

# Package ‘radiusmatching’

December 20, 2012

**Type** Package

**Title** What the package does (short line)

**Version** 1.0

**Date** 2012-12-19

**Author** Who wrote it

**Maintainer** Who to complain to <yourfault@somewhere.net>

**Description** More about what it does (maybe more than one line)

**License** What license is it under?

**LazyLoad** yes

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radiusmatching-package

*The radiusmatching package - radius matching with bias correction*

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## Description

Radius matching with bias correction as discussed in M. Huber, M. Lechner, and A. Steinmayr (2012): "Radius matching on the propensity score with bias adjustment: finite sample behaviour, tuning parameters and software implementation." and M. Huber, M. Lechner, and C. Wunsch (2012): "The performance of estimators based on the propensity score". The package currently contains the function "radiusmatch" and the data set "lalonge".

## Details

Package: radiusmatching  
 Type: Package  
 Version: 1.0  
 Date: 2012-12-19  
 License: What license is it under?  
 LazyLoad: yes

This package consists of the function "radiusmatch" and the dataset "lalonge".

## Author(s)

Martin Huber, Michael Lechner, and Andreas Steinmayr, Dept. of Economics, University of St. Gallen. Please write an e-mail to <martin.huber@unisg.ch> in case of problems, suggestions, etc.

## References

- M. Huber, M. Lechner, and A. Steinmayr (2012). Radius matching on the propensity score with bias adjustment: finite sample behaviour, tuning parameters and software implementation. University of St. Gallen Discussion Paper.
- M. Lechner, R. Miquel, and C. Wunsch (2011). Long-run effects of public sector sponsored training in West Germany. *Journal of the European Economic Association* volume 9: 742–784.
- M. Huber, M. Lechner, and C. Wunsch (2012). The performance of estimators based on the propensity score. Forthcoming in the *Journal of Econometrics*.

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lalonge

*LaLonde data*


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## Description

A data set on training participation which has been considered by Lalonde ("Evaluating the Econometric Evaluations of Training Programs with Experimental Data") and Dehejia and Wahba ("Causal Effects in Non-Experimental Studies: Reevaluating the Evaluation of Training Programs"), among others. Also used in the twang and MatchIt packages.

## Usage

```
data(lalonge)
```

## Format

Data frame with 10 variables and 614 observations.

```

treat a numeric vector
age a numeric vector
educ a numeric vector
black a numeric vector
hispan a numeric vector

```

married a numeric vector  
 nodegree a numeric vector  
 re74 a numeric vector  
 re75 a numeric vector  
 re78 a numeric vector

## Source

<http://www.columbia.edu/~rd247/nswdata.html> <http://cran.r-project.org/src/contrib/Descriptions/MatchIt.html>

## References

R. Lalonde (1986). Evaluating the econometric evaluations of training programs with experimental data. *American Economic Review* volume 76: 604-620.

R.H. Dehejia and S. Wahba. (1999). Causal effects in nonexperimental studies: Re-Evaluating the evaluation of training programs. *Journal of the American Statistical Association* volume 94: 1053-1062.

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radiusmatch	<i>Radius matching with bias correction</i>
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## Description

Radiusmatch estimates average treatment effects using radius matching with bias correction for both propensity score matching or Mahalanobis distance matching (on the propensity score and further variables). Radiusmatch is a one-to-many radius (or caliper) matching algorithm as, for example, discussed by Rosenbaum and Rubin (1985) and used by Dehejia and Wahba (1999, 2002). Radius matching uses all comparison observations within a predefined distance around the propensity score or based on the Mahalanobis distance of the respective treated. This allows for higher precision than fixed nearest neighbour matching in regions in which many similar comparison observations are available. Also, it may lead to a smaller bias in regions where similar controls are sparse. In other words, instead of fixing the number of matches globally, it is determined in the local neighbourhood of each treated observation. This estimator was proposed by Lechner, Miquel, and Wunsch (2011) and combines the features of radius matching with additional predictors and linear or nonlinear regression adjustment. After the first step of distance-weighted radius matching with predictors, this estimator uses the weights obtained from matching in a weighted linear or non-linear regression in order to remove biases due to mismatches.

## Usage

```
radiusmatch(y, d, x, xadd = NULL, radius = 3, quantile = 0.9, biascorr=1,
  ynonbin = 1, estimand = "ATET", commonsup = 1, maxwgt = 1, logit = 0,
  index = 0, boot = 299, scoreweight=5, se.kernel=1)
```

**Arguments**

y	Outcome variable
d	Binary treatment indicator
x	Covariates that enter propensity score estimation
xadd	Additional covariates to be controlled for on top of the propensity score. Under the default NULL, propensity score matching is performed. If not NULL, matching on the Mahalanobis distance defined by the propensity score and the additional covariates is performed.
radius	The multiplier of the maximum distance in pair matching (or a particular quantile, see argument "quantile") which defines the radius. E.g., setting radius=1 implies that the radius is equal to the maximum distance in pair matching (or a particular quantile). Setting radius=3 implies a radius of 3 times the maximum distance (or a particular quantile). Default is 3.
quantile	The quantile of the distances in pair matching to be used for the definition of the radius. Default is 0.9, i.e. the 0.9th quantile of the distances in pair matching are used. If "quantile" is smaller or equal to 0 or greater or equal 1, the maximum distance is chosen. The size of the radius obtained is a combination of the arguments "quantile" and "radius". E.g., "radius"=3 and "quantile"=0.9 defines the radius as three times the 0.9th quantile of differences in pair matching.
biascorr	If set to 1, linear or logit bias correction is performed. In either case, the outcome is regressed on the propensity score, its square, and (if xadd is not "NULL" such that Mahalanobis matching is used) on the variables in "xadd" within the counterfactual treatment state. Default is 1.
ynonbin	Type of outcome (multivalued or binary), which is relevant for the bias adjustment, which is based on a weighted regression of the non-treated outcomes on the p-score, its square, and all further covariates used in the Mahalanobis distance. Default is ynonbin=1, i.e., the outcome is not binary, such that OLS is used in the bias correction. If ynonbin=0 (or equal to any value other than 1), logit is used in the bias correction.
estimand	The estimand (or parameter) of interest. Must either be "ATET" (default) for the average treatment effect on the treated, or "ATENT" for the average treatment effect on the nontreated, or "ATE" for the average treatment effect.
commonsup	Specifies, whether common support is imposed. If commonsup=0, no common support restriction is imposed. If commonsup=1 and estimand="ATET", treated observations with propensity scores larger than the maximum propensity score among the nontreated are discarded. If commonsup=2 and estimand="ATET", treated observations with propensity scores larger than the second largest propensity score among the nontreated are discarded from the sample. If commonsup=1 and estimand="ATENT", nontreated observations with propensity scores smaller than the minimum propensity score among the treated are discarded. For estimand="ATE" common support is imposed for both the treated and the nontreated. Default is 1.
maxwgt	Maximum relative weight an observation may receive based on inverse probability weighting by the propensity score. E.g., if maxwgt=0.05, the maximum weight is 5 percent (compared to the joint weight of all other observations). The default is 1 (=100 percent), i.e., no restriction on the weight. If used together with common support (see argument "commonsup"), the weights are computed after imposing common support.

logit	If logit=1, the logit is used for propensity score estimation instead of the probit (probit is default).
index	If index=1, matching is done on the index of the probit estimation instead of the propensity score (matching on the propensity score is default).
boot	Number of bootstrap replications. If boot=0 (default), no bootstrap inference is performed. For any positive integer of boot, bootstrap standard errors and p-values are computed based on the number of bootstrap replications provided. The use of the bootstrap for estimating standard errors and p-values is highly recommended!
scoreweight	Weight of the p-score in Mahalanobis distance matching. E.g., setting the parameter to 1 implies equal weighting of the p-score and further covariates. 2 implies that the p-score gets twice the weight of any of the further covariates considered in Mahalanobis distance matching. Default is 5 (p-score gets 5 times the weight of any covariate).
se.kernel	If set to 1, local constant kernel regression (based on the Epanechnikov kernel and the rule of thumb for bandwidth choice) is used to estimate the conditional variance of the outcome given the matching weight under counterfactual treatment, which is required for estimating the standard error. The np package of T. Hayfield and J. Racine is used for estimation and is automatically loaded/installed. Otherwise a nearest neighbor matching algorithm is used for conditional variance estimation. Default is 1.

### Value

effect	Treatment effect estimate (bias corrected if "biascorr" is set to 1)
effect.unadjust	Unadjusted treatment effect estimate (without bias correction)
se	Approximation to the asymptotic standard error (not accounting for propensity score estimation)
se.boot	Standard error based on bootstrapping the effect
pval.t.boot	p-value based on bootstrapping the t-statistics
weights	Matching weights of the observations. If linear bias correction is used, it is accounted for in the matching weights. If logit bias correction is used, the reported matching weights are the unadjusted weights prior to bias correction.
dropped	Number of observations dropped due to common support and/or maximum weight restrictions
radius	Size of the radius/caliper (If the estimand is the ATE, it corresponds to the radius of the ATET estimation)
y1	Mean potential outcome under treatment
y0	Mean potential outcome under non-treatment

### Author(s)

Martin Huber, Michael Lechner, and Andreas Steinmayr, Dept. of Economics, University of St. Gallen. Please write an e-mail to <martin.huber@unisg.ch> in case of problems, suggestions, etc.

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- M. Huber, M. Lechner, and C. Wunsch (2012). The performance of estimators based on the propensity score. Forthcoming in the *Journal of Econometrics*.

## Examples

```
data(lalonde) #load the Lalonde (1986) data
attach(lalonde) #attach the data set

# estimate the average treatment effect on the treated (ATET) of the training (treat)
# on earnings in 1978 (re78) when controlling for age, education, ethnicity...
results<-radiusmatch(y=re78,d=treat,x=cbind(age, I(age^2), educ, I(educ^2),
black, hispan, married, nodegree, re74, re75), xadd=NULL, radius=1.5,
quantile=0.9, ynonbin=1, estimand="ATET", commonsup=1, maxwgt=0.1, logit=1, index=0, boot=19)
results$effect #bias adjusted ATET
results$se.boot # standard error based on 19 bootstraps
```

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