Package ‘MatchThem’

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Title Matching and Weighting Multiply Imputed Datasets

Description Provides the necessary tools for the pre-processing techniques of matching and weight-
ing multiply imputed datasets to control for effects of confounders and to reduce the de-
gree of dependence on certain modeling assumptions in studying the causal associations be-
tween an exposure and an outcome. This package includes functions to perform match-
ing within and across the multiply imputed datasets using several matching methods, to esti-
mate weights of units in the imputed datasets using several weighting methods, to calcu-
late the causal effect estimate in each matched or weighted dataset using parametric or non-
parametric statistical models, and to pool the obtained estimates from these models accord-
ing to Rubin's rules (please see <https://github.com/FarhadPishgar/MatchThem> for details).

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**complete**

*Extracts Imputed Datasets*

**Description**

The `complete()` function extracts data from an object of the `mimids` or `wimids` class.

**Usage**

```r
## S3 method for class 'mimids'
complete(data, n = 1, include = FALSE, mild = FALSE, all = TRUE, ...)

## S3 method for class 'wimids'
complete(data, n = 1, include = FALSE, mild = FALSE, all = TRUE, ...)
```

**Arguments**

- `data` This argument specifies an object of the `mimids` or `wimids` class.
- `n` This argument specifies the imputed dataset number, intended to extract its data, or an action. The input must be a positive integer or a keyword. The keywords include "all" (produces a mild object of the imputed datasets), "long" (produces a dataset with imputed datasets stacked vertically), and "broad" (produces a dataset with imputed datasets stacked horizontally). The default is 1.
- `include` This argument specifies whether the original data with the missing values should be included. The input must be a logical value. The default is FALSE.
- `mild` This argument specifies whether the return value should be an object of mild class. Please note that setting `mild = TRUE` overrides `n` keywords "long", "broad", and "repeated". The default is FALSE.
 This argument specifies whether to include observations with a zero estimated weight. The default is TRUE.

... Additional arguments to be passed to the function.

Details

The datasets within the \texttt{mimids} or \texttt{wimids} class objects are extracted.

Value

This function returns the imputed dataset within \texttt{mimids} or \texttt{wimids} class objects.

Author(s)

Extracted from the \texttt{mice} package written by Stef van Buuren et al. with changes

References


See Also

\texttt{mimids} \texttt{wimids}

Examples

#Loading libraries
library(mice)
library(MatchThem)

#Loading the dataset
data(osteoarthritis)

#Multiply imputing the missing values
imputed.datasets <- mice(osteoarthritis, m = 5, maxit = 10,
  method = c("","", "mean", "polyreg",
    "logreg", "logreg", "logreg"))

#Matching the multiply imputed datasets
matched.datasets <- matchthem(OSP ~ AGE + SEX + BMI + RAC + SMK, imputed.datasets,
  approach = 'within', method = 'nearest')

#Extracting the first imputed dataset
matched.dataset.1 <- complete(matched.datasets, n = 1)
is.mimids Checks for the mimids Class

Description
is.mimids() function checks whether class of objects is mimids or not.

Usage
is.mimids(object)

Arguments
object This argument specifies the object that should be checked to see if is of the mimids class or not.

Details
The class of objects is checked to be of the mimids.

Value
This function returns a logical value indicating whether object is of the mimids class.

Author(s)
Farhad Pishgar

See Also
matchthem
mimids

Examples
#Loading libraries
library(mice)
library(MatchThem)

#Loading the dataset
data(dataset)

#Multiply imputing the missing values
imputed.datasets <- mice(osteoarthritis, m = 5, maxit = 10,
                         method = c("", ",", "mean", "polyreg",
                         "logreg", "logreg", "logreg"))

#Matching the multiply imputed datasets
matched.datasets <- matchthem(OSP ~ AGE + SEX + BMI + RAC + SMK, imputed.datasets,


```r
approach = 'within', method = 'nearest')

#Checking the 'matched.datasets' object
is.mimids(matched.datasets)
is(matched.datasets)
```

---

### is.mimipo

**Checks for the mimipo Class**

**Description**

is.mimipo() function checks whether class of objects is `mimipo` or not.

**Usage**

```r
is.mimipo(object)
```

**Arguments**

- **object**
  
  This argument specifies the object that should be checked to see if is of the `mimipo` class or not.

**Details**

The class of objects is checked to be of the `mimipo`.

**Value**

This function returns a logical value indicating whether object is of the `mimipo` class.

**Author(s)**

Farhad Pishgar

**See Also**

- `pool`
- `mimipo`
is.mimira

Checks for the mimira Class

Description

is.mimira() function checks whether class of objects is mimira or not.

Usage

is.mimira(object)

Arguments

object

This argument specifies the object that should be checked to see if is of the mimira class or not.

Details

The class of objects is checked to be of the mimira.

Value

This function returns a logical value indicating whether object is of the mimira class.

Author(s)

Farhad Pishgar

See Also

with

mimira

Examples

#Loading libraries
library(mice)
library(MatchThem)
library(survey)

#Loading the dataset
data(osteoarthritis)

#Multiply imputing the missing values
imputed.datasets <- mice(osteoarthritis, m = 5, maxit = 10,
method = c("", ",", "mean", "polyreg",
"logreg", "logreg", "logreg"))

#Estimating weights of observations in the multiply imputed datasets
weighted.datasets <- weightthem(OSP ~ AGE + SEX + BMI + RAC + SMK, imputed.datasets, approach = 'within', method = 'ps')

#Analyzing the weighted datasets
models <- with(data = weighted.datasets, exp = svyglm(KOA ~ OSP, family = binomial))

#Checking the 'models' object
is.mimira(models)
is(models)

---

**is.wimids**

**Checks for the wimids Class**

**Description**

is.wimids() function checks whether class of objects is wimids or not.

**Usage**

is.wimids(object)

**Arguments**

object This argument specifies the object that should be checked to see if is of the wimids class or not.

**Details**

The class of objects is checked to be of the wimids.

**Value**

This function returns a logical value indicating whether object is of the wimids class.

**Author(s)**

Farhad Pishgar

**See Also**

weightthem
wimids
Examples

```r
# Loading libraries
library(mice)
library(MatchThem)

# Loading the dataset
data(osteoarthritis)

# Multiply imputing the missing values
imputed.datasets <- mice(osteoarthritis, m = 5, maxit = 10,
                          method = c("", ",", "mean", "polyreg",
                          "logreg", "logreg", "logreg"))

# Estimating weights of observations in the multiply imputed datasets
weighted.datasets <- weightthem(OSP ~ AGE + SEX + BMI + RAC + SMK, imputed.datasets,
                                 approach = 'within', method = 'ps')

# Checking the 'weighted.datasets' object
is.wimids(weighted.datasets)
is(weighted.datasets)
```

---

**matchthem**  
**Matches Multiply Imputed Datasets**

**Description**

`matchthem()` function enables parametric models for causal inference to work better by selecting matched subsets of the control and treated subgroups of imputed datasets of a `mids` or `amelia` class object.

**Usage**

```r
matchthem(
  formula,
  datasets,
  approach = "within",
  method = "nearest",
  distance = "logit",
  distance.options = list(),
  discard = "none",
  reestimate = FALSE,
  ...
)
```

**Arguments**

- `formula`  
  This argument takes the usual syntax of R formula, `z ~ x1 + x2`, where `z` is a binary exposure indicator and `x1` and `x2` are the potential confounders. Both
the exposure indicator and the potential confounders must be contained in the
imputed datasets, which is specified as datasets (see below). All of the usual
R syntax for formula works. For example, x1:x2 represents the first order inter-
action term between x1 and x2 and I(x1^2) represents the square term of x1.
See help(formula) for details.

datasets
This argument specifies the datasets containing the exposure indicator and the
potential confounders called in the formula. This argument must be an object
of the mids or amelia class, which is typically produced by a previous call to
mice() or mice.mids() functions from the mice package or to amelia() func-
tion from the Amelia package (the Amelia package is designed to impute miss-
ing data in a single cross-sectional dataset or in a time-series dataset, currently, the MatchThem package only supports the former datasets).

approach
This argument specifies a matching approach. Currently, "within" (calculat-
ing distance measures within each imputed dataset and matching observations
based on them) and "across" (calculating distance measures within each im-
puted dataset, averaging distance measure for each observation across imputed
datasets, and matching based on the averaged measures) approaches are avail-
able. The default is "within" which has been shown to produce unbiased re-
results.

method
This argument specifies a matching method. Currently, "nearest" (nearest
neighbor matching), "exact" (exact matching), "full" (full matching), "genetic"
(genetic matching), "subclass" (subclassification), "cem" (coarsened exact match-
ing), and "optimal" (optimal matching) methods are available (only the "nearest",
"full", "subclass", and "optimal" matching methods are compatible with the "across" approach). The default is "nearest". Note that within each of these matching methods, MatchThem offers a variety of options.

distance
This argument specifies the method that should be used to estimate the distance
measure (the "mahalanobis" method for distance measure is not compatible
with the "across" approach). The default is logistic regression, "logit". A
variety of other methods are available (please see the MatchIt package reference
manual <https://cran.r-project.org/package=MatchIt> for more details).

distance.options
This optional argument specifies the arguments that are passed to the model for
estimating the distance measure. The input to this argument should be a list.

discard
This argument specifies whether to discard observations that fall outside some
measure of support of the distance score before matching and not allow them to
be used at all in the matching procedure. Note that discarding observations may
change the quantity of interest being estimated. The current options are "none"
(discarding no observations before matching), "both" (discarding all observa-
tions, both the control and treated observations, that are outside the support of
the distance measure), "control" (discarding only control observations outside
the support of the distance measure of the treated observations), and "treat"
(discarding only treated observations outside the support of the distance measure
of the control observations). The default is "none".

reestimate
This argument specifies whether the model for estimating the distance measure
should be reestimated after observations are discarded. The input must be a
logical value. The default is FALSE.
Additional arguments to be passed to the matching method (please see the `MatchIt` package reference manual <https://cran.r-project.org/package=MatchIt> for more details).

Details

The matching is done using the `matchthem(z ~ x1,...)` command, where `z` is the exposure indicator and `x1` represents the potential confounder to be used in the matching model. There are a number of matching options. The default syntax is `matchthem(formula,datasets,approach = "within",method = "nearest",distance = "logit",...)`. Summaries of the results can be seen graphically using `plot()` or numerically using `summary()` functions. The `print()` function also prints out the output.

Value

This function returns an object of the `mimids` (matched multiply imputed datasets) class, that includes matched subsets of the imputed datasets primarily passed to the function by the `datasets` argument.

Author(s)

Farhad Pishgar and Noah Greifer

References


See Also

`mimids`

`with`

`pool`

Examples

```r
#Loading libraries
library(mice)
library(MatchThem)

#Loading the dataset
data(osteoarthritis)
```
# Multiply imputing the missing values
imputed.datasets <- mice(osteoarthritis, m = 5, maxit = 10,
    method = c("", "", "mean", "polyreg",
    "logreg", "logreg", "logreg"))

# Matching the multiply imputed datasets
matched.datasets <- matchthem(OSP ~ AGE + SEX + BMI + RAC + SMK, imputed.datasets,
    approach = 'within', method = 'nearest')

---

## `mimids` 

**Matched Multiply Imputed Datasets**

### Description

`mimids` object contains data of matched multiply imputed datasets. `mimids` objects are generated by calls to `matchthem()`.

### Details

`mimids` objects has methods for the `print()`, `summary()`, `plot()`, and `merge()` functions (please see `MatchIt` package reference manual for details).

### Note

The `MatchThem` package does not use the S4 class definitions and instead relies on the S3 list equivalents.

### Author(s)

Farhad Pishgar

### References


### See Also

`matchthem`
**mimipo**

*Multiply Imputed Pooled Outcome*

**Description**

*mimipo* object contains data of multiply imputed pooled outcome. *mimipo* objects are generated by calls to `pool()`.

**Details**

*mimipo* objects has methods for the `print()` and `summary()` functions (please see `mice` package reference manual for details).

**Note**

The **MatchThem** package does not use the S4 class definitions and instead relies on the S3 list equivalents.

**Author(s)**

Farhad Pishgar

**References**


**See Also**

`pool`

---

**mimira**

*Multiply Imputed Repeated Analyses*

**Description**

*mimira* object contains data of multiply imputed repeated analyses. *mimira* objects are generated by calls to `with()`.

**Details**

*mimira* objects has methods for the `print()` and `summary()` functions (please see `mice` package reference manual for details).
Note

The MatchThem package does not use the S4 class definitions and instead relies on the S3 list equivalents.

Author(s)

Farhad Pishgar

References


See Also

with

| osteoarthritis | Data of 2,585 Participants in the OAI Project |

Description

ostearthritis includes demographic data of 2,585 units (individuals) with or at risk of knee osteoarthritis. The recorded data has missing values in body mass index (BMI, a quantitative variable), race (RAC, a categorical qualitative variable), smoking status (SMK, a binary qualitative variable), osteoporosis status at baseline (OSP, a binary qualitative variable), and knee osteoarthritis status at follow-up (KOA, a binary qualitative variable).

Usage

ostearthritis

Format

This dataset contains 2,585 rows and 7 columns. Each row presents data of an unit (individual) and each column presents data of a characteristics of that individual. The columns are:

- **AGE**  Age of each unit (individual);
- **SEX**  Gender of each unit (individual), coded as 0 (female) and 1 (male);
- **BMI**  Estimated body mass index of each unit (individual);
- **RAC**  Race of each unit (individual), coded as 0 (other), 1 (caucasian), 2 (african american), and 3 (asian);
- **SMK**  The smoking status of each unit, coded as 0 (non-smoker) and 1 (smoker);
- **OSP**  Osteoporosis status of each unit (individual) at baseline, coded as 0 (negative) and 1 (positive); and
- **KOA**  Knee osteoarthritis status of each unit (individual) in the follow-up, coded as 0 (at risk) and 1 (diagnosed).
## Source

The information presented in the osteoarthritis dataset is based on the publicly available data of the Osteoarthritis Initiative (OAI) project (see [https://nda.nih.gov/oai/](https://nda.nih.gov/oai/) for details), with changes.

---

### pool

**Pools Estimates by Rubin’s Rules**

### Description

pool() function pools estimates from n repeated data analyses. The typical sequence of steps to do a matching procedure on the imputed datasets are:

1. Impute the missing values by the mice() function (from the mice package) or the amelia() function (from the Amelia package), resulting in a multiple imputed dataset (an object of the mids or amelia class);
2. Match each imputed dataset using a matching model by the matchthem() function, resulting in an object of the mimids class;
3. Check the extent of balance of covariates across the matched datasets;
4. Fit the statistical model of interest on each matched dataset by the with() function, resulting in an object of the mimira class; and
5. Pool the estimates from each model into a single set of estimates and standard errors, resulting in an object of the mimipo class.

### Usage

pool(object, dfcom = NULL)

### Arguments

- **object**: This argument specifies an object of the mimira class (produced by a previous call to with() function).
- **dfcom**: This argument specifies a positive number representing the degrees of freedom in the data analysis. The default is NULL, which means to extract this information from the fitted model with the lowest number of observations or the first fitted model (when that fails the warning The function cannot extract the dfcom from the datasets, hence, large sample is assumed. is printed and the parameter is set to 999999).

### Details

pool() function averages the estimates of the model and computes the total variance over the repeated analyses by Rubin’s rules.

### Value

This function returns an object of the mimipo class.
Author(s)

Extracted from the mice package written by Stef van Buuren et al. with changes

References


See Also

with

Examples

#Loading libraries
library(mice)
library(MatchThem)

#Loading the dataset
data(osteoarthritis)

#Multiply imputing the missing values
imputed.datasets <- mice(osteoarthritis, m = 5, maxit = 10,
   method = c("", "", "mean", "polyreg",
   "logreg", "logreg", "logreg"))

#Matching the multiply imputed datasets
matched.datasets <- matchthem(OSP ~ AGE + SEX + BMI + RAC + SMK, imputed.datasets,
   approach = 'within', method = 'nearest')

#Analyzing the matched datasets
models <- with(data = matched.datasets,
   exp = glm(KOA ~ OSP, family = binomial))

#Pooling results obtained from analysing the datasets
results <- pool(models)

weightthem

Weights Multiply Imputed Datasets

Description

weightthem() function enables parametric models for causal inference to work better by estimating weights of the control and treated units in each imputed dataset of a mids or amelia class object.
Usage

weightthem(
  formula,
  datasets,
  approach = "within",
  method = "ps",
  estimand = "ATE",
  ...
)

Arguments

formula This argument takes the usual syntax of R formula, \( z \sim x_1 + x_2 \), where \( z \) is a binary exposure indicator and \( x_1 \) and \( x_2 \) are the potential confounders. Both the exposure indicator and the potential confounders must be contained in the imputed datasets, which is specified as datasets (see below). All of the usual R syntax for formula works. For example, \( x_1:x_2 \) represents the first order interaction term between \( x_1 \) and \( x_2 \) and \( I(x_1^2) \) represents the square term of \( x_1 \). See help(formula) for details.

datasets This argument specifies the datasets containing the exposure indicator and the potential confounders called in the formula. This argument must be an object of the mids or amelia class, which is typically produced by a previous call to mice() or mice.mids() functions from the mice package or to amelia() function from the Amelia package (the Amelia package is designed to impute missing data in a single cross-sectional dataset or in a time-series dataset, currently, the MatchThem package only supports the former datasets).

approach This argument specifies a matching approach. Currently, "within" (calculating distance measures within each imputed dataset and weighting observations based on them) and "across" (calculating distance measures within each imputed dataset, averaging distance measure for each observation across imputed datasets, and weighting based on the averaged measures) approaches are available. The default is "within" which has been shown to produce unbiased results.

method This argument specifies the method that should be used to estimate weights. Currently, "ps" (propensity score weighting using generalized linear models), "gbm" (propensity score weighting using generalized boosted modeling), "cbps" (covariate balancing propensity score weighting), "npcbps" (non-parametric covariate balancing propensity score weighting), "ebal" (entropy balancing), "ebcw" (empirical balancing calibration weighting), "optweight" (optimization-based weighting), "super" (propensity score weighting using Super Learner), and "user-defined" (weighting using a user-defined weighting function) are available (only the "ps", "gbm", "cbps", and "super" weighting methods are compatible with the "across" approach). The default is "ps". Note that within each of these weighting methods, MatchThem offers a variety of options.

estimand This argument specifies the desired estimand. For binary and multinomial treatments, can be "ATE", "ATT", "ATC", and, for some weighting methods, "ATO" or
weightthem

"ATM". The default is "ATE". Please see the WeightIt package reference manual <https://cran.r-project.org/package=WeightIt> for more details.

... Additional arguments to be passed to the weighting method (please see the WeightIt package reference manual <https://cran.r-project.org/package=WeightIt> for more details).

Details

The weighting is done using the weightthem(z ~ x1,...) command, where z is the exposure indicator and x1 represents the potential confounders to be used in the weighting model. The default syntax is weightthem(formula,datasets,approach = "within",method = "ps",estimand = "ATE",...). Summaries of the results can be seen numerically using summary() function. The print() function also prints out the output.

Value

This function returns an object of the wimids (weighted multiply imputed datasets) class, that includes weights of observations of the imputed datasets (listed as the weights variables in each) primarily passed to the function by the datasets argument.

Author(s)

Farhad Pishgar and Noah Greifer

References


See Also

wimids
with
pool

Examples

#Loading libraries
library(mice)
library(MatchThem)

#Loading the dataset
data(osteoarthritis)

#Multiply imputing the missing values
imputed.datasets <- mice(osteoarthritis, m = 5, maxit = 10,
method = c("", ",", "mean", "polyreg",
"logreg", "logreg", "logreg"))
# Estimating weights of observations in the multiply imputed datasets
weighted.datasets <- weightthem(OSP ~ AGE + SEX + BMI + RAC + SMK, imputed.datasets,
                                   approach = 'within', method = 'ps', estimand = "ATT")

---

**wimids**  
*Weighted Multiply Imputed Datasets*

---

**Description**

* wimids object contains data of weighted multiply imputed datasets. The *wimids* object is generated by calls to the `weightthem()`.

**Details**

* wimids objects has methods for the `print()`, `summary()`, and `merge()` functions (please see *WeightIt* package reference manual for details).

**Note**

* The *MatchThem* package does not use the S4 class definitions and instead relies on the S3 list equivalents.

**Author(s)**

* Farhad Pishgar

**References**


**See Also**

* `weightthem`
**with**

Evaluates an Expression in Matched or Weighted Imputed Datasets

**Description**

with() function performs a statistical computation on the \( n \) imputed datasets of the \texttt{mimids} or \texttt{wimids} objects. The typical sequence of steps to do a matching or weighting procedure on the imputed datasets are:

1. Impute the missing values by the \texttt{mice()} function (from the \texttt{mice} package) or the \texttt{amelia()} function (from the \texttt{Amelia} package), resulting in a multiple imputed dataset (an object of the \texttt{mids} or \texttt{amelia} class);
2. Match or weight imputed datasets using a matching or weighting model by the \texttt{matchthem()} or \texttt{weightthem()} function, resulting in an object of the \texttt{mimids} or \texttt{wimids} class;
3. Check the extent of balance of covariates across the datasets;
4. Fit the statistical model of interest on each dataset by the \texttt{with()} function, resulting in an object of the \texttt{mimira} class; and
5. Pool the estimates from each model into a single set of estimates and standard errors, resulting in an object of the \texttt{mimipo} class.

**Usage**

```r
## S3 method for class 'mimids'
with(data, expr, ...)

## S3 method for class 'wimids'
with(data, expr, ...)
```

**Arguments**

- `data` This argument specifies an object of the \texttt{mimids} or \texttt{wimids} class, typically produced by a previous call to the \texttt{matchthem()} or \texttt{weightthem()}.
- `expr` This argument specifies an expression of the usual syntax of R formula (it also accepts expressions from \texttt{survey} package, like \texttt{svyglm()}, please note that you shouldn’t include the \texttt{weights = weights} argument, see the package vignette for details).
- `...` Additional arguments to be passed to \texttt{expr}.

**Details**

\texttt{with()} performs a computation on the imputed datasets.

**Value**

This function returns an object of the \texttt{mimira} class.
Author(s)
Farhad Pishgar

References

See Also
matchthem
weightthem

Examples
#Loading libraries
library(mice)
library(MatchThem)
library(survey)

#Loading the dataset
data(osteoarthritis)

#Multiply imputing the missing values
imputed.datasets <- mice(osteoarthritis, m = 5, maxit = 10,
    method = c("", ",", "mean", "polyreg",
                  "logreg", "logreg", "logreg"))

#Estimating weights of observations in the multiply imputed datasets
weighted.datasets <- weightthem(OSP ~ AGE + SEX + BMI + RAC + SMK, imputed.datasets,
                                  approach = 'within', method = 'ps')

#Analyzing the weighted datasets
models <- with(data = weighted.datasets,
              exp = svyglm(KOA ~ OSP, family = binomial))
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