

# Package: nearfar (via r-universe)

August 21, 2024

**Type** Package

**Title** Near-Far Matching

**Version** 1.3

**Date** 2024-01-22

**Author** Joseph Rigdon <jrigdon@wakehealth.edu>

**Maintainer** Joseph Rigdon <jrigdon@wakehealth.edu>

**Imports** GenSA, MASS, car, stats

**Description** Near-far matching is a study design technique for preprocessing observational data to mimic a pair-randomized trial. Individuals are matched to be near on measured confounders and far on levels of an instrumental variable. Methods outlined in further detail in Rigdon, Baiocchi, and Basu (2018) <[doi:10.18637/jss.v086.c05](https://doi.org/10.18637/jss.v086.c05)>.

**License** GPL-3

**Depends** nbpMatching

**NeedsCompilation** no

**Date/Publication** 2024-01-23 13:00:02 UTC

**Repository** <https://joerigdon.r-universe.dev>

**RemoteUrl** <https://github.com/cran/nearfar>

**RemoteRef** HEAD

**RemoteSha** cda395ce775de23b0d8205cfb3712386f29bb75f

## Contents

nearfar-package . . . . .	2
angrist . . . . .	3
calipers . . . . .	4
eff_ratio . . . . .	4
matches . . . . .	5
opt_nearfar . . . . .	7
smahal . . . . .	8

summary.nf . . . . .	9
summ_matches . . . . .	10

<b>Index</b>	<b>11</b>
--------------	-----------

---

nearfar-package	<i>Near-Far Matching</i>
-----------------	--------------------------

---

## Description

Near-far matching is a study design technique for preprocessing observational data to mimic a pair-randomized trial. Individuals are matched to be near on measured confounders and far on levels of an instrumental variable.

## Details

Package:	nearfar
Type:	Package
Version:	1.3
Date:	2024-01-15
License:	GPL-3

## Author(s)

Joseph Rigdon <jrigdon@wakehealth.edu>

## References

- Rigdon J, Baiocchi M, Basu S (2018). Near-far matching in R: The nearfar package. *Journal of Statistical Software*, 86(5), 1-21.
- Baiocchi M, Small D, Lorch S, Rosenbaum P (2010). Building a stronger instrument in an observational study of perinatal care for premature infants. *Journal of the American Statistical Association*, 105(492), 1285-1296.
- Baiocchi M, Small D, Yang L, Polsky D, Groeneveld P (2012). Near-far matching: a study design approach to instrumental variables. *Health Services and Outcomes Research Methodology*, 12(4), 237-253.

---

angrist

*Angrist data set for education and wages*

---

### Description

A random sample of 1000 observations from the data set used by Angrist and Krueger in their investigation of the impact of education on future wages.

### Format

A data frame with 1000 observations on the following 7 variables.

wage a numeric vector

educ a numeric vector

qob a numeric vector

IV a numeric vector

age a numeric vector

married a numeric vector

race a numeric vector

### Details

This data set is a random sample of 1000 observations from the URL listed below.

### Source

<https://economics.mit.edu/people/faculty/josh-angrist/angrist-data-archive>

### References

Angrist JD, Krueger AB (1991). Does Compulsory School Attendance Affect Schooling and Earnings? The Quarterly Journal of Economics, 106(4), 979-1014.

### Examples

```
library(nearfar)
str(angrist)
## maybe str(angrist) ; plot(angrist) ...
```

---

calipers	<i>Matching priority function</i>
----------	-----------------------------------

---

### Description

Updates given distance matrix to prioritize specified measured confounders in a pair match. Used in consort with [matches](#) function to prioritize specific measured confounders in a near-far match in the [opt\\_nearfar](#) function.

### Usage

```
calipers(distmat, variable, tolerance = 0.2)
```

### Arguments

distmat	An object of class distance matrix
variable	Named variable from list of measured confounders
tolerance	Penalty to apply to mismatched observations; values near 0 penalize mismatches more

### Value

Returns an updated distance matrix

### See Also

[matches](#), [opt\\_nearfar](#)

### Examples

```
dd = mtcars[1:4, 2:3]
cc = calipers(distmat=smahal(dd), variable=dd$cyl, tolerance=0.2)
cc
```

---

eff_ratio	<i>Inference for effect ratio</i>
-----------	-----------------------------------

---

### Description

Conducts inference on effect ratio as described in Section 3.3 of Baiocchi (2010), resulting in an estimate and a permutation based confidence interval for the effect ratio.

### Usage

```
eff_ratio(dta, match, outc, trt, alpha)
```

**Arguments**

dta	The name of the data frame object
match	Data frame where first column contains indices for those individuals encouraged into treatment by instrumental variable and second column contains indices for those individuals discouraged from treatment by instrumental variable; returned by both <code>opt_nearfar</code> and <code>matches</code>
outc	The name of the outcome variable in quotes, e.g., "wages"
trt	The name of the treatment variable, e.g., "educ"
alpha	Level of confidence interval

**Value**

est.emp	Empirical estimate of effect ratio
est.HL	Hodges-Lehmann type estimate of effect ratio
lower	Lower limit to 1-alpha/2 confidence interval for effect ratio
upper	Upper limit to 1-alpha/2 confidence interval for effect ratio

**Author(s)**

Joseph Rigdon <jrigdon@wakehealth.edu>

**References**

Baiocchi M, Small D, Lorch S, Rosenbaum P (2010). Building a stronger instrument in an observational study of perinatal care for premature infants. *Journal of the American Statistical Association*, 105(492), 1285-1296.

**Examples**

```
k2 = matches(dta=mtcars, covs=c("cyl", "disp"), sinks=0.2, iv="carb",
  cutpoint=2, imp.var=c("cyl"), tol.var=0.03)

eff_ratio(dta=mtcars, match=k2, outc="wt", trt="gear", alpha=0.05)
```

---

matches	<i>Function to find pair matches using a distance matrix. Called by <code>opt_nearfar</code> to discover optimal near-far matches.</i>
---------	--

---

**Description**

Given values of percent sinks and cutpoint, this function will find the corresponding near-far match

**Usage**

```
matches(dta, covs, iv = NA, imp.var = NA, tol.var = NA, sinks = 0,
  cutpoint = NA)
```

**Arguments**

<code>dta</code>	The name of the data frame on which to do the matching
<code>covs</code>	A vector of the names of the covariates to make “near”, e.g., <code>covs=c("age", "sex", "race")</code>
<code>iv</code>	The name of the instrumental variable, e.g., <code>iv="QOB"</code>
<code>imp.var</code>	A list of (up to 5) named variables to prioritize in the “near” matching
<code>tol.var</code>	A list of (up to 5) tolerances attached to the prioritized variables where 0 is highest penalty for mismatch
<code>sinks</code>	Percentage of the data to match to sinks (and thus remove) if desired; default is 0
<code>cutpoint</code>	Value below which individuals are too similar on <code>iv</code> ; increase to make individuals more “far” in match

**Details**

Default settings yield a "near" match on only observed confounders in X; add IV, sinks, and cutpoint to get near-far match.

**Value**

A two-column matrix of row indices of paired matches

**Author(s)**

Joseph Rigdon <[jrigdon@wakehealth.edu](mailto:jrigdon@wakehealth.edu)>

**References**

Lu B, Greevy R, Xu X, Beck C (2011). Optimal nonbipartite matching and its statistical applications. *The American Statistician*, 65(1), 21-30.

**See Also**

[opt\\_nearfar](#)

**Examples**

```
k2 = matches(dta=mtcars, covs=c("cyl", "disp"), sinks=0.2, iv="carb",
             cutpoint=2, imp.var=c("cyl"), tol.var=0.03)
k2[1:5, ]
```

---

opt_nearfar	<i>Finds optimal near-far match</i>
-------------	-------------------------------------

---

### Description

Discovers optimal near-far matches using the partial F statistic (for continuous treatments) or partial deviance (for binary and treatments)

### Usage

```
opt_nearfar(dta, trt, covs, iv, trt.type = "cont", imp.var = NA,
  tol.var = NA, adjust.IV = TRUE, sink.range = c(0, 0.5), cutp.range = NA,
  max.time.seconds = 300)
```

### Arguments

dta	The name of the data frame on which matching was performed
trt	The name of the treatment variable, e.g., "educ"
iv	The name of the instrumental variable, e.g., iv="QOB"
covs	A vector of the names of the covariates to make "near", e.g., covs=c("age", "sex", "race")
trt.type	Treatment variable type: "cont" for continuous, or "bin" for binary
imp.var	A list of (up to 5) named variables to prioritize in the "near" matching
tol.var	A list of (up to 5) tolerances attached to the prioritized variables where 0 is highest penalty for mismatch
adjust.IV	if TRUE, include measured confounders in treatment~IV model that is optimized; if FALSE, exclude
sink.range	A two element vector of (min, max) for range of sinks over which to optimize in the near-far match; default (0, 0.5) such that maximally 50% of observations can be removed
cutp.range	a two element vector of (min, max) for range of cutpoints (how far apart the IV will become) over which to optimize in the near-far match; default is (one SD of IV, range of IV)
max.time.seconds	How long to let the optimization algorithm run; default is 300 seconds = 5 minutes

### Value

n.calls	Number of calls made to the objective function
sink.range	A two element vector of (min, max) for range of sinks over which to optimize in the near-far match; default (0, 0.5) such that maximally 50% of observations can be removed

cutp.range	a two element vector of (min, max) for range of cutpoints (how far apart the IV will become) over which to optimize in the near-far match; default is (one SD of IV, range of IV)
pct.sink	Optimal percent sinks
cutp	Optimal cutpoint
maxF	Highest value of partial F-statistic (continuous treatment) or residual deviance (binary treatment) found by simulated annealing optimizer
match	A two column matrix where the first column is the index of an “encouraged” individual and the second column is the index of the corresponding “discouraged” individual from the pair matching
summ	A table of mean variable values for both the “encouraged” and “discouraged” groups across all variables plus absolute standardized differences for each variable

### Author(s)

Joseph Rigdon <jrigdon@wakehealth.edu>

### References

Lu B, Greevy R, Xu X, Beck C (2011). Optimal nonbipartite matching and its statistical applications. *The American Statistician*, 65(1), 21-30.

Xiang Y, Gubian S, Suomela B, Hoeng J (2013). Generalized Simulated Annealing for Efficient Global Optimization: the GenSA Package for R. *The R Journal*, 5(1). URL <http://journal.r-project.org/>.

### Examples

```
k = opt_nearfar(dta=mtcars, trt="drat", covs=c("cyl", "disp"),
  trt.type="cont", iv="carb", imp.var=NA, tol.var=NA, adjust.IV=TRUE,
  max.time.seconds=2)
summary(k)
```

---

smahal

*Compute rank-based Mahalanobis distance matrix between each pair*

---

### Description

This function computes the rank-based Mahalanobis distance matrix between each pair of observations in the data set. Called by `matches` (and ultimately `opt_nearfar`) function to set up a distance matrix used to create pair matches.

### Usage

```
smahal(X)
```



**Arguments**

X                    A matrix of observed confounders with n rows (observations) and p columns (variables)

**Value**

Returns the rank-based Mahalanobis distance matrix between every pair of observations

**Examples**

```
smahal(mtcars[1:4, 2:3])
```

---

summary.nf

*Summary method for object of class "nf"*

---

**Description**

Displays key information, e.g., number of matches tried, and post-match balance, for [opt\\_nearfar](#) function

**Usage**

```
## S3 method for class 'nf'
summary(object, ...)
```

**Arguments**

object                Object of class "nf" returned by [opt\\_nearfar](#)  
 ...                    additional arguments affecting the summary produced

**Value**

Returns a summary of results from [opt\\_nearfar](#) function

**Author(s)**

Joseph Rigdon <jrigdon@wakehealth.edu>

**See Also**

[opt\\_nearfar](#)

**Examples**

```
k = opt_nearfar(dta=mtcars, trt="drat", covs=c("cyl", "disp"),
  trt.type="cont", iv="carb", imp.var=NA, tol.var=NA, adjust.IV=TRUE,
  max.time.seconds=1)
summary(k)
```

---

summ_matches	<i>Computes table of absolute standardized differences</i>
--------------	--

---

**Description**

Computes absolute standardized differences for both continuous and binary variables. Called by [opt\\_nearfar](#) to summarize results of near-far match.

**Usage**

```
summ_matches(dta, iv, covs, match)
```

**Arguments**

dta	The name of the data frame on which matching was performed
iv	The name of the instrumental variable, e.g., iv="QOB"
covs	A vector of the names of the covariates to make "near", e.g., covs=c("age", "sex", "race")
match	A two-column matrix of row indices of paired matches

**Value**

A table of mean variable values for both the "encouraged" and "discouraged" groups across all variables plus absolute standardized differences for each variable

**Author(s)**

Joseph Rigdon <jrigdon@wakehealth.edu>

**See Also**

[opt\\_nearfar](#)

**Examples**

```
k2 = matches(dta=mtcars, covs=c("cyl", "disp"), sinks=0.2, iv="carb",
             cutpoint=2, imp.var=c("cyl"), tol.var=0.03)
summ_matches(dta=mtcars, iv="carb", covs=c("cyl", "disp"), match=k2)
```

# Index

\* **datasets**

    angrist, [3](#)

angrist, [3](#)

calipers, [4](#)

eff\_ratio, [4](#)

matches, [4](#), [5](#), [5](#), [8](#)

nearfar-package, [2](#)

opt\_nearfar, [4-6](#), [7](#), [8-10](#)

smahal, [8](#)

summ\_matches, [10](#)

summary.nf, [9](#)