ from that of the patients within the current study, that population weighted average would also be of interest. Thus the SPSloess() output object contains two data frames, logrid and lofit, useful in further computations.

- logridloess grid data.frame containing 11 variables and 100 observations. The PS variable contains propensity score "cell means" of 0.005 to 0.995 in steps of 0.010. Variables F0, S0 and C0 for treatment 0 and variables F1, S1 and C1 for treatment 1 contain fitted smooth spline values, standard error estimates and patient counts, respectively. The DIF variable is simply (F1-F0), the SED variable is sqrt(S1^2+S0^2), the HST variable is proportional to (C0+C1), and the DEN variable is the estimated probability density of patients along the PS axis. Observations with "NA" for variables F0, S0, F1 or S1 represent "extremes" where the lowess fits could not be extrapolated because no observed outcomes were available.

- losub0, losub1loess fit data.frame contains 4 variables for each distinct PS value in lofit. These 4 variables are named PS, YAVG, TRT==0 and 1, respectively, and FIT = spline prediction for the specified degrees-of-freedom (default df=1.)

- spanloess span setting.

- lotdifoutcome treatment difference mean.

- lotsdeoutcome treatment difference standard deviation.

**Author(s)**

Bob Obenchain <wizbob@att.net>

**References**


Ripley BD, loess() based on the 'cloess' package of Cleveland, Grosse and Shyu.
SPSlogit

Propensity Score prediction of Treatment Selection from Patient Baseline X-covariates

Description

Use a logistic regression model to predict Treatment Selection from Patient Baseline X-covariates in Supervised Propensity Scoring.

Usage

SPSlogit(envir, dframe, form, pfit, prank, qbin, bins = 5, appn = "")

Arguments

- **envir**: name of the working local control classic environment.
- **dframe**: data.frame containing X, t and Y variables.
- **form**: Valid formula for glm() with family = binomial(), with the two-level treatment factor variable as the left-hand-side of the formula.
- **pfit**: Name of variable to store PS predictions.
- **prnk**: Name of variable to store tied-ranks of PS predictions.
- **qbin**: Name of variable to store the assigned bin number for each patient.
- **bins**: optional; number of adjacent PS bins desired; default to 5.
- **appn**: optional; append the pfit, prank and qbin variables to the input dfname when appn=="", else save augmented data.frame to name specified within a non-blank appn string.

Details

The first phase of Supervised Propensity Scoring is to develop a logit (or probit) model predicting treatment choice from patient baseline X characteristics. SPSlogit uses a call to glm() with family = binomial() to fit a logistic regression.

Value

An output list object of class SPSlogit:

- **dframe**: Name of input data.frame containing X, t & Y variables.
- **dfoutnam**: Name of output data.frame augmented by pfit, prank and qbin variables.
- **trtm**: Name of two-level treatment factor variable.
- **formglm()**: formula for logistic regression.
- **pfit**: Name of predicted PS variable.
- **prank**: Name of variable containing PS tied-ranks.
- **qbin**: Name of variable containing assigned PS bin number for each patient.
- **bins**: Number of adjacent PS bins desired.
- **glmobj**: Output object from invocation of glm() with family = binomial().
SPSnbins

Author(s)
Bob Obenchain <wizbob@att.net>

References

See Also
SPSbalan, SPSnbins and SPSoutco.

---

SPSnbins
Change the Number of Bins in Supervised Propensiy Scoring

Description
Change the Number of Bins in Supervised Propensiy Scoring

Usage
SPSnbins(envir, dframe, prnk, qbin, bins = 8)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>envir</td>
<td>name of the working local control classic environment.</td>
</tr>
<tr>
<td>dframe</td>
<td>Name of data.frame of the form output by SPSlogit().</td>
</tr>
<tr>
<td>prnk</td>
<td>Name of PS tied-rank variable from previous call to SPSlogit().</td>
</tr>
<tr>
<td>qbin</td>
<td>Name of variable to contain the re-assigned bin number for each patient.</td>
</tr>
<tr>
<td>bins</td>
<td>Number of PS bins desired.</td>
</tr>
</tbody>
</table>

Details
Part or all of the first phase of Supervised Propensity Scoring will need to be redone if SPSbalan() detects dependence of within-bin X-covariate distributions upon treatment choice. Use SPSnbins() to change (increase) the number of adjacent PS bins. If this does not achieve balance, invoke SPSlogit() again to modify the form of your PS logistic model, typically by adding interaction and/or curvature terms in continuous X-covariates.
**Value**

An output data.frame with new variables inserted:

- dframe2Modified version of the data.frame specified as the first argument to SPSnbins().

**Author(s)**

Bob Obenchain <wizbob@att.net>

**References**


**See Also**

SPSlogit, SPSbalan and SPSoutco.

---

**SPSoutco**

*Examine Treatment Differences on an Outcome Measure in Supervised Propensity Scoring*

**Description**

Examine Within-Bin Treatment Differences on an Outcome Measure and Average these Differences across Bins.

**Usage**

```
SPSoutco(envir, dframe, trtm, qbin, yvar, faclev = 3)
```

**Arguments**

- **envir**
  name of the working local control classic environment.

- **dframe**
  Name of augmented data.frame written to the appn= argument of SPSlogit().

- **trtm**
  Name of treatment factor variable.

- **qbin**
  Name of variable containing the PS bin number for each patient.

- **yvar**
  Name of an outcome Y variable.

- **faclev**
  Maximum number of different numerical values an X-covariate can assume without automatically being converted into a "factor" variable; faclev=1 causes a binary indicator to be treated as a continuous variable determining an average or proportion.
Details

Once the second phase of Supervised Propensity Scoring confirms, using SPSbalan(), that X-covariate Distributions have been Balanced Within-Bins, the third phase can start: Examining Within-Bin Outcome Difference due to Treatment and Averaging these Differences across Bins. Graphical displays of SPSoutco() results feature R barplot() invocations.

Value

An output list object of class SPSoutco:

- dframeName of augmented data.frame written to the appn="" argument of SPSlogit().
- trtmName of the two-level treatment factor variable.
- yvarName of an outcome Y variable.
- binsNumber of variable containing bin numbers.
- PStdifCharacter string describing the treatment difference.
- rawmeanUnadjusted outcome mean by treatment group.
- rawvarsUnadjusted outcome variance by treatment group.
- rawfreqNumber of patients by treatment group.
- ratdifUnadjusted mean outcome difference between treatments.
- ratsdeStandard error of unadjusted mean treatment difference.
- binmeanUnadjusted mean outcome by cluster and treatment.
- binvarsUnadjusted variance by cluster and treatment.
- binfreqNumber of patients by bin and treatment.
- awbdifAcross cluster average difference with cluster size weights.
- awbsdeStandard error of awbdif.
- wwbdifAcross cluster average difference, inverse variance weights.
- wwbbsdeStandard error of wwbdif.
- formFormula for overall, marginal treatment difference on X-covariate.
- faclevMaximum number of different numerical values an X-covariate can assume without automatically being converted into a "factor" variable; faclev=1 causes a binary indicator to be treated as a continuous variable determining an average or proportion.
- youtypes"continuous" => only next six outputs; "factor" => only last four outputs.
- aovdiffANOVA output for marginal test.
- form2Formula for differences in X due to bins and to treatment nested within bins.
- bindiffANOVA summary for treatment nested within bin.
- pbindifUnadjusted treatment difference by cluster.
- pbinsdeStandard error of the unadjusted difference by cluster.
- pbinsizCluster radii measure: square root of total number of patients.
- factabMarginal table of counts by Y-factor level and treatment.
- tabThree-way table of counts by Y-factor level, treatment and bin.
- cumchiCumulative Chi-Square statistic for interaction in the three-way, nested table.
- cumdfDegrees of Freedom for the Cumulative Chi-Squared.
Author(s)

Bob Obenchain <wizbob@att.net>

References


See Also

SPSlogit, SPSbalan and SPSnbins.

---

**UPSaccum**

Prepare for Accumulation of (Outcome,Treatment) Results in Unsupervised Propensity Scoring

**Description**

Specify key result accumulation parameters: Treatment t-Factor, Outcome Y-variable, faclev setting, scedasticity assumption, and name of the UPSgraph() data accumulation object.

**Usage**

```r
UPSaccum(envir, dframe, trtm, yvar, faclev = 3, scedas = "homo")
```

**Arguments**

- `envir` : name of the working local control classic environment.
- `dframe` : Name of data.frame containing the X, t & Y variables.
- `trtm` : Name of treatment factor variable.
- `yvar` : Name of outcome Y variable.
- `faclev` : Maximum number of different numerical values an outcome variable can assume without automatically being converted into a "factor" variable; faclev=1 causes a binary indicator to be treated as a continuous variable determining an average or proportion.
- `scedas` : Scedasticity assumption: "homo" or "hete"
Details

The second phase in an Unsupervised Propensity Scoring analysis is to prepare to accumulate results over a wide range of values for "Number of Clusters." As the number of such clusters increases, individual clusters will tend to become smaller and smaller and, thus, more and more compact in covariate X-space.

Value

- hiclusName of a diana, agnes or hclust object created by UPShclus().
- dframeName of data.frame containing the X, t & Y variables.
- trtmName of treatment factor variable.
- yvarName of outcome Y variable.
- faclevMaximum number of different numerical values an outcome variable can assume without automatically being converted into a "factor" variable; faclev=1 causes a binary indicator to be treated as a continuous variable determining a proportion.
- scedasScedasticity assumption: "homo" or "hete"
- accobjName of the object for accumulation of I-plots to be ultimately displayed using UPSgraph().
- nnymaxMaximum NN LTD Standard Error observed; Upper NN plot limit; initialized to zero.
- nnxminMinimum NN LTD observed; Left NN plot limit; initialized to zero.
- nnxmaxMaximum NN LTD observed; Right NN plot limit; initialized to zero.

Author(s)

Bob Obenchain <wizbob@att.net>

References


See Also

UPSnnltd, UPSivadj and UPShclus.
Description

For a given number of clusters, UPSaltdd() characterizes the potentially biased distribution of "Local Treatment Differences" (LTDs) in a continuous outcome y-variable between two treatment groups due to Random Clusterings. When the NNobj argument is not NA and specifies an existing UPSnnltd() object, UPSaltdd() also computes a smoothed CDF for the NN/LTD distribution for direct comparison with the Artificial LTD distribution.

Usage

```r
UPSaltdd(
  envir,
  dframe,
  trtm,
  yvar,
  faclev = 3,
  scedas = "homo",
  NNobj = NA,
  clus = 50,
  reps = 10,
  seed = 12345
)
```

Arguments

- `envir` name of the working local control classic environment.
- `dframe` Name of data.frame containing a treatment-factor and the outcome y-variable.
- `trtm` Name of treatment factor variable with two levels.
- `yvar` Name of continuous outcome variable.
- `faclev` Maximum number of different numerical values an outcome variable can assume without automatically being converted into a "factor" variable; faclev=1 causes a binary indicator to be treated as a continuous variable determining an average or proportion.
- `scedas` Scedasticity assumption: "homo" or "hete"
- `NNobj` Name of an existing UPSnnltd object or NA.
- `clus` Number of Random Clusters requested per Replication; ignored when NNobj is not NA.
- `reps` Number of overall Replications, each with the same number of requested clusters.
- `seed` Seed for Monte Carlo random number generator.
Details

Multiple calls to UPSaltdd() for different UPSnnlttd objects or different numbers of clusters are typically made after first invoking UPSgraph().

Value

- dframeName of data.frame containing X, t & Y variables.
- trtmName of treatment factor variable.
- yvarName of outcome Y variable.
- faclevMaximum number of different numerical values an outcome variable can assume without automatically being converted into a "factor" variable; faclev=1 causes a binary indicator to be treated as a continuous variable determining an average or proportion.
- scedasScedasticity assumption: "homo" or "hete"
- NNobjName of an existing UPSnnlttd object or NA.
- clusNumber of Random Clusters requested per Replication.
- repsNumber of overall Replications, each with the same number of requested clusters.
- patsNumber of patients with no NAs in their yvar outcome and trtm factor.
- seedSeed for Monte Carlo random number generator.
- altdddMatrix of LTDs and relative weights from artificial clusters.
- alxminMinimum artificial LTD value.
- alxmaxMaximum artificial LTD value.
- alymaxMaximum weight among artificial LTDs.
- altdcdfVector of artificial LTD x-coordinates for smoothed CDF.
- qqVector of equally spaced CDF values from 0.0 to 1.0.
- nnltddOptional matrix of relevant NN/LTDs and relative weights.
- nnlxminOptional minimum NN/LTD value.
- nnlxmaxOptional maximum NN/LTD value.
- nnlymaxOptional maximum weight among NN/LTDs.
- nnltdcdfOptional vector of NN/LTD x-coordinates for smoothed CDF.
- nqOptional vector of equally spaced CDF values from 0.0 to 1.0.

Author(s)

Bob Obenchain <wizbob@att.net>

References

UPSboxplot

Returns a series of boxplots comparing LTD distributions given different numbers of clusters.

Description

Given the output of LocalControlClassic, this function uses all or some of the UPSnnltd objects contained to create a series of boxplots of the local treatment difference at each of the different numbers of requested clusters.

Usage

UPSboxplot(envir, clusterSubset = c())

Arguments

- envir: A LocalControlClassic environment containing UPSnnltd objects.
- clusterSubset: (optional) A vector containing requested cluster counts. If provided, the boxplot is created using only the UPSnnltd objects corresponding to the requested cluster counts.

Value

Returns the call to boxplot with the formula: "ltd ~ numclst".

Adds the "ltdds" object to the Local Control environment.

Examples

data(lindner)
cvars <- c("stent","height","female","diabetic","acutemi","ejectfrac","ves1proc")
numClusters <- c(1, 5, 10, 20, 40, 50)

results <- LocalControlClassic(data = lindner,
                                clusterVars = cvars,
                                treatmentColName = "abcix",
                                outcomeColName = "cardbill",
                                clusterCounts = numClusters)

bxp <- UPSboxplot(results)
**Description**

Plot summary of results from multiple calls to UPSnnltd() and/or UPSivadj() after an initial setup call to UPSaccum(). The UPSgraph() plot displays any sensitivity of the LTD and LOA Distributions to choice of Number of Clusters in X-space.

**Usage**

```r
UPSgraph(envir, nncol = "red", nwcol = "green3", ivcol = "blue", ...)
```

**Arguments**

<table>
<thead>
<tr>
<th>Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>envir</td>
<td>name of the working local control classic environment.</td>
</tr>
<tr>
<td>nncol</td>
<td>optional; string specifying color for display of the Mean of the LTD distribution when weighted by cluster size from any calls to UPSnnltd().</td>
</tr>
<tr>
<td>nwcol</td>
<td>optional; string specifying color for display of the Mean of the LTD distribution when weighted inversely proportional to variance from any calls to UPSnnltd().</td>
</tr>
<tr>
<td>ivcol</td>
<td>optional; string specifying color for display of the Difference in LOA predictions, at PS = 100% minus that at PS = 0%, from any calls to UPSivadj().</td>
</tr>
<tr>
<td>...</td>
<td>Additional arguments to pass to the plotting function.</td>
</tr>
</tbody>
</table>

**Details**

The third phase of Unsupervised Propensity Scoring is a graphical Sensitivity Analysis that depicts how the Overall Means of the LTD and LOA distributions change with the number of clusters.

**Author(s)**

Bob Obenchain <wizbob@att.net>

**References**


**See Also**

[UPSnnltd](#), [UPSivadj](#) and [UPSaccum](#).
Description

Derive a full, hierarchical clustering tree (dendrogram) for all patients (regardless of treatment received) using Mahalonobis between-patient distances computed from specified baseline X-covariate characteristics.

Usage

UPShclus(envir, dframe, xvars, method, metric)

Arguments

envir name of the working local control classic environment.
dframe Name of data.frame containing baseline X covariates.
xvars List of names of X variable(s).
method Hierarchical Clustering Method: "diana", "agnes" or "hclus".
metric A valid distance metric for clustering.

Details

The first step in an Unsupervised Propensity Scoring analysis is always to hierarchically cluster patients in baseline X-covariate space. UPShclus uses a Mahalanobis metric and clustering methods from the R "cluster" library for this key initial step.

Value

An output list object of class UPShclus:

- dframeName of data.frame containing baseline X covariates.
- xvarsList of names of X variable(s).
- methodHierarchical Clustering Method: "diana", "agnes" or "hclus".
- upshclHierarchical clustering object created by choice between three possible methods.

Author(s)

Bob Obenchain <wizbob@att.net>
References


See Also

UPSaccum, UPSnnltd and UPSgraph.

Description

For a given number of patient clusters in baseline X-covariate space and a specified Y-outcome variable, linearly smooth the distribution of Local Average Treatment Effects (LATEs) plotted versus Within-Cluster Treatment Selection (PS) Percentages.

Usage

UPSivadj(envir, numclust)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>envir</td>
<td>name of the working local control classic environment.</td>
</tr>
<tr>
<td>numclust</td>
<td>Number of clusters in baseline X-covariate space.</td>
</tr>
</tbody>
</table>

Details

Multiple calls to UPSivadj(n) for varying numbers of clusters n are made after first invoking UPSclus() to hierarchically cluster patients in X-space and then invoking UPSaccum() to specify a Y outcome variable and a two-level treatment factor t. UPSivadj(n) linearly smoothes the LATE distribution when plotted versus within cluster propensity score percentages.
Value

An output list object of class UPSivadj:

- `hiclusName` of clustering object created by UPShclus().
- `dframeName` of data.frame containing X, t & Y variables.
- `trtmName` of treatment factor variable.
- `yvarName` of outcome Y variable.
- `numclustNumber` of clusters requested.
- `actclustNumber` of clusters actually produced.
- `scedasScedasticity assumption: "homo" or "hete`.
- `PStdifCharacter string describing the treatment difference.`
- `ivhbindfVector` containing cluster number for each patient.
- `rawmeanUnadjusted outcome mean by treatment group`.
- `rawvarsUnadjusted outcome variance by treatment group`.
- `rawfreqNumber` of patients by treatment group.
- `ratdifUnadjusted mean outcome difference between treatments`.
- `ratsdeStandard error of unadjusted mean treatment difference`.
- `binmeanUnadjusted mean outcome by cluster and treatment`.
- `binfreqNumber` of patients by bin and treatment.
- `faclevMaximum number of different numerical values an outcome variable can assume without automatically being converted into a "factor" variable; faclev=1 causes a binary indicator to be treated as a continuous variable determining an average or proportion.`
- `youtype"contin"uous => next eleven outputs; "factor" => no additional output items.`
- `pbinoutLATE regardless of treatment by cluster`.
- `pbinpspWithin-Cluster Treatment Percentage = non-parametric Propensity Score`.
- `pbinsizCluster radii measure: square root of total number of patients`.
- `symmsizSymbol size of largest possible Snowball in a UPSivadj() plot with 1 cluster`.
- `ivfitlm() output` for linear smooth across clusters.
- `ivtzeroPredicted outcome at PS percentage zero`.
- `ivtxsdeStandard deviation of outcome prediction at PS percentage zero`.
- `ivtdiffPredicted outcome difference for PS percentage 100 minus that at zero`.
- `ivtdsdeStandard deviation of outcome difference`.
- `ivt100pPredicted outcome at PS percentage 100`.
- `ivt1pseStandard deviation of outcome prediction at PS percentage 100`.

Author(s)

Bob Obenchain <wizbob@att.net>
References


Obenchain RL. (2011) *USPSinR.pdf* USPS R-package vignette, 40 pages.-


See Also

*UPSnlnld, UPSaccum and UPSgraph.*

---

### UPSLTdist

- **Plot the LTD distribution as a function of the number of clusters.**

**Description**

This function creates a plot displaying the distribution of Local Treatment Differences (LTDs) as a function of the number of clusters created for all UPSnnltd objects in the provided environment. The hinges and whiskers are generated using `boxplot.stats`.

**Usage**

`UPSLTdist(envir, legloc = "bottomleft", ...)`

**Arguments**

- `envir` A LocalControlClassic environment containing UPSnnltd objects.
- `legloc` Where to place the legend in the returned plot. Defaults to "bottomleft".
- `...` Arguments passed on to `graphics::plot`

**Value**

Returns the LTD distribution plot.

Adds the "ltdds" object to `envir`. 
Examples

data(lindner)
cvars <- c("stent","height","female","diabetic","acutemi",
        "ejecfrac","ves1proc")
numClusters <- c(1, 2, 10, 15, 20, 25, 30, 35, 40, 45, 50)
results <- LocalControlClassic(data = lindner,
                              clusterVars = cvars,
                              treatmentColName = "abcix",
                              outcomeColName = "cardbill",
                              clusterCounts = numClusters)
UPSLTDdist(results,ylim=c(-15000,15000))

Description

For a given number of patient clusters in baseline X-covariate space, UPSnnltd() characterizes the
distribution of Nearest Neighbor "Local Treatment Differences" (LTDs) on a specified Y-outcome
variable.

Usage

UPSnnltd(envir, numclust)

Arguments

  envir       name of the working local control classic environment.
  numclust    Number of clusters in baseline X-covariate space.

Details

Multiple calls to UPSnnltd(n) for varying numbers of clusters, n, are typically made after first
invoking UPShclus() to hierarchically cluster patients in X-space and then invoking UPSaccum()
to specify a Y outcome variable and a two-level treatment factor t. UPSnnltd(n) then determines
the LTD Distribution corresponding to n clusters and, optionally, displays this distribution in a
"Snowball" plot.

Value

An output list object of class UPSnnltd:

- hiclusName of clustering object created by UPShclus().
- dframeName of data.frame containing X, t & Y variables.
• trtmName of treatment factor variable.
• yvarName of outcome Y variable.
• numclustNumber of clusters requested.
• actclustNumber of clusters actually produced.
• scedasScedasticity assumption: "homo" or "hete"
• PSstdifCharacter string describing the treatment difference.
• nnhbindfVector containing cluster number for each patient.
• rawmeanUnadjusted outcome mean by treatment group.
• rawvarsUnadjusted outcome variance by treatment group.
• rawfreqNumber of patients by treatment group.
• ratdifUnadjusted mean outcome difference between treatments.
• ratsdeStandard error of unadjusted mean treatment difference.
• binmeanUnadjusted mean outcome by cluster and treatment.
• binvarsUnadjusted variance by cluster and treatment.
• binfreqNumber of patients by bin and treatment.
• awbdifAcross cluster average difference with cluster size weights.
• awbsdeStandard error of awbdif.
• wwbdifAcross cluster average difference, inverse variance weights.
• wwbseStandard error of wwbdif.
• faclevMaximum number of different numerical values an outcome variable can assume without automatically being converted into a "factor" variable; faclev=1 causes a binary indicator to be treated as a continuous variable determining an average or proportion.
• youtype"contin"uous => only next eight outputs; "factor" => only last three outputs.
• aovdiffANOVA summary for treatment main effect only.
• form2Formula for outcome differences due to bins and to treatment nested within bins.
• bindiffANOVA summary for treatment nested within cluster.
• sig2Estimate of error mean square in nested model.
• pbndifUnadjusted treatment difference by cluster.
• pbwdsdeStandard error of the unadjusted difference by cluster.
• pbwsizCluster radii measure: square root of total number of patients.
• symsizSymbol size of largest possible Snowball in a UPSnnltd() plot with 1 cluster.
• factabMarginal table of counts by Y-factor level and treatment.
• cumchiCumulative Chi-Square statistic for interaction in the three-way, nested table.
• cumdfDegrees of Freedom for the Cumulative Chi-Squared.

Author(s)
Bob Obenchain <wizbob@att.net>
References


See Also

**UPSivadj, UPSaccum** and **UPSgraph**.
Index

* cluster
  UPSclus, 31
* data
  cardSim, 2
  framingham, 3
  lindner, 4
* design
  SPSnbins, 22
  UPSaccum, 25
  UPSclus, 31
* hplot
  SPSoutco, 23
  UPSgraph, 30
  UPSivadj, 32
* models
  SPSlogit, 21
* nonparametric
  SPSoutco, 23
  UPSivadj, 32
  UPSnlltd, 35
* univar
  UPSaccum, 25
  boxplot.stats, 34
  cardSim, 2
  framingham, 3
  graphics::plot, 15, 16, 34
  lindner, 4
  LocalControl, 4, 8, 11, 12
  LocalControl-deprecated, 7
  LocalControlClassic, 5, 8, 29
  localControlCompetingRisks
    (LocalControl-deprecated), 7
  localControlCompetingRisksConfidence, 11
  localControlNearestNeighbors
    (LocalControl-deprecated), 7
  plot.LocalControlCR, 8, 14
  plot.LocalControlCS, 5, 8, 16
  plotLocalControlCIF
    (LocalControl-deprecated), 7
  plotLocalControlLTD
    (LocalControl-deprecated), 7
  SPSbalan, 17, 22, 23, 25
  SPSloess, 19
  SPSlogit, 21, 23, 25
  SPSnbins, 22, 22, 25
  SPSoutco, 22, 23, 23
  UPSaccum, 25, 29, 30, 32, 34, 37
  UPSltdd, 27
  UPSboxplot, 29
  UPSgraph, 20, 30, 32, 34, 37
  UPSclus, 26, 31
  UPSivadj, 26, 30, 32, 37
  UPSLTdist, 34
  UPSnlltd, 26, 29, 30, 32, 34, 35