

Package ‘cem’

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Title Coarsened Exact Matching

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Suggests Amelia(>= 1.2-0)

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att

Example of ATT estimation from CEM output

Description

An example of ATT estimation from CEM output

Usage

```
att(obj, formula, data, model="linear", extrapolate=FALSE, ntree=2000)
## S3 method for class 'cem.att'
plot(x, obj, data, vars=NULL, plot=TRUE, ecolars, ...)
## S3 method for class 'cem.att'
summary(object, ...)
```

Arguments

obj	a cem.match or cem.match.list object
formula	a model formula. See Details.
data	a single data.frame or a list of data.frame's in case of cem.match.list
model	one model. See Details.
extrapolate	extrapolate the CEM restricted estimate to the whole data. Default = FALSE.
ntree	number of trees to generate in random forest model. Default = 2000.
x	the output from the att function
vars	a vector of variable names to be used in the parallel plots. By default all variables involved in data matching are used.
object	an object of class cem.att function
plot	if TRUE the plot is produced, otherwise only calculations are made.
ecolars	a vector of three colors respectively for positive, zero and negative treatment effect. Default c("blue", "black", "red").
...	passed to the plot function or to printCoefmat for the method summary

Details

Argument `model` can be `lm`, `linear` for linear regression model; `logit` for the the logistic model; `lme`, `linear-RE` for the linear model with random effects. Also `rf`, `forest` for the randomforest algorithm.

If the outcome is `y` and the treatment variable is `T`, then a formula like `y ~ T` will produce the simplest estimate the ATT: with `lm`, it is just the coefficient on `T`, which is the same as the difference in means, weighted by CEM stratum size. Users can add covariates to span any remaining imbalance after the match, such as `y ~ T + age + sex`, to adjust for variables `age` and `sex`.

In the case of multiply imputed datasets, the model is applied to each single matched data and the ATT and is the standard error estimated using the standard formulas for combining results of multiply imputed data.

When `extrapolate = TRUE`, the estimate model is extrapolated to the whole set of data.

There is a `print` method for the output of `att`. Specifying the option `TRUE` in a `print` command gives complete output from the estimated model when available.

Value

A matrix of estimates with their standard error, or a list in the case of `cem.match.list`. For `plot.att` a list of strata estimated treatment effect and group ("positive", "negative", "zero") and individual treatment and effect and group. The individual treatment effect and group is given by the treatment effect of the strata. Similarly for the group ("positive", "negative", "zero"). Also, colors associated to estimated treatment effects are returned for easy subsequent plotting.

Author(s)

Stefano Iacus, Gary King, and Giuseppe Porro

References

Stefano Iacus, Gary King, Giuseppe Porro, "Matching for Casual Inference Without Balance Checking: Coarsened Exact Matching," <http://gking.harvard.edu/files/abs/cem-abs.shtml>

Examples

```
data(LL)

# cem match: automatic bin choice
mat <- cem(treatment="treated",data=LL, drop="re78", keep.all=TRUE)
mat
mat$k2k

# ATT estimate
homo1 <- att(mat, re78~treated, data=LL)
rand1 <- att(mat, re78~treated, data=LL, model="linear-RE")
rf1 <- att(mat, re78~treated, data=LL, model="rf")

homo2 <- att(mat, re78~treated, data=LL, extra=TRUE)
rand2 <- att(mat, re78~treated, data=LL, model="linear-RE", extra=TRUE)
```

```

rf2 <- att(mat, re78~treated, data=LL, model="rf", extra=TRUE)

homo1
summary(homo1)

rand1
rf1

homo2
rand2
rf2

plot( homo1, mat, LL, vars=c("age","education","re74","re75"))
plot( rand1, mat, LL, vars=c("age","education","re74","re75"))
plot( rf1, mat, LL, vars=c("age","education","re74","re75"))

plot( homo2, mat, LL, vars=c("age","education","re74","re75"))
plot( rand2, mat, LL, vars=c("age","education","re74","re75"))
plot( rf2, mat, LL, vars=c("age","education","re74","re75"))

# reduce the match into k2k using euclidean distance within cem strata
mat2 <- k2k(mat, LL, "euclidean", 1)
mat2
mat2$k2k

# ATT estimate after k2k
att(mat2, re78~treated, data=LL)

# example with missing data
# using multiply imputed data
# we use Amelia for multiple imputation
## Not run:

if(require(Amelia)){
  data(LL)
  n <- dim(LL)[1]
  k <- dim(LL)[2]

# we generate missing values in 30
# randomly in one colum per row
LL1 <- LL
idx <- sample(1:n, .3*n)
invisible(sapply(idx, function(x) LL1[x,sample(2:k,1)] <- NA))

imputed <- amelia(LL1)
imputed <- imputed$imputations[1:5]

mat <- cem("treated", datalist=imputed, data=LL1, drop="re78")

print(mat)

```

```

  att(mat, re78 ~ treated, data=imputed)
}

## End(Not run)

```

cem

Coarsened Exact Matching

Description

Implementation of Coarsened Exact Matching

Usage

```

cem(treatment=NULL, data = NULL, datalist=NULL, cutpoints = NULL,
    grouping = NULL, drop=NULL, eval.imbalance = FALSE, k2k=FALSE,
    method=NULL, mpower=2, L1.breaks = NULL, L1.grouping = NULL,
    verbose = 0, baseline.group="1",keep.all=FALSE)

```

Arguments

treatment	character, name of the treatment variable
baseline.group	character, name of the baseline level treatment. See Details.
data	a data.frame
datalist	a list of optional multiply imputed data.frame's
cutpoints	named list each describing the cutpoints for numerical variables (the names are variable names). Each list element is either a vector of cutpoints, a number of cutpoints, or a method for automatic bin construction. See Details.
grouping	named list, each element of which is a list of groupings for a single categorical variable. See Details.
drop	a vector of variable names in the data frame to ignore during matching
eval.imbalance	Boolean. See Details.
k2k	boolean, restrict to k-to-k matching? Default = FALSE
method	distance method to use in k2k matching. See Details.
mpower	power of the Minkowski distance. See Details.
L1.breaks	list of cutpoints for the calculation of the L1 measure.
L1.grouping	as grouping but only needed in the calculation of the L1 measure not in matching.
verbose	controls level of verbosity. Default=0.
keep.all	if FALSE the coarsened dataset is not returned. Default=FALSE

Details

For multilevel (and a binary) treatment variables, the cem weights are calculated with respect to the baseline. Therefore, matched units with treatment variable equal to the baseline level receive weight 1, the others the usual cem weights. Unless specified, by default baseline is set to "1". If this level is not one of the possible values taken by the treatment variable, then the baseline is set to the first level of the treatment variable.

When specifying cutpoints, several automatic methods may be chosen, including "sturges" (Sturges' rule, the default), "fd" (Freedman-Diaconis' rule), "scott" (Scott's rule) and "ss" (Shimazaki-Shinomoto's rule). See references for a description of each rule.

The grouping option is a list where each element is itself a list. For example, suppose for variable `quest1` you have the following possible levels "no answer", NA, "negative", "neutral", "positive" and you want to collect ("no answer", NA, "neutral") into a single group, then the grouping argument should contain `list(quest1=list(c("no answer", NA, "neutral")))`. Or if you have a discrete variable elements with values 1:10 and you want to collect it into groups "1:3,NA", "4", "5:9", "10" you specify in grouping the following list `list(elements=list(c(1:3,NA), 5:9))`. Values not defined in the grouping are left as they are. If cutpoints and groupings are defined for the same variable, the groupings take precedence and the corresponding cutpoints are set to NULL.

`verbose`: a number greater or equal to 0. The higher, the more info are provided during the execution of the algorithm.

If `eval.imbalance = TRUE`, `cem$imbalance` contains the imbalance measure by absolute difference in means for numerical variables and chi-square distance for categorical variables. If FALSE (the default) then `cem$imbalance` is set to NULL. If data contains missing data, the imbalance measures are not calculated.

If `L1.breaks` is missing, the default rule to calculate cutpoints is the Scott's rule.

If `k2k` is set to TRUE, the algorithm return strata with the same number of treated and control units per stratum, otherwise all the matched units are returned (default). When `k2k = TRUE`, the user can choose a method (between 'euclidean', 'maximum', 'manhattan', 'canberra', 'binary' and 'minkowski') for nearest neighbor matching inside each cem strata. By default method is set to 'NULL', which means random matching inside cem strata. For the Minkowski distance the power can be specified via the argument `mpower`. For more information on method `!= NULL`, refer to [dist help page](#). If `k2k` is set to TRUE also `keep.all` is set to TRUE.

By default, cem treats missing values as distinct categories and matches observations with missing values in the same variable in the same stratum provided that all the remaining (corasened) covariates match.

If argument `data` is non-NULL and `datalist` is NULL, CEM is applied to the single data set in `data`.

Argument `datalist` is a list of (multiply imputed) data frames (i.e., with missing cell values imputed). If `data` is NULL, the function cem is applied independently to each element of the list, resulting in separately matched data sets with different numbers of treated and control units.

When `data` and `datalist` are both non-NULL, each multiply imputed observation is assigned to the stratum in which it has been matched most frequently. In this case, the algorithm outputs the same matching solution for each multiply imputed data set (i.e., an observation, and the number of treated and control units matched, in one data set has the same meaning in all, and is the same for all)

Value

Returns an object of class `cem.match` if only data is not NULL or an object of class `cem.match.list`, which is a list of objects of class `cem.match` plus a field called `unique` which is true only if data and `datalist` are not both NULL. A `cem.match` object is a list with the following slots:

<code>call</code>	the call
<code>strata</code>	vector of stratum number in which each observation belongs, NA if the observation has not been matched
<code>n.strata</code>	number of strata generated
<code>vars</code>	report variables names used for the match
<code>drop</code>	variables removed from the match
<code>X</code>	the coarsened dataset or NULL if <code>keep.all=FALSE</code>
<code>breaks</code>	named list of cutpoints, eventually NULL
<code>treatment</code>	name of the treatment variable
<code>groups</code>	factor, each observation belong to one group generated by the treatment variable
<code>n.groups</code>	number of groups identified by the treatment variable
<code>group.idx</code>	named list, index of observations belonging to each group
<code>group.len</code>	sizes of groups
<code>tab</code>	summary table of matched by group
<code>imbalance</code>	NULL or a vector of imbalances. See Details.

Author(s)

Stefano Iacus, Gary King, and Giuseppe Porro

References

Stefano Iacus, Gary King, Giuseppe Porro, "Matching for Casual Inference Without Balance Checking: Coarsened Exact Matching," <http://gking.harvard.edu/files/abs/cem-abs.shtml>

Examples

```
## Not run:
data(LL)

todrop <- c("treated","re78")

imbalance(LL$treated, LL, drop=todrop)

# cem match: automatic bin choice
mat <- cem(treatment="treated", data=LL, drop="re78")
mat

# cem match: user choiced coarsening
re74cut <- hist(LL$re74, br=seq(0,max(LL$re74)+1000, by=1000),plot=FALSE)$breaks
```

```

re75cut <- hist(LL$re75, br=seq(0,max(LL$re75)+1000, by=1000),plot=FALSE)$breaks
agecut <- hist(LL$age, br=seq(15,55, length=14),plot=FALSE)$breaks
mycp <- list(re75=re75cut, re74=re74cut, age=agecut)
mat <- cem(treatment="treated",data=LL, drop="re78",cutpoints=mycp)
mat

# cem match: user choiced coarsening, k-to-k matching
mat <- cem(treatment="treated",data=LL, drop="re78",cutpoints=mycp,k2k=TRUE)
mat

# mahalanobis matching: we use MatchIt
if(require(MatchIt)){
mah <- matchit(treated~age+education+re74+re75+black+hispanic+nodegree+married+u74+u75,
  distance="mahalanobis", data=LL)
mah
#imbalance
imbalance(LL$treated, LL, drop=todrop, weights=mah$weights)
}

# Multiply Imputed data
# making use of Amelia for multiple imputation
if(require(Amelia)){
  data(LL)
  n <- dim(LL)[1]
  k <- dim(LL)[2]

  set.seed(123)

  LL1 <- LL
  idx <- sample(1:n, .3*n)
  invisible(sapply(idx, function(x) LL1[x,sample(2:k,1)] <- NA))

  imputed <- amelia(LL1,noms=c("black","hispanic","treated","married",
    "nodegree","u74","u75"))
  imputed <- imputed$imputations[1:5]
# without information on which observation has missing values
mat1 <- cem("treated", datalist=imputed, drop="re78")
mat1

# ATT estimation
out <- att(mat1, re78 ~ treated, data=imputed)

# with information about missingness
mat2 <- cem("treated", datalist=imputed, drop="re78", data=LL1)
mat2

# ATT estimation
out <- att(mat2, re78 ~ treated, data=imputed)
}

## End(Not run)

```


Description

Exploration tool for CEM

Usage

```
cemspace(treatment=NULL, data = NULL, R=100, grouping = NULL, drop=NULL,
L1.breaks = NULL, L1.grouping=NULL, plot = TRUE, fixed = NULL,
minimal = 1, maximal = 5, M=250, raw.profile=NULL, keep.weights=FALSE)
```

Arguments

treatment	character, name of the treatment variable.
data	a data.frame.
R	number of possible random coarsening for the CEM.
grouping	named list, each element of which is a list of groupings for a single categorical variable. For more details see cem .
drop	a vector of variable names in the data frame to ignore during matching
L1.breaks	list of cutpoints for the calculation of the L1 measure.
L1.grouping	as grouping but only needed in the calculation of the L1 measure not in matching.
plot	plot the space of solutions?
fixed	vector of variable names which will not be relaxed.
minimal	the minimal number of intervals acceptable after relaxation. Should be a named list of positive integers or if a number, this is applied to all variables.
maximal	the maximal number of intervals acceptable after relaxation. Should be a named list of positive integers or if a number, this is applied to all variables.
M	number of possible random coarsening for the L1 measure
raw.profile	an object of class L1profile. If passed, the L1.breaks are ignored and set to median cutpoints of L1 profile.
keep.weights	if TRUE, for each matching solutions the CEM-weights are stored.

Details

This is a tool to help the user to explore different cem solutions by choosing random coarsenings. The algorithm tries R random choices of coarsenings into intervals between minimal and maximal for numerical, integer or ordered factors. It drops or include dichotomous or boolean variables.

Calling directly plot on the output of cemspace has the same effect of calling directly [imbospace.plot](#).

If you want to relax a given cem solution, use the function [imbospace](#) instead.

Value

val an invisible object of class imbalance.space.

Author(s)

Stefano Iacus, Gary King, and Giuseppe Porro

References

Stefano Iacus, Gary King, Giuseppe Porro, "Matching for Casual Inference Without Balance Checking: Coarsened Exact Matching," <http://gking.harvard.edu/files/abs/cem-abs.shtml>

See Also

[imbospace.plot](#), [cemspace](#)

Examples

```
## Not run:  
data(LL)  
tmp <- cemspace("treated", LL, drop="re78", M=50)  
  
## End(Not run)
```

combine.spacegraphs *Combine two spacegraph objects.*

Description

Combine two spacegraph objects so that their results can be plotted together. Both spacegraphs must be from the same dataset using the same distance metric.

Usage

```
combine.spacegraphs(x,y)
```

Arguments

x a spacegraph object to be combined
y a spacegraph object to be combined

Details

This allows users to combine two spacegraph objects rather than having to re-run the spacegraph command from the start.

Inputs must be created using [spacegraph](#).

Value

val an object of class spacegraph.

Author(s)

Richard Nielsen

See Also

[spacegraph](#)

Examples

```
## Not run:
data(LL)

sp1 <- spacegraph("treated", LL, drop="re78", M=5,
                 R=list(cem=5,psm=5, mdm=0))

## Note that we must use the same L1 measure from the first spacegraph!
sp2 <- spacegraph("treated", LL, drop="re78", raw.profile=sp1$raw.profile,
                 R=list(cem=0,psm=0, mdm=5))

sp3 <- combine.spacegraphs(sp1,sp2)

plot(sp3)

## End(Not run)
```

DW

Dehejia-Wahba dataset

Description

A subset of the Lalonde dataset (see cited reference).

Usage

```
data(DW)
```

Format

A data frame with 445 observations on the following 10 variables.

treated treated variable indicator

age age

education years of education

black race indicator variable

married marital status indicator variable
 nodegree indicator variable of not possessing a degree
 re74 real earnings in 1974
 re75 real earnings in 1975
 re78 real earnings in 1978 (post treatment outcome)
 hispanic ethnic indicator variable
 u74 unemployment in 1974 indicator variable
 u75 unemployment in 1975 indicator variable

Source

see references

References

Dehejia, R., Wahba, S. (1999) "Causal Effects in Nonexperimental Studies: Reevaluating the Evaluation of Training Programs," *Journal of the American Statistical Association*, 94, 1053-1062.

imbalance	<i>Calculates several imbalance measures</i>
-----------	----------------------------------------------

Description

Calculates several imbalance measures for the original and matched data sets

Usage

```
imbalance(group, data, drop=NULL, breaks = NULL, weights, grouping = NULL)
```

Arguments

group	the group variable
data	the data
drop	a vector of variable names in the data frame to ignore
breaks	a list of vectors of cutpoints used to calculate the L1 measure. See Details.
weights	weights
grouping	named list, each element of which is a list of groupings for a single categorical variable. See Details.

Details

This function calculates several imbalance measures. For numeric variables, the difference in means (under the column statistic), the difference in quantiles and the L1 measure is calculated. For categorical variables the L1 measure and the Chi-squared distance (under column statistic) is calculated. Column type reports either (diff) or (Chi2) to indicate the type of statistic being calculated.

If breaks is not specified, the Scott automated bin calculation is used (which coarsens less than Sturges, which used in `cem`). Please refer to `cem` help page. In this case, breaks are used to calculate the L1 measure.

This function also calculate the global L1 imbalance measure. If breaks is missing, the default rule to calculate cutpoints is the Scott's rule.

The grouping option is a list where each element is itself a list. For example, suppose for variable `quest1` you have the following possible levels "no answer", NA, "negative", "neutral", "positive" and you want to collect ("no answer", NA, "neutral") into a single group, then the grouping argument should contain `list(quest1=list(c("no answer", NA, "neutral")))`. Or if you have a discrete variable elements with values 1:10 and you want to collect it into groups "1:3, NA", "4", "5:9", "10" you specify in grouping the following list `list(elements=list(c(1:3, NA), 5:9))`. Values not defined in the grouping are left as they are. If cutpoints and groupings are defined for the same variable, the groupings take precedence and the corresponding cutpoints are set to NULL.

See [L1.meas](#) help page for details.

Value

An object of class `imbalance` which is a list with the following two elements

<code>tab</code>	Table of imbalance measures
<code>L1</code>	The global L1 measure of imbalance

Author(s)

Stefano Iacus, Gary King, and Giuseppe Porro

References

Stefano Iacus, Gary King, Giuseppe Porro, "Matching for Casual Inference Without Balance Checking: Coarsened Exact Matching," <http://gking.harvard.edu/files/abs/cem-abs.shtml>

Examples

```
## Not run:

data(LL)

todrop <- c("treated", "re78")

imbalance(LL$treated, LL, drop=todrop)
```

```
# cem match: automatic bin choice
mat <- cem(treatment="treated", data=LL, drop="re78")

## End(Not run)
```

imbspace

Diagnostic tool for CEM

Description

Diagnostic tools for CEM

Usage

```
imbspace(obj, data, depth = 1, L1.breaks = NULL,
plot = TRUE, fixed = NULL, minimal = 1, maximal = 6,
M=250, raw.profile=NULL)
```

Arguments

obj	an object of class <code>cem.match</code>
data	the original data.
depth	if 1, relaxes up to dropping one var, if 2 relaxes (up to dropping) two vars, etc.
L1.breaks	list of cutpoints for the calculation of the L1 measure.
plot	plot the space of solutions?
fixed	vector of variable names which will not be relaxed.
minimal	the minimal number of intervals acceptable after relaxation. Should be a named list of positive integers or if a number, this is applied to all variables.
maximal	the maximal number of intervals acceptable after relaxation. Should be a named list of positive integers or if a number, this is applied to all variables.
M	number of possible random coarsening for the L1 measure
raw.profile	and object of class <code>L1profile</code> . If passed, the <code>L1.breaks</code> are ignored.

Details

This is a diagnostic tool to help the user in the search of different choices of coarsenings. The algorithm tries all possible combination of coarsenings into intervals between `minimal` and `maximal` one variable at time, for pairs, triplets, etc depending on the value of `depth`.

Calling directly `plot` on the output of `imbspace` has the same effect of calling directly `imbspace.plot`.

Value

`val` an invisible object of class `imbalance.space`.

Author(s)

Stefano Iacus, Gary King, and Giuseppe Porro

References

Stefano Iacus, Gary King, Giuseppe Porro, “Matching for Casual Inference Without Balance Checking: Coarsened Exact Matching,” <http://gking.harvard.edu/files/abs/cem-abs.shtml>

See Also

[imbspace.plot](#)

imbspace.plot

Plot of imbalance space diagnostic tool for CEM

Description

Plot of imbalance space diagnostic tool for CEM

Usage

```
imbspace.plot(obj, group="1", data, explore=TRUE)
```

Arguments

obj	an object of class <code>imbalance.space</code>
group	character string denoting group id. Defaults to "1".
data	data for running additional matching solutions.
explore	if TRUE the user can interact and find new solutions.

Details

For an interactive device a two panels plot is given. On the left panel the user can select a CEM solution and the number of cutpoints used in that matching solution is plotted as a parallel plot on the right plot. On exit (right-click on the left panel), the function returns all the cem solutions highlighted in the last selection of the user.

For non-interactive devices, only the space of the solutions are plotted.

This plot shows the tradeoff in matching as a function of imbalance and sample size.

The imbalance of the raw data is represented as a red plot and the initial CEM solution as a green plot. All solutions below the green dot and left to it are better than the user choice in terms of imbalance and number of units matched.

Value

tab	an invisible object containing the selection of cem solutions and their coarsenings.
-----	--------------------------------------------------------------------------------------

Author(s)

Stefano Iacus, Gary King, and Giuseppe Porro

References

Stefano Iacus, Gary King, Giuseppe Porro, “Matching for Casual Inference Without Balance Checking: Coarsened Exact Matching,” <http://gking.harvard.edu/files/abs/cem-abs.shtml>

See Also

[imbospace](#)

Examples

```
## Not run:
require(cem)

data(LL)

mat <- cem("treated", LL, drop=c("re78","treated"),
  cut=list(age=4, edu=4, re74=3, re75=3), keep.all=TRUE)
mat

imb.raw <- L1.profile(LL$treated, LL[, mat$vars], M=250, plot=FALSE)

imbsp <- imbospace(mat, LL,depth=2, raw.profile=imb.raw,
  maximal=6, minimal=2, fixed=c("hispanic", "black", "married",
  "nodegree","u74","u75"), plot=FALSE)

tmp <- plot(imbsp,data=LL,explore=interactive())
tmp

## End(Not run)
```

k2k

Reduction to k2k Matching

Description

Reduces a CEM output to a k2k matching

Usage

```
k2k(obj, data, method=NULL, mpower=2, verbose=0)
```


Arguments

obj	an object as output from cem
data	the original data.frame used by cem
method	distance method to use in k2k matching. See Details.
mpower	power of the Minkowski distance. See Details.
verbose	controls level of verbosity. Default=0.

Details

This function transforms a typical cem matching solution to a k-to-k match, with k variable along strata: i.e., in each stratum generated by cem, the match is reduce to have the same number of treated and control units. (This option will delete some data that matched well, and thus likely increase the variance, but it means that subsequent analyses do not require weights.)

The user can choose a method (between 'euclidean', 'maximum', 'manhattan', 'canberra', 'binary' and 'minkowski') for nearest neighbor matching inside each cem strata. By default method is set to 'NULL', which means random matching inside cem strata. For the Minkowski distance the power can be specified via the argument 'mpower'. For more information on method != NULL, refer to [dist](#) help page.

After k2k the weights of each matched observation are set to unity. Please notice that option `keep.all=TRUE` must be used in cem calls otherwise k2k will not work.

Value

obj	an object of class <code>cem.match</code>
-----	-------------------------------------------

Author(s)

Stefano Iacus, Gary King, and Giuseppe Porro

References

Stefano Iacus, Gary King, Giuseppe Porro, "Matching for Casual Inference Without Balance Checking: Coarsened Exact Matching," <http://gking.harvard.edu/files/abs/cem-abs.shtml>

Examples

```
data(LL)

# cem match: automatic bin choice
mat <- cem(treatment="treated", data=LL, drop="re78", keep.all=TRUE)
mat
mat$k2k

# ATT estimate
att(mat, re78 ~ treated, data=LL)

# transform the match into k2k
```

```
mat2 <- k2k(mat, LL, "euclidean", 1)
mat2
mat2$k2k

# ATT estimate after k2k
att(mat2, re78 ~ treated, data=LL)
```

L1.meas

Evaluates L1 distance between multidimensional histograms

Description

Evaluates L1 distance between multidimensional histograms

Usage

```
L1.meas(group, data, drop=NULL, breaks = NULL, weights, grouping = NULL)
```

Arguments

group	the group variable
data	the data
drop	a vector of variable names in the data frame to ignore
breaks	a list of vectors of cutpoints; if not specified, automatic choice will be made
weights	weights
grouping	named list, each element of which is a list of groupings for a single categorical variable. See Details.

Details

This function calculates the L1 distance on the k-dimensional histogram in order to measure the level of imbalance in a matching solution.

If `breaks` is not specified, the Scott automated bin calculation is used (which coarsens less than Sturges, which used in [cem](#)). Please refer to [cem](#) help page. In this case, `breaks` are used to calculate the L1 measure.

When choosing `breaks` for L1, a very fine coarsening (many cut points) produces values of L1 close to 1. A very mild coarsening (very few cutpoints), is not able to discriminate, i.e. L1 close to 0 (particularly true when the number of observations is small with respect to the number of continuous variables).

The `grouping` option is a list where each element is itself a list. For example, suppose for variable `quest1` you have the following possible levels "no answer", NA, "negative", "neutral", "positive" and you want to collect ("no answer", NA, "neutral") into a single group, then the `grouping` argument should contain `list(quest1=list(c("no answer", NA, "neutral")))`. Or if you have a discrete variable `elements` with values 1:10 and you want to collect it into groups "1:3, NA", "4", "5:9", "10" you specify in `grouping` the following list `list(elements=list(c(1:3, NA), 5:9))`.

Values not defined in the grouping are left as they are. If cutpoints and groupings are defined for the same variable, the groupings take precedence and the corresponding cutpoints are set to NULL.

The `L1.profile` function shows how to compare matching solutions for any level of (i.e., without regard to) coarsening.

This code also calculate the Local Common Support (LCS) measure, which is the proportion of non empty k-dimensional cells of the histogram which contain at least one observation per group.

Value

An object of class `L1.meas` which is a list with the following fields

L1	The numerical value of the L1 measure
breaks	A list of cutpoints used to calculate the L1 measure
LCS	The numerical value of the Local Common Support proportion

Author(s)

Stefano Iacus, Gary King, and Giuseppe Porro

References

Stefano Iacus, Gary King, Giuseppe Porro, "Matching for Casual Inference Without Balance Checking: Coarsened Exact Matching," <http://gking.harvard.edu/files/abs/cem-abs.shtml>

Examples

```
data(LL)
L1.meas(LL$treated,LL, drop=c("treated","re78"))
```

L1.profile

Calculates L1 distance for different coarsenings

Description

Calculates L1 distance for different coarsenings

Usage

```
L1.profile(group, data, drop = NULL, min.cut = 2, max.cut = 12,
weights, plot = TRUE, add = FALSE, col = "red",
lty = 1, M=100, useCP=NULL, grouping=NULL, progress=TRUE)
```

Arguments

group	the group variable
data	the data
drop	a vector of variable names in the data frame to ignore
min.cut	minimum number of cut points per variable
max.cut	maximum number of cut points per variable
weights	weights
useCP	a list which elements is a list of cutpoints, usually passed from a previous instance of <code>L1.profile</code> . If not NULL these coarsenings are used instead of generating them randomly.
M	number of random coarsenings
plot	plot a graph?
add	add graph to an existing plot? Makes sense only if plot is TRUE
col	draw in specified color
lty	draw using specified lty
grouping	named list, each element of which is a list of groupings for a single categorical variable. See Details.
progress	if TRUE, feedback on progress is given. See Details.

Details

The L1 measure depends on the coarsening chosen to calculate it, and as such the comparison of different matching solutions may differ depending on this somewhat arbitrary choice. This function computes L1 for a random range of possible coarsenings. The point of this function is that if one matching solution has a lower L1 than another, then it dominates without regard to the choice of coarsening. A graphic display conveys the results succinctly. (The logic is similar to that for ROC curves used for classification algorithms.) (This degree of coarsening should remain fixed for different CEM runs.)

For each variables the function generates a random number of cutpoints between `min.cut` and `max.cut` in which to cut the support of each variable. This procedure is repeated M times. The out is sorted in increasing values of L1 just for graphical representation.

Non numeric variables are grouped randomly unless they appear specified in the grouping argument.

A plot method exists for the returned object.

Value

An invisible object of class `L1profile` which contains a named list of coarsenings and values of the L1 measure for each coarsening.

Author(s)

Stefano Iacus, Gary King, and Giuseppe Porro

References

Stefano Iacus, Gary King, Giuseppe Porro, “Matching for Casual Inference Without Balance Checking: Coarsened Exact Matching,” <http://gking.harvard.edu/files/abs/cem-abs.shtml>

Examples

```
## Not run:
data(LL)
for(i in c(4:6,10:12))
  LL[[i]] <- factor(LL[[i]])

imb0 <- L1.profile(LL$treated,LL, drop=c("treated","re78"))

if(require(MatchIt)){
  m2 <- matchit(treated ~ black + hispanic + married + nodegree +
    u74 + u75 + education + age + re74 + re75, data=LL,
    distance="logit")

  m3 <- matchit(treated ~ black + hispanic + married + nodegree +
    u74 + u75 + education + age + re74 + re75, data=LL,
    distance="mahalanobis")

  L1.profile(LL$treated,LL, drop=c("treated","re78"),
    weights=m2$w, add=TRUE, col="green", lty=2, useCP=imb0$CP)

  L1.profile(LL$treated,LL, drop=c("treated","re78"),
    weights=m3$w, add=TRUE, col="orange", lty=3, useCP=imb0$CP)
}

m1 <- cem("treated", LL, drop="re78")

L1.profile(LL$treated,LL, drop=c("treated","re78"),
  weights=m1$w>0, add=TRUE, col="blue", lty=4, useCP=imb0$CP)

legend(5, 0.9, legend=c("raw data", "pscore", "mahalanobis", "cem"),
  lty=1:4, col=c("red", "green", "orange", "blue"))

## End(Not run)
```

LeLonde

Modified Lalonde dataset

Description

This is a modified version of the Lalonde experimental dataset used for explanatory reasons only.

Usage

```
data(LL)
```

Format

A data frame with 722 observations on the following 11 variables.

treated treatment variable indicator

age age

education years of education

black race indicator variable

married marital status indicator variable

nodegree indicator variable for not possessing a degree

re74 real earnings in 1974

re75 real earnings in 1975

re78 real earnings in 1978 (post-treatment outcome)

hispanic ethnic indicator variable

u74 unemployment in 1974 indicator variable

u75 unemployment in 1975 indicator variable

q1 answer to survey question n1

Details

This data is a copy of the original Lalonde (1986) data set (see [LL](#)) with 10% of missing data and an additional variable q1 which is the fictitious answer to the questionnaire on “Agreement on this job training program”.

Source

see references

References

Lalonde, R. (1986) “Evaluating the Econometric Evaluations of Training Programs,” *American Economic Review*, 76, 604-620.

LL

Lalonde dataset

Description

Lalonde experimental dataset (see cited reference).

Usage

data(LL)

Format

A data frame with 722 observations on the following 10 variables.

treated treatment variable indicator
 age age
 education years of education
 black race indicator variable
 married marital status indicator variable
 nodegree indicator variable for not possessing a degree
 re74 real earnings in 1974
 re75 real earnings in 1975
 re78 real earnings in 1978 (post-treatment outcome)
 hispanic ethnic indicator variable
 u74 unemployment in 1974 indicator variable
 u75 unemployment in 1975 indicator variable

Source

see references

References

Lalonde, R. (1986) "Evaluating the Econometric Evaluations of Training Programs," *American Economic Review*, 76, 604-620.

 LLvsPSID

Lalonde treated units versus PSID control individuals

Description

The Lalonde set of treated units versus PSID (Panel Study of Income Dynamics) control individuals

Usage

data(LLvsPSID)

Format

A data frame with 2787 observations on the following 10 variables.

treated treated variable indicator
 age age
 education years of education
 black race indicator variable

married marital status indicator variable
 nodegree indicator variable of not possessing a degree
 re74 real earnings in 1974
 re75 real earnings in 1975
 re78 real earnings in 1978 (post treatment outcome)
 hispanic ethnic indicator variable
 u74 unemployment in 1974 indicator variable
 u75 unemployment in 1975 indicator variable

Details

These two sets of treated and control units can be hardly matched.

Source

see references

References

Lalonde, R. (1986) Evaluating the Econometric Evaluations of Training Programs, *American Economic Review*, 76, 604-620.

pair	<i>Produces a paired sample out of a CEM match solution</i>
------	-------------------------------------------------------------

Description

Produces a paired sample out of a CEM match solution

Usage

```
pair(obj, data, method=NULL, mpower=2, verbose=0)
```

Arguments

obj	an object as output from cem
data	the original data.frame used by cem
method	distance method to use in k2k matching. See Details.
mpower	power of the Minkowski distance. See Details.
verbose	controls level of verbosity. Default=0.

Details

This function returns a vector of paired matched units index.

The user can choose a method (between 'euclidean', 'maximum', 'manhattan', 'canberra', 'binary' and 'minkowski') for nearest neighbor matching inside each cem strata. By default method is set to 'NULL', which means random matching inside cem strata. For the Minkowski distance the power can be specified via the argument `mpower`'. For more information on method != NULL, refer to [dist](#) help page.

Value

`obj` a list with the fields `paired`, `full.paired`, `reservoir` and `reservoir2`. The latter contain the indexes of the unmatched units.

Author(s)

Stefano Iacus, Gary King, and Giuseppe Porro

References

Stefano Iacus, Gary King, Giuseppe Porro, "Matching for Casual Inference Without Balance Checking: Coarsened Exact Matching," <http://gking.harvard.edu/files/abs/cem-abs.shtml>

Examples

```
## Not run:
data(LL)

# cem match: automatic bin choice
mat <- cem(data=LL, drop="re78")

# we want a set of paired units
psample <- pair(mat, data=LL)
table(psample$paired)
psample$paired[1:100]

table(psample$full.paired)
psample$full.paired[1:10]

# cem match: automatic bin choice, we drop one row from the data set
mat1 <- cem(data=LL[-1,], drop="re78")

# we want a set of paired units but we have an odd number of units in the data
psample <- pair(mat1, data=LL[-1,])
table(psample$full.paired)

## End(Not run)
```

`pscoreSelect`*Heuristic search of the best propensity score model specification*

Description

Heuristic search of the best propensity score model specification

Usage

```
pscoreSelect(formula, data, C.L=2*(pnorm(-1,0,1)), C.Q=0.1)
```

Arguments

<code>data</code>	the original data.
<code>formula</code>	formula type specification.
<code>C.L</code>	if at least one likelihood ration test statistic is greater than C.L, then the covariate with higher likelihood ration test statistic is added linearly to the model.
<code>C.Q</code>	if the highest likelihood ratio statistic is greater than C.Q, then interaction terms are included in the pscore model specification.

Details

This is a tool to help the user to the search for the best propensity score model specification along the lines suggested by Imbens and Rubin (forthcoming). The output of the function is a model formula to be passed to `glm` or such, in order to estimate the propensity score model and then perform propensity score matching.

This tool is useful in combination with [imbspace.plot](#).

Value

`val` an invisible object of class `list`.

Author(s)

Richard Nielsen

References

Guido Imbens, Donald Rubin, “Causal Inference”, Chapter 13, forthcoming.

See Also

[cemspace](#)

Examples

```
## Not run:
data(LL)
mod <- pscoreSelect( treated ~ age + education + black+ married + nodedegree +
  re74 + re75 + hispanic + u74 + u75, data=LL)
print(mod)

## End(Not run)
```

relax.cem

*Diagnostic tool for CEM***Description**

Diagnostic tools for CEM

Usage

```
relax.cem(obj, data, depth=1, verbose = 1, L1.breaks=NULL, plot=TRUE,
  fixed=NULL, shifts=NULL, minimal=NULL, use.coarsened=TRUE,
  eval.imbalance=TRUE, use.weights=FALSE, ...)
relax.plot(tab, group="1", max.terms=50, perc=.5, unique=FALSE, colors=TRUE)
```

Arguments

obj	an object of class cem.
data	the original data.
verbose	controls the level of verbosity.
L1.breaks	list of cutpoints for the calculation of the L1 measure.
plot	plot the solutions?
tab	the output table from relax.cem.
fixed	vector of variable names which will not be relaxed.
max.terms	plot only the last best results of relax.cem.
shifts	a vector of proportions of shifts.
minimal	the minimal number of intervals acceptable after relaxation. Should be a named list of positive integers.
group	character string denoting group id. Defaults to "1".
perc	only plot if percentage of matched units is greater than perc.
unique	only plot different solutions (in terms of matched units).
depth	if 1, relaxes up to dropping one var, if 2 relaxes (up to dropping) two vars, etc.
use.coarsened	used coarsened values for continuous variables.
colors	If TRUE each variable is plotted in a different colour.

eval.imbalance If TRUE L1 measure is evaluated at each iteration.
 use.weights If TRUE L1 measure is evaluated with weights calculated at each iteration. Slows down the execution.
 ... passed to the relax.plot function.

Details

relax.cem starts from a cem solution (as given by [cem](#)) which has to be run with argument keep.all=TRUE. relax.cem tries several relaxed coarsenings on the variables. Coarsenings corresponds to dividing the support of each variable into a decreasing number of intervals of the same length (even if in the starting solution intervals are of different lengths). Because CEM is MIB, the number of matched units increases as the number of intervals decrease. All variables are coarsened into k intervals along a sequence which starts from the original number of intervals and decreases to 10 intervals by 2, then continues from 10 down to 1 intervals by 1. If minimal is specified, variables are coarsened down to that minimal value.

To observe MIB property of CEM use.coarsened (default) should be set to TRUE; otherwise the coarsening of the continuous variable will be recalculated at each iteration and there is no guarantee of monotonicity.

relax.cem outputs a list of tables. Each table is named Ggroup where group is the id of the group. Each Ggroup table is ordered in increasing order of matched units of group group. Columns PercGgroup and Ggroup report percentage and absolute number of matched units for each group. Column Relaxed indicates which relaxation has been done, with something like "V1(4),V3(5)", which means "variable V1 has been split in 4 intervals of the same length and variable V3 into five intervals". Thus, the number of intervals is reported in parentheses and if equal to 1 means that the corresponding variable is excluded from affecting the match (i.e. all observations are assigned to the same interval).

If shifts is not null, each coarsening is shifted accordingly (see [shift.cem](#) for additional details). In case of shifting "S:" appears in the labels.

The relax.plot, plot all the different relaxation in increasing order of number of treated units matched. For each coarsening it also reports the value of the L1 measure. The table generated by relax.cem may contain many entries. By default, only a portion of best coarsenings are plotted (option max.terms). In addition, the user can specify to plot the coarsening for which at least a certain percentage of treated units have been matched (option perc, by default 50). In addition, of several different coarsenings which lead to the same number of treated units matched, the user can specify to plot only one of them using the option unique = TRUE (default).

If L1.breaks are NULL they are taken from the cem object if available or calculated automatically as in cem.

Calling directly plot on the output of cem.relax has the same effect of calling directly relax.plot.

Value

tab an invisible object containing the tabs and the L1breaks used

Author(s)

Stefano Iacus, Gary King, and Giuseppe Porro

References

Stefano Iacus, Gary King, Giuseppe Porro, “Matching for Casual Inference Without Balance Checking: Coarsened Exact Matching,” <http://gking.harvard.edu/files/abs/cem-abs.shtml>

See Also

[cem](#)

Examples

```
## Not run:
data(LL)

mat <- cem(treatment="treated",data=LL, drop="re78", keep.all=TRUE)
mat
tab <- relax.cem(mat, LL, depth=1, plot=FALSE)

relax.plot(tab, group="1")
plot(tab, group="1")
relax.plot(tab, group="1", unique=TRUE)
relax.plot(tab, group="1", perc=0.6)
relax.plot(tab, group="1", perc=0.6,unique=TRUE)

tab1 <- relax.cem(mat, LL, depth=1, minimal=list(re74=6, age=3, education=3, re75=5))
tab2 <- relax.cem(mat, LL, depth=1, minimal=list(re74=6, age=3,
education=3, re75=5), shifts=0.01)
tab3 <- relax.cem(mat, LL, depth=1, minimal=list(age=3, education=3),
fixed=c("re74","re75"))
tab4 <- relax.cem(mat, LL, depth=2, minimal=list(age=4,
education=3,re75=6),plot=FALSE, fixed="re74")
relax.plot(tab4)
relax.plot(tab4, unique=TRUE)
relax.plot(tab4, perc=0.7)

## End(Not run)
```

search.match

Heuristic search of match solutions

Description

Heuristic search of match solutions

Usage

```
search.match(data, treatment, vars, depth=3, min.vars =1, group=1, useCP, ...)
```

Arguments

data	the original data.
treatment	name of the treatment variable.
depth	level of interaction and squares. See Details.
vars	vector of variables' names to match on.
min.vars	minimum number of variables to consider in the model.
group	the identifier of the treated group, usually 1 or the level of the fact variable treatment.
useCP	the cutpoints for the calculation of the L1 measure
...	passed to matchit

Details

This is a tool to help the user in the search of different choices models for matching. For example, for the search of different propensity score models. The tool tries all submodels of k variables starting from one covariate up to the full model. Then adds interactions to the full model trying all pairs, triplets etc according to the parameter depth. Then, for continuous variables only, adds squared terms to the full model.

This tool is useful in combination with [imbospace.plot](#).

Value

val an invisible object of class list.

Author(s)

Stefano Iacus, Gary King, and Giuseppe Porro

References

Stefano Iacus, Gary King, Giuseppe Porro, "Matching for Casual Inference Without Balance Checking: Coarsened Exact Matching," <http://gking.harvard.edu/files/abs/cem-abs.shtml>

See Also

[imbospace.plot](#)

`shift.cem`*Diagnostic tool for CEM*

Description

Diagnostic tools for CEM. Applies leftward and rightward shifts of the cutpoints.

Usage

```
shift.cem(obj, data, shifts=NULL, verbose=0, plot=TRUE)
```

Arguments

<code>obj</code>	and object of class <code>cem</code>
<code>data</code>	the original data
<code>shifts</code>	a vector of proportions of shifts
<code>verbose</code>	controls the level of verbosity
<code>plot</code>	whether to plot a graphic representation of the search

Details

For each variable, shift all the cutpoints left and right by `shifts` times the smallest epsilon of the coarsening. Shifting to the right produces a new cell on the left; shift to the left, adds a new cell to the coarsening on the right. Only positive proportions should be used; the algorithm will produce shifting on the left or on the right. The best shifting of the original `cem` match is produced as output, where best is defined in terms of the maximal total number of matched units m_T+m_C (see below).

By default, the function returns minimal information about the execution of the algorithm. By setting a value greater than 0 in option `verbose` more feedback on the process is returned.

Option `plot = TRUE` plots the number of treated units matched m_T , the number of control units matched m_C , and the sum m_T+m_C , as a function of the shifts.

Value

<code>tab</code>	an invisible object containing a new <code>cem</code> object
------------------	--------------------------------------------------------------

Author(s)

Stefano Iacus, Gary King, and Giuseppe Porro

References

Stefano Iacus, Gary King, Giuseppe Porro, "Matching for Casual Inference Without Balance Checking: Coarsened Exact Matching," <http://gking.harvard.edu/files/abs/cem-abs.shtml>

See Also

[cem](#)

Examples

```
## Not run:
data(LL)

m74 <- max(LL$re74, na.rm=TRUE)
s74 <- seq(0,m74,by=sd(LL$re74))
l74 <- length(s74)
if(max(s74) < m74) s74 <- c(s74, m74)

m75 <- max(LL$re75, na.rm=TRUE)
s75 <- seq(0,m75,by=sd(LL$re75))
l75 <- length(s75)
if(max(s75) < m75) s75 <- c(s75, m75)

mybr = list(re74=s74,
            re75 = s75,
            age = hist(LL$age,plot=FALSE)$breaks,
            education = hist(LL$education,plot=FALSE)$breaks)

mat <- cem(treatment="treated",data=LL, drop="re78",cut=mybr)
mat

shift.cem(mat, data=LL, shifts=seq(0.01, 0.5, length=10), verb=1)

## End(Not run)
```

spacegraph

Randomly compute many different matching solutions

Description

Randomly compute many different matching solutions

Usage

```
spacegraph(treatment=NULL, data = NULL,
            R=list("cem"=50,"psm"=0,"mdm"=0,"matchit"=0),
            grouping = NULL, drop=NULL,
            L1.breaks = NULL, L1.grouping=NULL, fixed = NULL,
            minimal = 1, maximal = 15, M=100,
            raw.profile=NULL, keep.weights=FALSE, progress=TRUE,
            rgroupping=FALSE, groups=NULL, psmpoly=1, mdmpoly=1,
            other.matches=NULL, heuristic=FALSE, linear.pscore=FALSE)
```

Arguments

treatment character, name of the treatment variable

<code>data</code>	a <code>data.frame</code>
<code>drop</code>	a vector of variable names in the data frame to ignore during matching.
<code>R</code>	a named list that gives the number of possible random solutions for each matching method. Allowed methods are <code>cem</code> , <code>psm</code> , <code>mdm</code> , and <code>matchit</code> .
<code>grouping</code>	named list, each element of which is a list of groupings for a single categorical variable. For more details see cem .
<code>L1.breaks</code>	list of cutpoints for the calculation of the L1 measure.
<code>L1.grouping</code>	as <code>grouping</code> but only needed in the calculation of the L1 measure not in matching.
<code>fixed</code>	vector of variable names which will not be relaxed.
<code>minimal</code>	the minimal number of intervals acceptable after relaxation. Should be a named list of positive integers or if a number, this is applied to all variables.
<code>maximal</code>	the maximal number of intervals acceptable after relaxation. Should be a named list of positive integers or if a number, this is applied to all variables.
<code>M</code>	number of possible random coarsening for the L1 measure
<code>raw.profile</code>	an object of class <code>L1profile</code> . If passed, the <code>L1.breaks</code> are ignored and set to median cutpoints of L1 profile.
<code>keep.weights</code>	if TRUE, for each matching solutions the CEM-weights are stored.
<code>rgrouping</code>	Boolean, specifies whether levels of categorical variables should be randomly grouped together by CEM.
<code>groups</code>	named list, each element of which is a list of allowable groupings for a single categorical variable.
<code>psmpoly</code>	numeric, specifying the order of polynomials to include in the propensity score models. At the moment, only <code>psmpoly=1</code> is available and other values will throw warnings.
<code>mdmpoly</code>	numeric, specifying the order of polynomials to include in Mahalanobis matching. At the moment, only <code>mdmpoly=1</code> is available and other values will throw warnings.
<code>other.matches</code>	This argument allows plotting of user-specified matching solutions. The solutions must be supplied in a specific format: as a list of data frames, where each data frame contains the observation IDs, observations weights, and the method. These must be provided in three columns of the data frame, with names (exactly) "id", "weight", "method". See the example.
<code>heuristic</code>	Boolean, if TRUE <code>spacegraph</code> uses a heuristic method to randomly select covariates for MDM and PSM rather than sampling from all possible combinations of covariates. The heuristic tends to select most of the main effects and a small number of interactions. This method is automatically applied with large numbers of covariates.
<code>progress</code>	show progress bars.
<code>linear.pscore</code>	does <code>linear.pscore</code>

Details

Spacegraph is a tool to help the user to the search for optimal matching solutions by generating many matching solutions from a variety of matching algorithms (currently CEM, Mahalanobis distance matching, and propensity score matching are supported). The resulting object can be plotted with `plot()` to show where each solution falls along the bias-variance tradeoff.

The `spacegraph` function currently calculates two measures of balance for each solution: the L1 metric (see [L1.meas](#)) and the difference in means of the covariates. Typically, analysts look at the difference in means separately for each variable, but this can't be plotted on a two-dimensional graph. We summarize the difference in means by calculating the average difference in means for all of the covariates. Specifically, we calculate the difference in means for each variable as $\text{mean}(\text{treated}) - \text{mean}(\text{control}) / \text{sd}(\text{treated})$ and then average across all covariates.

Value

`val` an object of class `spacegraph` that can be used directly with `plot()` to produce a `spacegraph`.

Author(s)

Richard Nielsen, Stephano Iacus, Gary King, and Guiseppe Porro

See Also

[combine.spacegraphs](#)

Examples

```
## Not run:
data(LL)

sp <- spacegraph("treated", LL, drop="re78", M=5,
                 R=list(cem=5,psm=5, mdm=5))

plot(sp)
## ABOUT THE PLOTTING TOOL:
## The circled solution is the current selection.
## Solutions that are strictly better are also circled.
## The gui provides the exact call to re-run the selected matching solution.
## The call can also be edited, re-run by clicking the button, and
## automatically added to the existing spacegraph.
## CEM solutions can also be adjusted variable by variable and re-run.

## Some plotting parameters can be changed
plot(sp, main="Comparison of Matching Methods",
      ylab="L1", xlim=c(300,50), ylim=c(0,.7))

## You can specify whether the x-axis shows treated units,
## control units, or all units using the argument N, which
## can take the values "treated", "control", or "all".
```

```
## Default is "treated".

plot(sp, N="all")

## You can specify how the x-axis is scaled. Setting scale.var=T
## gives you the scaling as 1/sqrt(n). Setting scale.var=F gives
## scales it linearly. Default is scale.var=T.

plot(sp, scale.var=F)

## You can also specify which measure of balance to use
## by specifying the argument "balance.metric" as
## "L1", "mdiff" (Avg. standardized difference in means),
## or "mdisc" (Average Malanobis Discrepancy). Default is "L1".

plot(sp, balance.metric="mdiff")
plot(sp, balance.metric="mdisc")

## Matching solutions from other methods can be included in
## a spacegraph by using the argument "other.matches".
## First, Run a matching method. Here, propensity scores from MatchIt.
library(MatchIt)
m.out <- matchit(formula=treated ~ education+age, data=LL, method = "nearest")

## Put the required information into a list of data frames.
## Note, there are many ways to do this.
mymatches <- list(data.frame(names(m.out$w)))
names(mymatches[[1]])[1] <- "id"
mymatches[[1]]$weight <- m.out$w
mymatches[[1]]$method <- "matchit psm"

sp <- spacegraph("treated", LL, drop="re78", M=5,
  R=list(cem=5,psm=5, mdm=5), other.matches=mymatches)
plot(sp)

## End(Not run)
```

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