Package ‘mice’

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R topics documented:

.pmm.match ................................................................. 5
ampute ................................................................. 6
anova.mira .......................................................... 10
appendbreak .......................................................... 11
as.mids ............................................................... 11
as.mira ............................................................... 13
as.mitml.result ..................................................... 14
boys ................................................................. 15
brandsma ............................................................ 16
bwplot.mads .......................................................... 18
bwplot.mids .......................................................... 19
cbind.mids .......................................................... 22
cc ................................................................. 24
cci ................................................................. 25
complete.mids ....................................................... 26
construct.blocks ................................................... 27
D1 ................................................................. 29
D2 ................................................................. 30
D3 ................................................................. 31
densityplot.mids ................................................... 32
employee ............................................................ 35
estimice ............................................................ 36
extractBS ............................................................ 37
fdd ................................................................. 38
R topics documented:

fdgs .......................................................... 40
fico ............................................................ 41
filter.mids .................................................. 42
fix.coef ....................................................... 44
flux ............................................................ 45
fluxplot ....................................................... 46
getfit .......................................................... 48
getqbar ......................................................... 49
glm.mids ...................................................... 50
ibind ............................................................ 51
ic ............................................................... 52
ici ............................................................... 53
is.mads ....................................................... 53
is.mids ........................................................ 54
is.mipo ........................................................ 54
is.mira ........................................................ 55
is.mitml.result ............................................. 55
leiden85 ...................................................... 56
lm.mids ........................................................ 56
mads-class ................................................... 57
make.blocks ................................................... 59
make.blots .................................................... 60
make.formulas ............................................... 61
make.method ................................................ 62
make.post .................................................... 63
make.predictorMatrix ..................................... 64
make.visitSequence ....................................... 64
make.where ................................................ 65
mammalsleep ............................................... 66
matchindex .................................................. 67
md.pairs ...................................................... 68
md.pattern ................................................... 70
mdc ............................................................ 71
mice ........................................................... 72
mice.impute.2l.bin ........................................ 79
mice.impute.2l.lmer ...................................... 81
mice.impute.2l.norm ...................................... 82
mice.impute.2l.pan ....................................... 83
mice.impute.2lonly.mean ................................ 86
mice.impute.2lonly.norm ................................ 87
mice.impute.2lonly.pmm ................................ 90
mice.impute.cart ......................................... 93
mice.impute.jomoImpute .................................. 94
mice.impute.lda ........................................... 96
mice.impute.logreg ....................................... 97
mice.impute.logreg.boot .................................. 99
mice.impute.mean ......................................... 100
mice.impute.midastouch ................................ 101
R topics documented:

mice.impute.mnar.logreg .............................................. 104
mice.impute.norm .................................................. 107
mice.impute.norm.boot ............................................... 108
mice.impute.norm.nob ................................................ 109
mice.impute.norm.predict ........................................... 111
mice.impute.panImpute ................................................ 112
mice.impute.passive .................................................. 114
mice.impute.pmm ...................................................... 115
mice.impute.polr ....................................................... 117
mice.impute.polyreg .................................................. 119
mice.impute.quadratic .............................................. 121
mice.impute.rf ........................................................ 123
mice.impute.ri ......................................................... 125
mice.impute.sample ................................................... 126
mice.mids ............................................................. 127
mice.theme ............................................................ 128
mids-class ............................................................. 129
mids2mplus ............................................................. 131
mids2spss .............................................................. 132
mira-class ............................................................... 133
mnar_demo_data ....................................................... 134
name.blocks ............................................................. 135
name.formulas ........................................................ 136
ncc ................................................................. 137
nelsonaalen ............................................................ 138
nhanes ................................................................. 139
nhanes2 ............................................................... 140
nic ................................................................. 141
nimp ................................................................. 141
norm.draw .............................................................. 142
parlmice ............................................................... 143
pattern ............................................................... 145
plot.mids .............................................................. 146
pool ............................................................... 148
pool.compare ........................................................ 150
pool.r.squared ....................................................... 151
pool.scalar ........................................................... 153
popmis ............................................................... 154
pops ............................................................... 155
potthoffroy ........................................................... 156
print.mads ............................................................ 157
print.mids ............................................................. 158
quickpred ............................................................. 159
rbind.mids ............................................................ 161
selfreport ............................................................. 163
squeeze ............................................................. 165
stripplot.mids ......................................................... 165
summary.mira ........................................................ 169
.pmm.match

Finds an imputed value from matches in the predictive metric (deprecated)

Description
This function finds matches among the observed data in the predictive mean metric. It selects the donors closest matches, randomly samples one of the donors, and returns the observed value of the match.

Usage
.pmm.match(z, yhat = yhat, y = y, donors = 5, ...)

Arguments
- `z`: A scalar containing the predicted value for the current case to be imputed.
- `yhat`: A vector containing the predicted values for all cases with an observed outcome.
- `y`: A vector of length(yhat) elements containing the observed outcome
- `donors`: The size of the donor pool among which a draw is made. The default is donors = 5. Setting donors = 1 always selects the closest match. Values between 3 and 10 provide the best results. Note: This setting was changed from 3 to 5 in version 2.19, based on simulation work by Tim Morris (UCL).
- `...`: Other parameters (not used).

Details
This function is included for backward compatibility. It was used up to mice 2.21. The current `mice.impute.pmm()` function calls the faster C function matcher instead of `.pmm.match()`.

Value
A scalar containing the observed value of the selected donor.
ampute

Generate missing data for simulation purposes

Description

This function generates multivariate missing data under a MCAR, MAR or MNAR missing data mechanism. Imputation of data sets containing missing values can be performed with mice.

Usage

ampute(
  data,
  prop = 0.5,
  patterns = NULL,
  freq = NULL,
  mech = "MAR",
  weights = NULL,
  std = TRUE,
  cont = TRUE,
  type = NULL,
  odds = NULL,
  bycases = TRUE,
  run = TRUE
)

Arguments

data A complete data matrix or data frame. Values should be numeric. Categorical variables should have been transformed to dummies.

prop A scalar specifying the proportion of missingness. Should be a value between 0 and 1. Default is a missingness proportion of 0.5.

patterns A matrix or data frame of size #patterns by #variables where 0 indicates that a variable should have missing values and 1 indicates that a variable should remain complete. The user may specify as many patterns as desired. One pattern (a vector) is possible as well. Default is a square matrix of size #variables where each pattern has missingness on one variable only (created with

Author(s)

Stef van Buuren

References


After the amputation procedure, `md.pattern` can be used to investigate the missing data patterns in the data.

**freq**  
A vector of length `#patterns` containing the relative frequency with which the patterns should occur. For example, for three missing data patterns, the vector could be `c(0.4, 0.4, 0.2)`, meaning that of all cases with missing values, 40 percent should have pattern 1, 40 percent pattern 2 and 20 percent pattern 3. The vector should sum to 1. Default is an equal probability for each pattern, created with `ampute.default.freq`.

**mech**  
A string specifying the missingness mechanism, either "MCAR" (Missing Completely At Random), "MAR" (Missing At Random) or "MNAR" (Missing Not At Random). Default is a MAR missingness mechanism.

**weights**  
A matrix or data frame of size `#patterns` by `#variables`. The matrix contains the weights that will be used to calculate the weighted sum scores. For a MAR mechanism, the weights of the variables that will be made incomplete should be zero. For a MNAR mechanism, these weights could have any possible value. Furthermore, the weights may differ between patterns and between variables. They may be negative as well. Within each pattern, the relative size of the values are of importance. The default weights matrix is made with `ampute.default.weights` and returns a matrix with equal weights for all variables. In case of MAR, variables that will be amputed will be weighted with 0. For MNAR, variables that will be observed will be weighted with 0. If the mechanism is MCAR, the weights matrix will not be used.

**std**  
Logical. Whether the weighted sum scores should be calculated with standardized data or with non-standardized data. The latter is especially advised when making use of train and test sets in order to prevent leakage.

**cont**  
Logical. Whether the probabilities should be based on a continuous or a discrete distribution. If TRUE, the probabilities of being missing are based on a continuous logistic distribution function. `ampute.continuous` will be used to calculate and assign the probabilities. These probabilities will then be based on the argument type. If FALSE, the probabilities of being missing are based on a discrete distribution (`ampute.discrete`) based on the odds argument. Default is TRUE.

**type**  
A string or vector of strings containing the type of missingness for each pattern. Either "LEFT", "MID", "TAIL" or "RIGHT". If a single missingness type is given, all patterns will be created with the same type. If the missingness types should differ between patterns, a vector of missingness types should be given. Default is RIGHT for all patterns and is the result of `ampute.default.type`.

**odds**  
A matrix where `#patterns` defines the `#rows`. Each row should contain the odds of being missing for the corresponding pattern. The number of odds values defines in how many quantiles the sum scores will be divided. The odds values are relative probabilities: a quantile with odds value 4 will have a probability of being missing that is four times higher than a quantile with odds 1. The number of quantiles may differ between the patterns, specify NA for cells remaining empty. Default is 4 quantiles with odds values 1, 2, 3 and 4 and is created by `ampute.default.odds`.

**bycases**  
Logical. If TRUE, the proportion of missingness is defined in terms of cases.
If FALSE, the proportion of missingness is defined in terms of cells. Default is TRUE.

run Logical. If TRUE, the amputations are implemented. If FALSE, the return object will contain everything except for the amputed data set.

Details

This function generates missing values in complete data sets. Amputation of complete data sets is useful for the evaluation of imputation techniques, such as multiple imputation (performed with function `mice` in this package).

The basic strategy underlying multivariate imputation was suggested by Don Rubin during discussions in the 90’s. Brand (1997) created one particular implementation, and his method found its way into the FCS paper (Van Buuren et al, 2006).

Until recently, univariate amputation procedures were used to generate missing data in complete, simulated data sets. With this approach, variables are made incomplete one variable at a time. When more than one variable needs to be amputed, the procedure is repeated multiple times.

With the univariate approach, it is difficult to relate the missingness on one variable to the missingness on another variable. A multivariate amputation procedure solves this issue and moreover, it does justice to the multivariate nature of data sets. Hence, `ampute` is developed to perform multivariate amputation.

The idea behind the function is the specification of several missingness patterns. Each pattern is a combination of variables with and without missing values (denoted by 0 and 1 respectively). For example, one might want to create two missingness patterns on a data set with four variables. The patterns could be something like: 0,0,1,1 and 1,0,1,0. Each combination of zeros and ones may occur.

Furthermore, the researcher specifies the proportion of missingness, either the proportion of missing cases or the proportion of missing cells, and the relative frequency each pattern occurs. Consequently, the data is split into multiple subsets, one subset per pattern. Now, each case is candidate for a certain missingness pattern, but whether the case will have missing values eventually depends on other specifications.

The first of these specifications is the missing mechanism. There are three possible mechanisms: the missingness depends completely on chance (MCAR), the missingness depends on the values of the observed variables (i.e. the variables that remain complete) (MAR) or on the values of the variables that will be made incomplete (MNAR). For a discussion on how missingness mechanisms are related to the observed data, we refer to Schouten and Vink, 2018.

When the user specifies the missingness mechanism to be "MCAR", the candidates have an equal probability of becoming incomplete. For a "MAR" or "MNAR" mechanism, weighted sum scores are calculated. These scores are a linear combination of the variables.

In order to calculate the weighted sum scores, the data is standardized. For this reason, the data has to be numeric. Second, for each case, the values in the data set are multiplied with the weights, specified by argument `weights`. These weighted scores will be summed, resulting in a weighted sum score for each case.

The weights may differ between patterns and they may be negative or zero as well. Naturally, in case of a MAR mechanism, the weights corresponding to the variables that will be made incomplete, have a 0. Note that this may be different for each pattern. In case of MNAR missingness, especially
the weights of the variables that will be made incomplete are of importance. However, the other variables may be weighted as well.

It is the relative difference between the weights that will result in an effect in the sum scores. For example, for the first missing data pattern mentioned above, the weights for the third and fourth variables could be set to 2 and 4. However, weight values of 0.2 and 0.4 will have the exact same effect on the weighted sum score: the fourth variable is weighted twice as much as variable 3.

Based on the weighted sum scores, either a discrete or continuous distribution of probabilities is used to calculate whether a candidate will have missing values.

For a discrete distribution of probabilities, the weighted sum scores are divided into subgroups of equal size (quantiles). Thereafter, the user specifies for each subgroup the odds of being missing. Both the number of subgroups and the odds values are important for the generation of missing data. For example, for a RIGHT-like mechanism, scoring in one of the higher quantiles should have high missingness odds, whereas for a MID-like mechanism, the central groups should have higher odds. Again, not the size of the odds values are of importance, but the relative distance between the values.

The continuous distributions of probabilities are based on the logistic distribution function. The user can specify the type of missingness, which, again, may differ between patterns.

For an example and more explanation about how the arguments interact with each other, we refer to the vignette Generate missing values with ampute The amputation methodology is published in Schouten, Lugtig and Vink, 2018.

Value

Returns an S3 object of class mads-class (multivariate amputed data set)

Author(s)

Rianne Schouten [aut, cre], Gerko Vink [aut], Peter Lugtig [ctb], 2016

References


See Also

`mads-class, bwplot, xyplot, mice`

Examples

```r
# start with a complete data set
cmpl_boys <- cc(boys)[1:3]

# Perform amputation with default settings
mads_boys <- ampute(data = cmpl_boys)
mads_boys$amp

# Change default matrices as desired
my_patterns <- mads_boys$patterns
my_patterns[1:3, 2] <- 0

my_weights <- mads_boys$weights
my_weights[2, 1] <- 2
my_weights[3, 1] <- 0.5

# Rerun amputation
my_mads_boys <- ampute(data = cmpl_boys, patterns = my_patterns, freq =
c(0.3, 0.3, 0.4), weights = my_weights, type = c("RIGHT", "TAIL", "LEFT"))
my_mads_boys$amp
```

---

### Description

Compare several nested models

#### Usage

```r
## S3 method for class 'mira'
anova(object, ..., method = "D1", use = "wald")
```

#### Arguments

- **object**: Two or more objects of class `mira`
- **...**: Other parameters passed down to `D1()`, `D2()`, `D3()` and `mitml::testModels`.
- **method**: Either "D1", "D2" or "D3"
- **use**: An character indicating the test statistic

#### Value

Object of class `mice.anova`
appendbreak

Description

A custom function to insert rows in long data with new pseudo-observations that are being done on the specified break ages. There should be a column called `first` in data with logical data that codes whether the current row is the first for subject `id`. Furthermore, the function assumes that columns `age`, `occ`, `hgt.z`, `wgt.z` and `bmi.z` are available. This function is used on the tbc data in FIMD chapter 9. Check that out to see it in action.

Usage

```r
appendbreak(data, brk, warp.model = warp.model, id = NULL, typ = "pred")
```

Arguments

data A data frame in the long long format
brk A vector of break ages
warp.model A time warping model
id The subject identifier
typ Label to signal that this is a newly added observation

Value

A long data frame with additional rows for the break ages

as.mids

Converts an imputed dataset (long format) into a mids object

Description

This function converts imputed data stored in long format into an object of class `mids`. The original incomplete dataset needs to be available so that we know where the missing data are. The function is useful to convert back operations applied to the imputed data back in a `mids` object. It may also be used to store multiply imputed data sets from other software into the format used by `mice`.

Usage

```r
as.mids(long, where = NULL, .imp = ".imp", .id = ".id")
```
Arguments

long A multiply imputed data set in long format, for example produced by a call to complete(...,action = 'long',include = TRUE), or by other software.

where A data frame or matrix with logicals of the same dimensions as data indicating where in the data the imputations should be created. The default, where = is.na(data), specifies that the missing data should be imputed. The where argument may be used to overimpute observed data, or to skip imputations for selected missing values.

.imp An optional column number or column name in long, indicating the imputation index. The values are assumed to be consecutive integers between 0 and m. Values 1 through m correspond to the imputation index, value 0 indicates the original data (with missings). By default, the procedure will search for a variable named ".imp".

.id An optional column number or column name in long, indicating the subject identification. If not specified, then the function searches for a variable named ".id". If this variable is found, the values in the column will define the row names in the data element of the resulting mids object.

Value

An object of class mids

Note

The function expects the input data long to be sorted by imputation number (variable ".imp" by default), and in the same sequence within each imputation block.

Author(s)

Gerko Vink

Examples

# impute the nhanes dataset
imp <- mice(nhanes, print = FALSE)
# extract the data in long format
X <- complete(imp, action = "long", include = TRUE)
# create dataset with .imp variable as numeric
X2 <- X

# nhanes example without .id
test1 <- as.mids(X)
is.mids(test1)
identical(complete(test1, action = "long", include = TRUE), X)

# nhanes example without .id where .imp is numeric
test2 <- as.mids(X2)
is.mids(test2)
identical(complete(test2, action = "long", include = TRUE), X)
# nhanes example, where we explicitly specify .id as column 2
test3 <- as.mids(X, .id = ".id")
is.mids(test3)
identical(complete(test3, action = "long", include = TRUE), X)

# nhanes example with .id where .imp is numeric
test4 <- as.mids(X2, .id = 2)
is.mids(test4)
identical(complete(test4, action = "long", include = TRUE), X)

# example without an .id variable
# variable .id not preserved
X3 <- X[, -2]
test5 <- as.mids(X3)
is.mids(test5)
identical(complete(test5, action = "long", include = TRUE)[, -2], X[, -2])

# as() syntax has fewer options
test7 <- as(X, "mids")
test8 <- as(X2, "mids")
test9 <- as(X2[, -2], "mids")
rev <- ncol(X):1
test10 <- as(X[, rev], "mids")

# where argument copies also observed data into $imp element
where <- matrix(TRUE, nrow = nrow(nhanes), ncol = ncol(nhanes))
colnames(where) <- colnames(nhanes)
test11 <- as.mids(X, where = where)
identical(complete(test11, action = "long", include = TRUE), X)

--

as.mira

Create a mira object from repeated analyses

Description

The as.mira() function takes the results of repeated complete-data analysis stored as a list, and turns it into a mira object that can be pooled.

Usage

as.mira(fitlist)

Arguments

fitlist A list containing $m$ fitted analysis objects

Value

An S3 object of class mira.
Description

The `as.mitml.result()` function takes the results of repeated complete-data analysis stored as a list, and turns it into an object of class `mitml.result`.

Usage

```r
as.mitml.result(x)
```

Arguments

- `x` An object of class `mira`

Value

An S3 object of class `mitml.result`, a list containing $m$ fitted analysis objects.

Author(s)

Stef van Buuren

See Also

`with.mitml.list`
Description

Height, weight, head circumference and puberty of 748 Dutch boys.

Format

A data frame with 748 rows on the following 9 variables:

- **age**: Decimal age (0-21 years)
- **hgt**: Height (cm)
- **wgt**: Weight (kg)
- **bmi**: Body mass index
- **hc**: Head circumference (cm)
- **gen**: Genital Tanner stage (G1-G5)
- **phb**: Pubic hair (Tanner P1-P6)
- **tv**: Testicular volume (ml)
- **reg**: Region (north, east, west, south, city)

Details

Random sample of 10% from the cross-sectional data used to construct the Dutch growth references 1997. Variables gen and phb are ordered factors. reg is a factor.

Source


Examples

# create two imputed data sets
imp <- mice(boys, m = 1, maxit = 2)
z <- complete(imp, 1)

# create imputations for age <8yrs
plot(z$age, z$gen,
     col = mdc(1:2)[1 + is.na(boys$gen)],
     xlab = "Age (years)", ylab = "Tanner Stage Genital"
# figure to show that the default imputation method does not impute BMI consistently
plot(z$bmi, z$wgt / (z$hgt / 100)^2,
     col = mdc(1:2)[1 + is.na(boys$bmi)],
     xlab = "Imputed BMI", ylab = "Calculated BMI"
)

# also, BMI distributions are somewhat different
oldpar <- par(mfrow = c(1, 2))
MASS::truehist(z$bmi[!is.na(boys$bmi)],
               h = 1, xlim = c(10, 30), ymax = 0.25,
               col = mdc(1), xlab = "BMI observed"
)
MASS::truehist(z$bmi[is.na(boys$bmi)],
               h = 1, xlim = c(10, 30), ymax = 0.25,
               col = mdc(2), xlab = "BMI imputed"
)
par(oldpar)

# repair the inconsistency problem by passive imputation
meth <- imp$meth
meth["bmi"] <- "~I(wgt/(hgt/100)^2)"
pred <- imp$predictorMatrix
pred["hgt", "bmi"] <- 0
pred["wgt", "bmi"] <- 0
imp2 <- mice(boys, m = 1, maxit = 2, meth = meth, pred = pred)
z2 <- complete(imp2, 1)

# show that new imputations are consistent
plot(z2$bmi, z2$wgt / (z2$hgt / 100)^2,
     col = mdc(1:2)[1 + is.na(boys$bmi)],
     ylab = "Calculated BMI"
)

# and compare distributions
oldpar <- par(mfrow = c(1, 2))
MASS::truehist(z2$bmi[!is.na(boys$bmi)],
               h = 1, xlim = c(10, 30), ymax = 0.25, col = mdc(1),
               xlab = "BMI observed"
)
MASS::truehist(z2$bmi[is.na(boys$bmi)],
               h = 1, xlim = c(10, 30), ymax = 0.25, col = mdc(2),
               xlab = "BMI imputed"
)
par(oldpar)

brandsma

Brandsma school data used Snijders and Bosker (2012)
Description

Dataset with raw data from Snijders and Bosker (2012) containing data from 4106 pupils attending 216 schools. This dataset includes all pupils and schools with missing data.

Format

brandsma is a data frame with 4106 rows and 14 columns:

- sch  School number
- pup  Pupil ID
- iqv  IQ verbal
- iqp  IQ performal
- sex  Sex of pupil
- ses  SES score of pupil
- min  Minority member 0/1
- rpg  Number of repeated groups, 0, 1, 2
- lpr  language score PRE
- lpo  language score POST
- apr  Arithmetic score PRE
- apo  Arithmetic score POST
- den  Denomination classification 1-4 - at school level
- ssi  School SES indicator - at school level

Note

This dataset is constructed from the raw data. There are a few differences with the data set used in Chapter 4 and 5 of Snijders and Bosker:

1. All schools are included, including the five school with missing values on langpost.
2. Missing denomina codes are left as missing.
3. Aggregates are undefined in the presence of missing data in the underlying values. Variables ses, iqv and iqp are in their original scale, and not globally centered. No aggregate variables at the school level are included.
4. There is a wider selection of original variables. Note however that the source data contain an even wider set of variables.

Source

References


descriptive

bwplot.mads  Box-and-whisker plot of amputed and non-amputed data

Description

Plotting method to investigate the relation between the data variables and the amputed data. The function shows how the amputed values are related to the variable values.

Usage

```
## S3 method for class 'mads'
bwplot(
x, data,
which.pat = NULL,
standardized = TRUE,
descriptives = TRUE,
layout = NULL,
...
)
```

Arguments

- **x**: A mads (mads-class) object, typically created by ampute.
- **data**: A string or vector of variable names that needs to be plotted. As a default, all variables will be plotted.
- **which.pat**: A scalar or vector indicating which patterns need to be plotted. As a default, all patterns are plotted.
- **standardized**: Logical. Whether the box-and-whisker plots need to be created from standardized data or not. Default is TRUE.
- **descriptives**: Logical. Whether the mean, variance and n of the variables need to be printed. This is useful to examine the effect of the amputation. Default is TRUE.
- **layout**: A vector of two values indicating how the boxplots of one pattern should be divided over the plot. For example, c(2, 3) indicates that the boxplots of six variables need to be placed on 3 rows and 2 columns. Default is 1 row and an amount of columns equal to #variables. Note that for more than 6 variables, multiple plots will be created automatically.
- **...**: Not used, but for consistency with generic
Value

A list containing the box-and-whisker plots. Note that a new pattern will always be shown in a new plot.

Note

The mads object contains all the information you need to make any desired plots. Check mads-class or the vignette Multivariate Amputation using Ampute to understand the contents of class object mads.

Author(s)

Rianne Schouten, 2016

See Also

ampute, bwplot, Lattice for an overview of the package, mads-class

Description

Plotting methods for imputed data using lattice. bwplot produces box-and-whisker plots. The function automatically separates the observed and imputed data. The functions extend the usual features of lattice.

Usage

```r
## S3 method for class 'mids'
bwplot(
  x,
  data,
  na.groups = NULL,
  groups = NULL,
  as.table = TRUE,
  theme = mice.theme(),
  mayreplicate = TRUE,
  allow.multiple = TRUE,
  outer = TRUE,
  drop.unused.levels = lattice::lattice.getOption("drop.unused.levels"),
  ...
)
```

bwplot.mids  

Box-and-whisker plot of observed and imputed data

---

**bwplot.mids**  

**Box-and-whisker plot of observed and imputed data**

---

**Description**

Plotting methods for imputed data using lattice. bwplot produces box-and-whisker plots. The function automatically separates the observed and imputed data. The functions extend the usual features of lattice.

**Usage**

```r
## S3 method for class 'mids'
bwplot(
  x,
  data,
  na.groups = NULL,
  groups = NULL,
  as.table = TRUE,
  theme = mice.theme(),
  mayreplicate = TRUE,
  allow.multiple = TRUE,
  outer = TRUE,
  drop.unused.levels = lattice::lattice.getOption("drop.unused.levels"),
  ...
)
```
Arguments

x

A mids object, typically created by mice() or mice.mids().

data

Formula that selects the data to be plotted. This argument follows the lattice rules for formulas, describing the primary variables (used for the per-panel display) and the optional conditioning variables (which define the subsets plotted in different panels) to be used in the plot.

The formula is evaluated on the complete data set in the long form. Legal variable names for the formula include names(x$data) plus the two administrative factors .imp and .id.

Extended formula interface: The primary variable terms (both the LHS y and RHS x) may consist of multiple terms separated by a ‘+’ sign, e.g., y1 + y2 ~ x | a * b. This formula would be taken to mean that the user wants to plot both y1 ~ x | a * b and y2 ~ x | a * b, but with the y1 ~ x and y2 ~ x in separate panels. This behavior differs from standard lattice. Only combine terms of the same type, i.e. only factors or only numerical variables. Mixing numerical and categorical data occasionally produces odds labeling of vertical axis.

For convenience, in stripplot() and bwplot the formula y~.imp may be abbreviated as y. This applies only to a single y, and does not (yet) work for y1+y2~.imp.

na.groups

An expression evaluating to a logical vector indicating which two groups are distinguished (e.g. using different colors) in the display. The environment in which this expression is evaluated is the response indicator is.na(x$data).

The default na.group = NULL contrasts the observed and missing data in the LHS y variable of the display, i.e. groups created by is.na(y). The expression y creates the groups according to is.na(y). The expression y1 & y2 creates groups by is.na(y1) & is.na(y2), and y1 | y2 creates groups as is.na(y1) | is.na(y2), and so on.

groups

This is the usual groups arguments in lattice. It differs from na.groups because it evaluates in the completed data. frame(complete(x,"long",inc=TRUE)) (as usual), whereas na.groups evaluates in the response indicator. See xyplot for more details. When both na.groups and groups are specified, na.groups takes precedence, and groups is ignored.

as.table

See xyplot.

theme

A named list containing the graphical parameters. The default function mice.theme produces a short list of default colors, line width, and so on. The extensive list may be obtained from trellis.par.get(). Global graphical parameters like col or cex in high-level calls are still honored, so first experiment with the global parameters. Many setting consists of a pair. For example, mice.theme defines two symbol colors. The first is for the observed data, the second for the imputed data. The theme settings only exist during the call, and do not affect the trellis graphical parameters.

mayreplicate

A logical indicating whether color, line widths, and so on, may be replicated. The graphical functions attempt to choose "intelligent" graphical parameters. For example, the same color can be replicated for different element, e.g. use all reds for the imputed data. Replication may be switched off by setting the flag to FALSE, in order to allow the user to gain full control.
allow.multiple  See xyplot.
outer            See xyplot.
drop.unused.levels See xyplot.

... Further arguments, usually not directly processed by the high-level functions documented here, but instead passed on to other functions.
subscripts       See xyplot.
subset           See xyplot.

Details

The argument na.groups may be used to specify (combinations of) missingness in any of the variables. The argument groups can be used to specify groups based on the variable values themselves. Only one of both may be active at the same time. When both are specified, na.groups takes precedence over groups.

Use the subset and na.groups together to plots parts of the data. For example, select the first imputed data set by by subset=.imp==1.

Graphical parameters like col, pch and cex can be specified in the arguments list to alter the plotting symbols. If length(col)==2, the color specification to define the observed and missing groups. col[1] is the color of the ‘observed’ data, col[2] is the color of the missing or imputed data. A convenient color choice is col=mdc(1:2), a transparent blue color for the observed data, and a transparent red color for the imputed data. A good choice is col=mdc(1:2),pch=20,cex=1.5. These choices can be set for the duration of the session by running mice.theme().

Value

The high-level functions documented here, as well as other high-level Lattice functions, return an object of class "trellis". The update method can be used to subsequently update components of the object, and the print method (usually called by default) will plot it on an appropriate plotting device.

Note

The first two arguments (x and data) are reversed compared to the standard Trellis syntax implemented in lattice. This reversal was necessary in order to benefit from automatic method dispatch.

In mice the argument x is always a mids object, whereas in lattice the argument x is always a formula.

In mice the argument data is always a formula object, whereas in lattice the argument data is usually a data frame.

All other arguments have identical interpretation.

Author(s)

Stef van Buuren
cbin.mids

Combine mids objects by columns

Description
This function combines two mids objects columnwise into a single object of class mids, or combines a single mids object with a vector, matrix, factor or data.frame columnwise into a mids object.

Usage

cbind.mids(x, y = NULL, ...)

Arguments

x A mids object.

y A mids object, or a data.frame, matrix, factor or vector.

... Additional data.frame, matrix, vector or factor. These can be given as named arguments.
cbind.mids

Details

Pre-requisites: If y is a mids-object, the rows of $x$data and $y$data should match, as well as the number of imputations (m). Other y are transformed into a data.frame whose rows should match with $x$data.

The function renames any duplicated variable or block names by appending ".1", ".2" to duplicated names.

Value

An S3 object of class mids

Note

The function constructs the elements of the new mids object as follows:

data      Columnwise combination of the data in x and y
imp       Combines the imputed values from x and y
m         Taken from x$m
where      Columnwise combination of x$where and y$where
blocks    Combines x$blocks and y$blocks
call      Vector, call[1] creates x, call[2] is call to cbind.mids
nmis      Equals c(x$nmis, y$nmis)
method    Combines x$method and y$method
predictorMatrix  Combination with zeroes on the off-diagonal blocks
visitSequence Combined as c(x$visitSequence, y$visitSequence)
formulas   Combined as c(x$formulas, y$formulas)
post       Combined as c(x$post, y$post)
blots      Combined as c(x$blots, y$blots)
ignore     Taken from x$ignore
seed       Taken from x$seed
iteration  Taken from x$iteration
lastSeedValue Taken from x$lastSeedValue
chainMean  Combined from x$chainMean and y$chainMean
chainVar   Combined from x$chainVar and y$chainVar
loggedEvents Taken from x$loggedEvents
version    Current package version
date       Current date

Author(s)

Karin Groothuis-Oudshoorn, Stef van Buuren

See Also

cbind, rbind.mids, ibind, mids
Examples

```r
# impute four variables at once (default)
imp <- mice(nhanes, m = 1, maxit = 1, print = FALSE)
imp$predictorMatrix

# impute two by two
data1 <- nhanes[, c("age", "bmi")]
data2 <- nhanes[, c("hyp", "chl")]
imp1 <- mice(data1, m = 2, maxit = 1, print = FALSE)
imp2 <- mice(data2, m = 2, maxit = 1, print = FALSE)

# Append two solutions
imp12 <- cbind(imp1, imp2)

# This is a different imputation model
imp12$predictorMatrix

# Append the other way around
imp21 <- cbind(imp2, imp1)
imp21$predictorMatrix

# Append 'forgotten' variable chl
data3 <- nhanes[, 1:3]
imp3 <- mice(data3, maxit = 1, m = 2, print = FALSE)
imp4 <- cbind(imp3, chl = nhanes$chl)

# Of course, chl was not imputed
head(complete(imp4))

# Combine mids object with data frame
imp5 <- cbind(imp3, nhanes2)
head(complete(imp5))
```

cc

Select complete cases

Description

Extracts the complete cases, also known as *listwise deletion*. `cc(x)` is similar to `na.omit(x)`, but returns an object of the same class as the input data. Dimensions are not dropped. For extracting incomplete cases, use `ici`.

Usage

`cc(x)`

Arguments

- `x` An R object. Methods are available for classes `mids`, `data.frame` and `matrix`. Also, `x` could be a vector.
cci

Value

A vector, matrix or data.frame containing the data of the complete cases.

Author(s)

Stef van Buuren, 2017.

See Also

na.omit, cci, ici

Examples

# cc(nhanes)  # get the 13 complete cases
# cc(nhanes$bmi)  # extract complete bmi

cci

Complete case indicator

Description

The complete case indicator is useful for extracting the subset of complete cases. The function cci(x) calls complete.cases(x). The companion function ici() selects the incomplete cases.

Usage

ci(x)

Arguments

x  An R object. Currently supported are methods for the following classes: mids.

Value

Logical vector indicating the complete cases.

Author(s)

Stef van Buuren, 2017.

See Also

complete.cases, ici, cc
Examples

cci(nhanes) # indicator for 13 complete cases
cci(mice(nhanes, maxit = 0))
f <- cci(nhanes[, c("bmi", "hyp")]) # complete data for bmi and hyp
nhanes[f, ] # obtain all data from those with complete bmi and hyp

complete.mids

Extracts the completed data from a mids object

Description

Takes an object of class mids, fills in the missing data, and returns the completed data in a specified format.

Usage

## S3 method for class 'mids'
complete(data, action = 1L, include = FALSE, mild = FALSE, ...)

Arguments

data An object of class mids as created by the function mice().
action A numeric vector or a keyword. Numeric values between 1 and data$m return the data with imputation number action filled in. The value of action = 0 return the original data, with missing values. action can also be one of the following keywords: "all", "long", "broad" and "repeated". See the Details section for the interpretation. The default is action = 1L returns the first imputed data set.
include A logical to indicate whether the original data with the missing values should be included.
mild A logical indicating whether the return value should always be an object of class mild. Setting mild = TRUE overrides action keywords "long", "broad" and "repeated". The default is FALSE.
...

Additional arguments. Not used.

Details

The argument action can be length-1 character, which is matched to one of the following keywords:
"all" produces a mild object of imputed data sets. When include = TRUE, then the original data are appended as the first list element;
"long" produces a data set where imputed data sets are stacked vertically. The columns are added:
1) .imp, integer, referring the imputation number, and 2) .id, character, the row names of data$data;
"stacked" same as "long" but without the two additional columns;
"broad" produces a data set with where imputed data sets are stacked horizontally. Columns are ordered as in the original data. The imputation number is appended to each column name;
"repeated" same as "broad", but with columns in a different order.
Value

Complete data set with missing values replaced by imputations. A data.frame, or a list of data frames of class mild.

Note

Technical note: mice 3.7.5 renamed the complete() function to complete.mids() and exported it as an S3 method of the generic tidyr::complete(). Name clashes between mice::complete() and tidyr::complete() should no longer occur.

See Also

mice, mids

Examples

```r
# obtain first imputed data set
sum(is.na(nhanes2))
imp <- mice(nhanes2, print = FALSE, maxit = 1)
dat <- complete(imp)
sum(is.na(dat))

# obtain stacked third and fifth imputation
dat <- complete(imp, c(3, 5))

# obtain all datasets, with additional identifiers
head(complete(imp, "long"))

# same, but now as list, mild object
dslist <- complete(imp, "all")
length(dslist)

# same, but also include the original data
dslist <- complete(imp, "all", include = TRUE)
length(dslist)

# select original + 3 + 5, store as mild
dslist <- complete(imp, c(0, 3, 5), mild = TRUE)
names(dslist)
```
Description

This helper function attempts to find blocks of variables in the specification of the `formulas` and/or `predictorMatrix` objects. Blocks specified by `formulas` may consist of multiple variables. Blocks specified by `predictorMatrix` are assumed to consist of single variables. Any duplicates in names are removed, and the formula specification is preferred. When both arguments specify models for the same block, the model for the `predictorMatrix` is removed, and priority is given to the specification given in `formulas`.

Usage

```r
construct.blocks(formulas = NULL, predictorMatrix = NULL)
```

Arguments

- **formulas**: A named list of formula’s, or expressions that can be converted into formula’s by `as.formula`. List elements correspond to blocks. The block to which the list element applies is identified by its name, so list names must correspond to block names. The `formulas` argument is an alternative to the `predictorMatrix` argument that allows for more flexibility in specifying imputation models, e.g., for specifying interaction terms.

- **predictorMatrix**: A numeric matrix of `length(blocks)` rows and `ncol(data)` columns, containing 0/1 data specifying the set of predictors to be used for each target column. Each row corresponds to a variable block, i.e., a set of variables to be imputed. A value of 1 means that the column variable is used as a predictor for the target block (in the rows). By default, the `predictorMatrix` is a square matrix of `ncol(data)` rows and columns with all 1’s, except for the diagonal. Note: For two-level imputation models (which have "2l" in their names) other codes (e.g., 2 or -2) are also allowed.

Value

A `blocks` object.

See Also

`make.blocks`, `name.blocks`

Examples

```r
form <- name.formulas(list(bmi + hyp ~ chl + age, chl ~ bmi))
pred <- make.predictorMatrix(nhanes[, c("age", "chl")])
construct.blocks(formulas = form, pred = pred)
```
**D1**

**Compare two nested models using D1-statistic**

**Description**

The D1-statistics is the multivariate Wald test.

**Usage**

D1(fit1, fit0 = NULL, dfcom = NULL, df.com = NULL)

**Arguments**

- **fit1**: An object of class `mira`, produced by `with()`.
- **fit0**: An object of class `mira`, produced by `with()`. The model in `fit0` is a nested within `fit1`. The default null model `fit0 = NULL` compares `fit1` to the intercept-only model.
- **dfcom**: A single number denoting the complete-data degrees of freedom of model `fit1`. If not specified, it is set equal to `df.residual` of model `fit1`. If that cannot be done, the procedure assumes (perhaps incorrectly) a large sample.
- **df.com**: Deprecated

**References**


https://stefvanbuuren.name/fimd/sec-multiparameter.html#sec:wald

**See Also**

testModels

**Examples**

# Compare two linear models:
imp <- mice(nhanes2, seed = 51009, print = FALSE)
mi1 <- with(data = imp, expr = lm(bmi ~ age + hyp + chl))
mi0 <- with(data = imp, expr = lm(bmi ~ age + hyp))
D1(mi1, mi0)

## Not run:
# Compare two logistic regression models
imp <- mice(boys, maxit = 2, print = FALSE)
fit1 <- with(imp, glm(gen > levels(gen)[1] ~ hgt + hc + reg, family = binomial))
fit0 <- with(imp, glm(gen > levels(gen)[1] ~ hgt + hc, family = binomial))
D1(fit1, fit0)

## End(Not run)
Compare two nested models using D2-statistic

Description

The D2-statistic pools test statistics from the repeated analyses. The method is less powerful than the D1- and D3-statistics.

Usage

D2(fit1, fit0 = NULL, use = "wald")

Arguments

- fit1: An object of class mira, produced by with().
- fit0: An object of class mira, produced by with(). The model in fit0 is a nested within fit1. The default null model fit0 = NULL compares fit1 to the intercept-only model.
- use: A character string denoting Wald- or likelihood-based based tests. Can be either "wald" or "likelihood". Only used if method = "D2".

References


https://stefvanbuuren.name/fimd/sec-multiparameter.html#sec:chi

See Also

testModels

Examples

# Compare two linear models:
imp <- mice(nhanes2, seed = 51009, print = FALSE)
mi1 <- with(data = imp, expr = lm(bmi ~ age + hyp + chl))
mi0 <- with(data = imp, expr = lm(bmi ~ age + hyp))
D2(mi1, mi0)

# Compare two logistic regression models
imp <- mice(boys, maxit = 2, print = FALSE)
fit1 <- with(imp, glm(gen > levels(gen)[1] ~ hgt + hc + reg, family = binomial))
fit0 <- with(imp, glm(gen > levels(gen)[1] ~ hgt + hc, family = binomial))
D2(fit1, fit0)
Compare two nested models using D3-statistic

Description
The D3-statistic is a likelihood-ratio test statistic.

Usage
D3(fit1, fit0 = NULL, dfcom = NULL, df.com = NULL)

Arguments
fit1 An object of class mira, produced by with().
fit0 An object of class mira, produced by with(). The model in fit0 is a nested
within fit1. The default null model fit0 = NULL compares fit1 to the intercept-
only model.
dfcom A single number denoting the complete-data degrees of freedom of model
fit1. If not specified, it is set equal to df.residual of model fit1. If that cannot be
done, the procedure assumes (perhaps incorrectly) a large sample.
df.com Deprecated

Details
The D3() function implement the LR-method by Meng and Rubin (1992). The implementation of
the method relies on the broom package, the standard update mechanism for statistical models in R
and the offset function.

The function calculates m repetitions of the full (or null) models, calculates the mean of the estimates
of the (fixed) parameter coefficients β. For each imputed imputed dataset, it calculates the likelihood
for the model with the parameters constrained to β.

The mitml::testModels() function offers similar functionality for a subset of statistical models. Results of mice::D3() and mitml::testModels() differ in multilevel models because the
testModels() also constrains the variance components parameters. For more details on

Value
An object of class mice.anova

References
https://stefvanbuuren.name/fimd/sec-multiparameter.html#sec:likelihoodratio
http://bbolker.github.io/mixedmodels-misc/glmmFAQ.html#setting-residual-variances-to-a-fixed-value
See Also

fix.coef

Examples

# Compare two linear models:
imp <- mice(nhanes2, seed = 51009, print = FALSE)
mi1 <- with(data = imp, expr = lm(bmi ~ age + hyp + chl))
mi0 <- with(data = imp, expr = lm(bmi ~ age + hyp))
D3(mi1, mi0)

# Compare two logistic regression models
imp <- mice(boys, maxit = 2, print = FALSE)
fit1 <- with(imp, glm(gen > levels(gen)[1] ~ hgt + hc + reg, family = binomial))
fit0 <- with(imp, glm(gen > levels(gen)[1] ~ hgt + hc, family = binomial))
D3(fit1, fit0)

densityplot.mids  

Density plot of observed and imputed data

Description

Plotting methods for imputed data using lattice. densityplot produces plots of the densities. The function automatically separates the observed and imputed data. The functions extend the usual features of lattice.

Usage

## S3 method for class 'mids'
densityplot(
x,  
data,  
augmented as.groups = NULL,  
groups = NULL,  
subscripts = TRUE,  
panel = lattice::lattice.getOption("panel.densityplot"),  
default.prepanel = lattice::lattice.getOption("prepanel.default.densityplot"),  
...  

subscripts = TRUE,
densityplot.mids

subset = TRUE

Arguments

- **x**: A mids object, typically created by `mice()` or `mice.mids()`.
- **data**: Formula that selects the data to be plotted. This argument follows the `lattice` rules for `formulas`, describing the primary variables (used for the per-panel display) and the optional conditioning variables (which define the subsets plotted in different panels) to be used in the plot.

The formula is evaluated on the complete data set in the long form. Legal variable names for the formula include `names(x$data)` plus the two administrative factors `.imp` and `.id`.

**Extended formula interface:** The primary variable terms (both the LHS `y` and RHS `x`) may consist of multiple terms separated by a `+` sign, e.g., `y1 + y2 ~ x | a * b`. This formula would be taken to mean that the user wants to plot both `y1 ~ x | a * b` and `y2 ~ x | a * b`, but with the `y1 ~ x` and `y2 ~ x` in separate panels. This behavior differs from standard `lattice`. Only combine terms of the same type, i.e. only factors or only numerical variables. Mixing numerical and categorical data occasionally produces odds labeling of vertical axis.

The function `densityplot` does not use the `y` terms in the formula. Density plots for `x1` and `x2` are requested as `~ x1 + x2`.

- **na.groups**: An expression evaluating to a logical vector indicating which two groups are distinguished (e.g. using different colors) in the display. The environment in which this expression is evaluated is the response indicator `is.na(x$data)`.

The default `na.group = NULL` contrasts the observed and missing data in the LHS `y` variable of the display, i.e. groups created by `is.na(y)`. The expression `y` creates the groups according to `is.na(y)`. The expression `y1 & y2` creates groups by `is.na(y1) & is.na(y2)`, and `y1 | y2` creates groups as `is.na(y1) | is.na(y2)`, and so on.

- **groups**: This is the usual `groups` arguments in `lattice`. It differs from `na.groups` because it evaluates in the completed data `data.frame(complete(x,"long",inc=TRUE))` (as usual), whereas `na.groups` evaluates in the response indicator. See `xyplot` for more details. When both `na.groups` and `groups` are specified, `na.groups` takes precedence, and `groups` is ignored.

- **as.table**: A logical used in `densityplot` that signals whether the points should be plotted.

- **plot.points**: A logical used in `densityplot` that signals whether the points should be plotted.

- **theme**: A named list containing the graphical parameters. The default function `mice.theme` produces a short list of default colors, line width, and so on. The extensive list may be obtained from `trellis.par.get()`. Global graphical parameters like `col` or `cex` in high-level calls are still honored, so first experiment with the global parameters. Many setting consists of a pair. For example, `mice.theme` defines two symbol colors. The first is for the observed data, the second for the imputed data. The theme settings only exist during the call, and do not affect the trellis graphical parameters.
mayreplicate

A logical indicating whether color, line widths, and so on, may be replicated. The graphical functions attempt to choose "intelligent" graphical parameters. For example, the same color can be replicated for different element, e.g. use all reds for the imputed data. Replication may be switched off by setting the flag to FALSE, in order to allow the user to gain full control.

thicker

Used in densityplot. Multiplication factor of the line width of the observed density. thicker=1 uses the same thickness for the observed and imputed data.

allow.multiple

See xyplot.

outer

See xyplot.

drop.unused.levels

See xyplot.

panel

See xyplot.

default.prepanel

See xyplot.

...

Further arguments, usually not directly processed by the high-level functions documented here, but instead passed on to other functions.

subscripts

See xyplot.

subset

See xyplot.

Details

The argument na.groups may be used to specify (combinations of) missingness in any of the variables. The argument groups can be used to specify groups based on the variable values themselves. Only one of both may be active at the same time. When both are specified, na.groups takes precedence over groups.

Use the subset and na.groups together to plots parts of the data. For example, select the first imputed data set by by subset=.imp==1.

Graphical parameters like col, pch and cex can be specified in the arguments list to alter the plotting symbols. If length(col)==2, the color specification to define the observed and missing groups. col[1] is the color of the 'observed' data, col[2] is the color of the missing or imputed data. A convenient color choice is col=mdc(1:2), a transparent blue color for the observed data, and a transparent red color for the imputed data. A good choice is col=mdc(1:2),pch=20,cex=1.5. These choices can be set for the duration of the session by running mice.theme().

Value

The high-level functions documented here, as well as other high-level Lattice functions, return an object of class "trellis". The update method can be used to subsequently update components of the object, and the print method (usually called by default) will plot it on an appropriate plotting device.

Note

The first two arguments (x and data) are reversed compared to the standard Trellis syntax implemented in lattice. This reversal was necessary in order to benefit from automatic method dispatch.
In **mice** the argument `x` is always a `mids` object, whereas in **lattice** the argument `x` is always a formula.

In **mice** the argument `data` is always a formula object, whereas in **lattice** the argument `data` is usually a data frame.

All other arguments have identical interpretation.

densityplot errs on empty groups, which occurs if all observations in the subgroup contain NA. The relevant error message is: Error in density.default: ... need at least 2 points to select a bandwidth automatically. There is yet no workaround for this problem. Use the more robust `bwplot` or `stripplot` as a replacement.

**Author(s)**

Stef van Buuren

**References**


**See Also**

`mice`, `xyplot`, `stripplot`, `bwplot`, `lattice` for an overview of the package, as well as `densityplot`, `panel.densityplot`, `print.trellis`, `trellis.par.set`

**Examples**

```r
imp <- mice(boys, maxit = 1)

### density plot of head circumference per imputation
### blue is observed, red is imputed
densityplot(imp, ~ hc | .imp)

### All combined in one panel.
densityplot(imp, ~hc)
```

---

**employee**

*Employee selection data*

**Description**

A toy example from Craig Enders.

**Usage**

`employee`
Estimice

Format

A data frame with 20 rows and 3 variables:

- **IQ**: candidate IQ score
- **wbeing**: candidate well-being score
- **jobperf**: candidate job performance score

Details

Enders describes these data as follows: I designed these data to mimic an employee selection scenario in which prospective employees complete an IQ test and a psychological well-being questionnaire during their interview. The company subsequently hires the applications that score in the upper half of the IQ distribution, and a supervisor rates their job performance following a 6-month probationary period. Note that the job performance scores are missing at random (MAR) (i.e. individuals in the lower half of the IQ distribution were never hired, and thus have no performance rating). In addition, I randomly deleted three of the well-being scores in order to mimic a situation where the applicant’s well-being questionnaire is inadvertently lost.

A larger version of this data set is present as `data.enders.employee`.

Source

Enders (2010), Applied Missing Data Analysis, p. 218

---

estimice

**Computes least squares parameters**

Description

This function computes least squares estimates, variance/covariance matrices, residuals and degrees of freedom according to ridge regression, QR decomposition or Singular Value Decomposition. This function is internally called by `.norm.draw()`, but can be called by any user-specified imputation function.

Usage

```
estimice(x, y, ls.meth = "qr", ridge = 1e-05, ...)
```

Arguments

- **x**: Matrix (n x p) of complete covariates.
- **y**: Incomplete data vector of length n
- **ls.meth**: the method to use for obtaining the least squares estimates. By default parameters are drawn by means of QR decomposition.
- **ridge**: A small numerical value specifying the size of the ridge used. The default value `ridge = 1e-05` represents a compromise between stability and unbiasedness. Decrease `ridge` if the data contain many junk variables. Increase `ridge` for highly collinear data.
- **...**: Other named arguments.
Details
When calculating the inverse of the crossproduct of the predictor matrix, problems may arise. For example, taking the inverse is not possible when the predictor matrix is rank deficient, or when the estimation problem is computationally singular. This function detects such error cases and automatically falls back to adding a ridge penalty to the diagonal of the crossproduct to allow for proper calculation of the inverse.

Value
A list containing components c (least squares estimate), r (residuals), v (variance/covariance matrix) and df (degrees of freedom).

Note
This functions adds a star to variable names in the mice iteration history to signal that a ridge penalty was added. In that case, it also adds an entry to loggedEvents.

Author(s)
Gerko Vink, 2018

---

**extractBS**

Extract broken stick estimates from a lmer object

Description
Extract broken stick estimates from a lmer object

Usage
```
extractBS(fit)
```

Arguments

<table>
<thead>
<tr>
<th>Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>fit</td>
<td>An object of class lmer</td>
</tr>
</tbody>
</table>

Value
A matrix containing broken stick estimates

Author(s)
Stef van Buuren, 2012
**Description**

Multiple outcomes of a randomized study to reduce post-traumatic stress.

**Format**

`fdd` is a data frame with 52 rows and 65 columns:

- **id** Client number
- **trt** Treatment (E=EMDR, C=CBT)
- **pp** Per protocol (Y/N)
- **trtp** Number of parental treatments
- **sex** Sex: M/F
- **etn** Ethnicity: NL/OTHER
- **age** Age (years)
- **trauma** Trauma count (1-5)
- **prop1** PROPS total score T1
- **prop2** PROPS total score T2
- **prop3** PROPS total score T3
- **crop1** CROPS total score T1
- **crop2** CROPS total score T2
- **crop3** CROPS total score T3
- **masc1** MASC score T1
- **masc2** MASC score T2
- **masc3** MASC score T3
- **cbcl1** CBCL T1
- **cbcl3** CBCL T3
- **prs1** PRS total score T1
- **prs2** PRS total score T2
- **prs3** PRS total score T3
- **ypa1** PTSD-RJ B intrusive recollection parent T1
- **ypb1** PTSD-RJ C avoidant/numbing parent T1
- **ypc1** PTSD-RJ D hyper-arousal parent T1
- **yp1** PTSD-RJ B+C+D parent T1
- **ypa2** PTSD-RJ B intrusive recollection parent T2
- **ypb2** PTSD-RJ C avoidant/numbing parent T2
fdd.pred is the 65 by 65 binary predictor matrix used to impute fdd.
Details

Data from a randomized experiment to reduce post-traumatic stress by two treatments: Eye Movement Desensitization and Reprocessing (EMDR) (experimental treatment), and cognitive behavioral therapy (CBT) (control treatment). 52 children were randomized to one of these two treatments. Outcomes were measured at three time points: at baseline (pre-treatment, T1), post-treatment (T2, 4-8 weeks), and at follow-up (T3, 3 months). For more details, see de Roos et al (2011). Some person covariates were reshuffled. The imputation methodology is explained in Chapter 9 of van Buuren (2012).

Source


Examples

data <- fdgs
md.pattern(fdgs)

```
fdgs                Fifth Dutch growth study 2009

```

Description

Age, height, weight and region of 10030 children measured within the Fifth Dutch Growth Study 2009

Format

fdgs is a data frame with 10030 rows and 8 columns:

- **id** Person number
- **reg** Region (factor, 5 levels)
- **age** Age (years)
- **sex** Sex (boy, girl)
- **hgt** Height (cm)
- **wgt** Weight (kg)
- **hgt.z** Height Z-score
- **wgt.z** Weight Z-score
Details

The data set contains data from children of Dutch descent (biological parents are born in the Netherlands). Children with growth-related diseases were excluded. The data were used to construct new growth charts of children of Dutch descent (Schonbeck 2013), and to calculate overweight and obesity prevalence (Schonbeck 2011).

Some groups were underrepresented. Multiple imputation was used to create synthetic cases that were used to correct for the nonresponse. See Van Buuren (2012), chapter 8 for details.

Source


Examples

data <- data(fdgs)
summary(data)

<table>
<thead>
<tr>
<th>fico</th>
<th>Fraction of incomplete cases among cases with observed</th>
</tr>
</thead>
</table>

Description

FICO is an outbound statistic defined by the fraction of incomplete cases among cases with Yj observed (White and Carlin, 2010).

Usage

fico(data)

Arguments

data A data frame or a matrix containing the incomplete data. Missing values are coded as NA’s.

Value

A vector of length ncol(data) of FICO statistics.
filter.mids

Subset rows of a mids object

Description

This function takes a mids object and returns a new mids object that pertains to the subset of the data identified by the expression in .... The expression may use column values from the incomplete data in .data$data.

Usage

```r
## S3 method for class 'mids'
filter(.data, ..., .preserve = FALSE)
```

Arguments

- `.data`: A mids object.
- `...`: Expressions that return a logical value, and are defined in terms of the variables in .data$data. If multiple expressions are specified, they are combined with the & operator. Only rows for which all conditions evaluate to TRUE are kept.
- `.preserve`: Relevant when the .data input is grouped. If .preserve = FALSE (the default), the grouping structure is recalculated based on the resulting data, otherwise the grouping is kept as is.

Value

An S3 object of class mids

Note

The function calculates a logical vector include of length nrow(.data$data). The function constructs the elements of the filtered mids object as follows:
data Select rows in .data$data for which include == TRUE
imp Select rows each imputation data.frame in .data$imp for which include == TRUE
m Equals .data$m
where Select rows in .data$where for which include == TRUE
blocks Equals .data$blocks
call Equals .data$call
nmis Recalculate nmis based on the selected data rows
method Equals .data$method
predictorMatrix Equals .data$predictorMatrix
visitSequence Equals .data$visitSequence
formulas Equals .data$formulas
post Equals .data$post
blots Equals .data$blots
ignore Select positions in .data$ignore for which include == TRUE
seed Equals .data$seed
iteration Equals .data$iteration
lastSeedValue Equals .data$lastSeedValue
chainMean Set to NULL
chainVar Set to NULL
loggedEvents Equals .data$loggedEvents
version Replaced with current version
date Replaced with current date

Author(s)

Patrick Rockenschaub

See Also

filter

Examples

imp <- mice(nhanes, m = 2, maxit = 1, print = FALSE)

# example with external logical vector
imp_f <- filter(imp, c(rep(TRUE, 13), rep(FALSE, 12)))

nrow(complete(imp))
nrow(complete(imp_f))

# example with calculated include vector
imp_f2 <- filter(imp, age >= 2 & hyp == 1)
nrow(complete(imp_f2))  # should be 5
Description
Refits a model with a specified set of coefficients.

Usage
fix.coef(model, beta = NULL)

Arguments
- model: An R model, e.g., produced by lm or glm
- beta: A numeric vector with length(coef) model coefficients. If the vector is not named, the coefficients should be given in the same order as in coef(model). If the vector is named, the procedure attempts to match on names.

Details
The function calculates the linear predictor using the new coefficients, and reformulates the model using the offset argument. The linear predictor is called offset, and its coefficient will be 1 by definition. The new model only fits the intercept, which should be 0 if we set beta = coef(model).

Value
An updated R model object

Author(s)
Stef van Buuren, 2018

Examples
```r
model0 <- lm(Volume ~ Girth + Height, data = trees)
formula(model0)
coef(model0)
deviance(model0)

# refit same model
model1 <- fix.coef(model0)
formula(model1)
coef(model1)
deviance(model1)

# change the beta's
model2 <- fix.coef(model0, beta = c(-50, 5, 1))
coef(model2)
deviance(model2)
```
# compare predictions
plot(predict(model0), predict(model1))
abline(0, 1)
plot(predict(model0), predict(model2))
abline(0, 1)

# compare proportion explained variance
cor(predict(model0), predict(model0) + residuals(model0))^2
cor(predict(model1), predict(model1) + residuals(model1))^2
cor(predict(model2), predict(model2) + residuals(model2))^2

# extract offset from constrained model
summary(model2$offset)

# it also works with factors and missing data
model0 <- lm(bmi ~ age + hyp + chl, data = nhanes2)
model1 <- fix.coef(model0)
model2 <- fix.coef(model0, beta = c(15, -8, -8, 2, 0.2))

---

**Description**

Influx and outflux are statistics of the missing data pattern. These statistics are useful in selecting predictors that should go into the imputation model.

**Usage**

flux(data, local = names(data))

**Arguments**

- **data**: A data frame or a matrix containing the incomplete data. Missing values are coded as NA's.
- **local**: A vector of names of columns of data. The default is to include all columns in the calculations.

**Details**

Influx and outflux have been proposed by Van Buuren (2018), chapter 4. Influx is equal to the number of variable pairs \((Y_j, Y_k)\) with \(Y_j\) missing and \(Y_k\) observed, divided by the total number of observed data cells. Influx depends on the proportion of missing data of the variable. Influx of a completely observed variable is equal to 0, whereas for completely missing variables we have influx = 1. For two variables with the same proportion of missing data, the variable with higher influx is better connected to the observed data, and might thus be easier to impute.
Outflux is equal to the number of variable pairs with $Y_j$ observed and $Y_k$ missing, divided by the total number of incomplete data cells. Outflux is an indicator of the potential usefulness of $Y_j$ for imputing other variables. Outflux depends on the proportion of missing data of the variable. Outflux of a completely observed variable is equal to 1, whereas outflux of a completely missing variable is equal to 0. For two variables having the same proportion of missing data, the variable with higher outflux is better connected to the missing data, and thus potentially more useful for imputing other variables.

FICO is an outbound statistic defined by the fraction of incomplete cases among cases with $Y_j$ observed (White and Carlin, 2010).

**Value**

A data frame with `ncol(data)` rows and six columns: `pobs` = Proportion observed, `influx` = Influx `outflux` = Outflux `ainb` = Average inbound statistic `aout` = Average outbound statistic `fico` = Fraction of incomplete cases among cases with $Y_j$ observed

**Author(s)**

Stef van Buuren, 2012

**References**


**See Also**

`fluxplot, md.pattern, fico`

**fluxplot**

*Fluxplot of the missing data pattern*

**Description**

Influx and outflux are statistics of the missing data pattern. These statistics are useful in selecting predictors that should go into the imputation model.

**Usage**

```r
fluxplot(
  data,
  local = names(data),
  plot = TRUE,
  labels = TRUE,
  xlim = c(0, 1),
```

```r
```
fluxplot

ylim = c(0, 1),
las = 1,
xlab = "Influx",
ylab = "Outflux",
main = paste("Influx-outflux pattern for", deparse(substitute(data))),
eqscplot = TRUE,
pty = "s",
lwd = 1,

Arguments

data A data frame or a matrix containing the incomplete data. Missing values are coded as NA's.
local A vector of names of columns of data. The default is to include all columns in the calculations.
plot Should a graph be produced?
labels Should the points be labeled?
xlim See par.
ylim See par.
las See par.
xlab See par.
ylab See par.
main See par.
eqscplot Should a square plot be produced?
pty See par.
lwd See par. Controls axis line thickness and diagonal

Details

Infux and outflux have been proposed by Van Buuren (2012), chapter 4.
Infux is equal to the number of variable pairs \((Y_j, Y_k)\) with \(Y_j\) missing and \(Y_k\) observed, divided by the total number of observed data cells. Infux depends on the proportion of missing data of the variable. Infux of a completely observed variable is equal to 0, whereas for completely missing variables we have infux = 1. For two variables with the same proportion of missing data, the variable with higher infux is better connected to the observed data, and might thus be easier to impute.

Outflux is equal to the number of variable pairs with \(Y_j\) observed and \(Y_k\) missing, divided by the total number of incomplete data cells. Outflux is an indicator of the potential usefulness of \(Y_j\) for imputing other variables. Outflux depends on the proportion of missing data of the variable. Outflux of a completely observed variable is equal to 1, whereas outflux of a completely missing variable is equal to 0. For two variables having the same proportion of missing data, the variable with higher outflux is better connected to the missing data, and thus potentially more useful for imputing other variables.
getfit

Value
An invisible data frame with \( \text{ncol(data)} \) rows and six columns: 
- \( \text{pobs} \) = Proportion observed
- \( \text{influx} \) = Influx
- \( \text{outflux} \) = Outflux
- \( \text{ainb} \) = Average inbound statistic
- \( \text{aout} \) = Average outbound statistic
- \( \text{fico} \) = Fraction of incomplete cases among cases with \( Y_j \) observed

Author(s)
Stef van Buuren, 2012

References


See Also
- flux
- md.pattern
- fico

Description
Function `getfit()` returns the list of objects containing the repeated analysis results, or optionally, one of these fitted objects. The function looks for a list element called `analyses`, and return this component as a list with `mira` class. If element `analyses` is not found in `x`, then it returns `x` as a `mira` object.

Usage
`getfit(x, i = -1L, simplify = FALSE)`

Arguments
- `x` An object of class `mira`, typically produced by a call to `with()`.
- `i` An integer between 1 and \( x@m \) signalling the index of the repeated analysis. The default \( i = -1 \) return a list with all analyses.
- `simplify` Should the return value be unlisted?

Details
No checking is done for validity of objects. The function also processes objects of class `mitml.result` from the `mitml` package.
getqbar

Value

If \( i = -1 \) an object of class `mira` containing all analyses. If \( i \) selects one of the analyses, then it return an object whose with class inherited from that element.

Author(s)

Stef van Buuren, 2012, 2020

See Also

`mira`, `with.mids`

Examples

```r
imp <- mice(nhanes, print = FALSE, seed = 21443)
fit <- with(imp, lm(bmi ~ chl + hyp))
f1 <- getfit(fit)
class(f1)
f2 <- getfit(fit, 2)
class(f2)
```

---

**getqbar** *Extract estimate from mipo object*

Description

`getqbar` returns a named vector of pooled estimates.

Usage

```r
getqbar(x)
```

Arguments

- \( x \) An object of class `mipo`
glm.mids  Generalized linear model for mids object

Description
Applies glm() to a multiply imputed data set

Usage
glm.mids(formula, family = gaussian, data, ...)

Arguments

formula  
a formula expression as for other regression models, of the form response ~ predictors. See the documentation of \texttt{lm} and \texttt{formula} for details.

family  
The family of the glm model

data  
An object of type \texttt{mids}, which stands for 'multiply imputed data set', typically created by function \texttt{mice}().

...  
Additional parameters passed to \texttt{glm}.

Details
This function is included for backward compatibility with V1.0. The function is superseded by \texttt{with.mids}.

Value
An objects of class \texttt{mira}, which stands for 'multiply imputed repeated analysis'. This object contains data$m distinct glm.objects, plus some descriptive information.

Author(s)
Stef van Buuren, Karin Groothuis-Oudshoorn, 2000

References

See Also
\texttt{with.mids, glm.mids, mira}
Examples

```r
imp <- mice(nhanes)
# logistic regression on the imputed data
fit <- glm.mids((hyp == 2) ~ bmi + chl, data = imp, family = binomial)
fit
```

ibind

**Enlarge number of imputations by combining mids objects**

Description

This function combines two mids objects `x` and `y` into a single mids object, with the objective of increasing the number of imputed data sets. If the number of imputations in `x` and `y` are `m(x)` and `m(y)`, then the combined object will have `m(x)+m(y)` imputations.

Usage

```r
ibind(x, y)
```

Arguments

- `x` A mids object.
- `y` A mids object.

Details

The two mids objects are required to have the same underlying multiple imputation model and should be fitted on the same data.

Value

An S3 object of class mids

Author(s)

Karin Groothuis-Oudshoorn, Stef van Buuren

See Also

mids, rbind.mids, cbind.mids
ic

Select incomplete cases

Examples

```r
data(nhanes)
imp1 <- mice(nhanes, m = 1, maxit = 2, print = FALSE)
imp1$m

imp2 <- mice(nhanes, m = 3, maxit = 3, print = FALSE)
imp2$m

imp12 <- ibind(imp1, imp2)
imp12$m
plot(imp12)
```

ic

Select incomplete cases

Description

Extracts incomplete cases from a data set. The companion function for selecting the complete cases is `cc`.

Usage

`ic(x)`

Arguments

- `x` An R object. Methods are available for classes `mids`, `data.frame` and `matrix`. Also, `x` could be a vector.

Value

A vector, matrix or `data.frame` containing the data of the complete cases.

Author(s)

Stef van Buuren, 2017.

See Also

`cc`, `ici`

Examples

```r
ic(nhanes) # get the 12 rows with incomplete cases
ic(nhanes[1:10, ]) # incomplete cases within the first ten rows
ic(nhanes[, c("bmi", "hyp")]) # restrict extraction to variables bmi and hyp
```
ici

Incomplete case indicator

Description
This array is useful for extracting the subset of incomplete cases. The companion function cci() selects the complete cases.

Usage
ici(x)

Arguments
x An R object. Currently supported are methods for the following classes: mids.

Value
Logical vector indicating the incomplete cases,

Author(s)
Stef van Buuren, 2017.

See Also
ci, ic

Examples
ici(nhanes) # indicator for 12 rows with incomplete cases

is.mads

Check for mads object

Description
Check for mads object

Usage
is.mads(x)

Arguments
x An object
is.mipo

Value
A logical indicating whether \( x \) is an object of class \texttt{mads}

\begin{verbatim}
is.mids  \texttt{Check for mids object}
\end{verbatim}

Description
Check for \texttt{mids} object

Usage
\texttt{is.mids(x)}

Arguments
\begin{verbatim}
x  \texttt{An object}
\end{verbatim}

Value
A logical indicating whether \( x \) is an object of class \texttt{mads}

\begin{verbatim}
is.mipo  \texttt{Check for mipo object}
\end{verbatim}

Description
Check for \texttt{mipo} object

Usage
\texttt{is.mipo(x)}

Arguments
\begin{verbatim}
x  \texttt{An object}
\end{verbatim}

Value
A logical indicating whether \( x \) is an object of class \texttt{mipo}
is.mira  

**Description**

Check for \texttt{mira} object

**Usage**

\texttt{is.mira(x)}

**Arguments**

\texttt{x} \hspace{1cm} An object

**Value**

A logical indicating whether \texttt{x} is an object of class \texttt{mira}

---

is.mitml.result  

**Description**

Check for \texttt{mitml.result} object

**Usage**

\texttt{is.mitml.result(x)}

**Arguments**

\texttt{x} \hspace{1cm} An object

**Value**

A logical indicating whether \texttt{x} is an object of class \texttt{mitml.result}
lm.mids

Description

Applies `lm()` to multiply imputed data set

Usage

`lm.mids(formula, data, ...)`

---

leiden85

*Leiden 85+ study*

**Description**

Subset of data from the Leiden 85+ study

**Format**

`leiden85` is a data frame with 956 rows and 336 columns.

**Details**

The data set concerns of subset of 956 members of a very old (85+) cohort in Leiden.

Multiple imputation of this data set has been described in Boshuizen et al (1998), Van Buuren et al (1999) and Van Buuren (2012), chapter 7.

The data set is not available as part of `mice`.

**Source**


Arguments

- formula: a formula object, with the response on the left of a ~ operator, and the terms, separated by + operators, on the right. See the documentation of `lm` and `formula` for details.
- data: An object of type ‘mids’, which stands for ‘multiply imputed data set’, typically created by a call to function `mice()`.
- ... Additional parameters passed to `lm`.

Details

This function is included for backward compatibility with V1.0. The function is superseded by `with.mids`.

Value

An objects of class `mira`, which stands for ‘multiply imputed repeated analysis’. This object contains data$m distinct lm.objects, plus some descriptive information.

Author(s)

Stef van Buuren, Karin Groothuis-Oudshoorn, 2000

References


See Also

- `lm`, `mids`, `mira`

Examples

```r
imp <- mice(nhanes)
fit <- lm.mids(bmi ~ hyp + chl, data = imp)
fit
```

mads-class

Multivariate amputed data set (mads)

Description

The mads object contains an amputed data set. The mads object is generated by the ampute function. The mads class of objects has methods for the following generic functions: `print`, `summary`, `bwplot` and `xyplot`. 
Contents

call: The function call.

prop: Proportion of cases with missing values. Note: even when the proportion is entered as the proportion of missing cells (when bycases == TRUE), this object contains the proportion of missing cases.

patterns: A data frame of size #patterns by #variables where 0 indicates a variable has missing values and 1 indicates a variable remains complete.

freq: A vector of length #patterns containing the relative frequency with which the patterns occur. For example, if the vector is c(0.4, 0.4, 0.2), this means that of all cases with missing values, 40 percent is candidate for pattern 1, 40 percent for pattern 2 and 20 percent for pattern 3. The vector sums to 1.

mech: A string specifying the missingness mechanism, either "MCAR", "MAR" or "MNAR".

weights: A data frame of size #patterns by #variables. It contains the weights that were used to calculate the weighted sum scores. The weights may differ between patterns and between variables.

cont: Logical, whether probabilities are based on continuous logit functions or on discrete odds distributions.

type: A vector of strings containing the type of missingness for each pattern. Either "LEFT", "MID", "TAIL" or "RIGHT". The first type refers to the first pattern, the second type to the second pattern, etc.

odds: A matrix where #patterns defines the #rows. Each row contains the odds of being missing for the corresponding pattern. The amount of odds values defines in how many quantiles the sum scores were divided. The values are relative probabilities: a quantile with odds value 4 will have a probability of being missing that is four times higher than a quantile with odds 1. The #quantiles may differ between patterns, NA is used for cells remaining empty.

amp: A data frame containing the input data with NAs for the amputed values.

cand: A vector that contains the pattern number for each case. A value between 1 and #patterns is given. For example, a case with value 2 is candidate for missing data pattern 2.

scores: A list containing vectors with weighted sum scores of the candidates. The first vector refers to the candidates of the first pattern, the second vector refers to the candidates of the second pattern, etc. The length of the vectors differ because the number of candidates is different for each pattern.

data: The complete data set that was entered in ampute.

Note

Many of the functions of the mice package do not use the S4 class definitions, and instead rely on the S3 list equivalent oldClass(obj) <-"mads".

Author(s)

Rianne Schouten, 2016

See Also

ampute, Vignette titled "Multivariate Amputation using Ampute".
make.blocks  Creates a blocks argument

Description

This helper function generates a list of the type needed for blocks argument in the [=mice]{mice} function.

Usage

```r
make.blocks(
  data,
  partition = c("scatter", "collect", "void"),
  calltype = "type"
)
```

Arguments

- **data**: A data.frame, character vector with variable names, or list with variable names.
- **partition**: A character vector of length 1 used to assign variables to blocks when data is a data.frame. Value "scatter" (default) will assign each column to its own block. Value "collect" assigns all variables to one block, whereas "void" produces an empty list.
- **calltype**: A character vector of length(block) elements that indicates how the imputation model is specified. If calltype = "type" (the default), the underlying imputation model is called by means of the type argument. The type argument for block h is equivalent to row h in the predictorMatrix. The alternative is calltype = "formula". This will pass formulas[[h]] to the underlying imputation function for block h, together with the current data. The calltype of a block is set automatically during initialization. Where a choice is possible, calltype "formula" is preferred over "type" since this is more flexible and extendable. However, what precisely happens depends also on the capabilities of the imputation function that is called.

Details

Choices "scatter" and "collect" represent two extreme scenarios for assigning variables to imputation blocks. Use "scatter" to create an imputation model based on fully conditionally specification (FCS). Use "collect" to gather all variables to be imputed by a joint model (JM). Scenario’s in-between these two extremes represent hybrid imputation models that combine FCS and JM.

Any variable not listed in will not be imputed. Specification "void" represents the extreme scenario that skips imputation of all variables.

A variable may be a member of multiple blocks. The variable will be re-imputed in each block, so the final imputations for variable will come from the last block that was executed. This scenario may be useful where the same complete background factors appear in multiple imputation blocks.
A variable may appear multiple times within a given block. If a univariate imputation model is applied to such a block, then the variable is re-imputed each time as it appears in the block.

Value

A named list of character vectors with variables names.

Examples

```r
make.blots(nhanes)
make.blots(c("age", "sex", "edu"))
```

make.blots

Creates a blots argument

Description

This helper function creates a valid blots object. The blots object is an argument to the mice function. The name blots is a contraction of blocks-dots. Through blots, the user can specify any additional arguments that are specifically passed down to the lowest level imputation function.

Usage

```r
make.blots(data, blocks = make.blocks(data))
```

Arguments

data A data.frame with the source data
blocks An optional specification for blocks of variables in the rows. The default assigns each variable in its own block.

Value

A matrix

See Also

make.blocks

Examples

```r
make.predictorMatrix(nhanes)
make.blots(nhanes, blocks = name.blocks(c("age", "hyp"), "xxx"))
```
Description

This helper function creates a valid formulas object. The formulas object is an argument to the mice function. It is a list of formula's that specifies the target variables and the predictors by means of the standard ~ operator.

Usage

make.formulas(data, blocks = make.blocks(data), predictorMatrix = NULL)

Arguments

data A data.frame with the source data
blocks An optional specification for blocks of variables in the rows. The default assigns each variable in its own block.
predictorMatrix A predictorMatrix specified by the user.

Value

A list of formula's.

See Also

make.blocks, make.predictorMatrix

Examples

f1 <- make.formulas(nhanes)
f1
f2 <- make.formulas(nhanes, blocks = make.blocks(nhanes, "collect"))
f2

# for editing, it may be easier to work with the character vector
c1 <- as.character(f1)
c1

# fold it back into a formula list
f3 <- name.formulas(lapply(c1, as.formula))
f3
**make.method**

*Creates a method argument*

**Description**

This helper function creates a valid method vector. The method vector is an argument to the mice function that specifies the method for each block.

**Usage**

```r
make.method(
  data,
  where = make.where(data),
  blocks = make.blocks(data),
  defaultMethod = c("pmm", "logreg", "polyreg", "polr")
)
```

**Arguments**

- `data` A data frame or a matrix containing the incomplete data. Missing values are coded as NA.
- `where` A data frame or matrix with logicals of the same dimensions as `data` indicating where in the data the imputations should be created. The default, `where = is.na(data)`, specifies that the missing data should be imputed. The `where` argument may be used to overimpute observed data, or to skip imputations for selected missing values.
- `blocks` List of vectors with variable names per block. List elements may be named to identify blocks. Variables within a block are imputed by a multivariate imputation method (see method argument). By default each variable is placed into its own block, which is effectively fully conditional specification (FCS) by univariate models (variable-by-variable imputation). Only variables whose names appear in `blocks` are imputed. The relevant columns in the `where` matrix are set to FALSE of variables that are not block members. A variable may appear in multiple blocks. In that case, it is effectively re-imputed each time that it is visited.
- `defaultMethod` A vector of length 4 containing the default imputation methods for 1) numeric data, 2) factor data with 2 levels, 3) factor data with > 2 unordered levels, and 4) factor data with > 2 ordered levels. By default, the method uses pmm, predictive mean matching (numeric data) logreg, logistic regression imputation (binary data, factor with 2 levels) polyreg, polytomous regression imputation for unordered categorical data (factor > 2 levels) polr, proportional odds model for (ordered, > 2 levels).

**Value**

Vector of length(blocks) element with method names
This helper function creates a valid post vector. The post vector is an argument to the `mice` function that specifies post-processing for a variable just after imputation.

Usage

```r
make.post(data)
```

Arguments

data A data frame or a matrix containing the incomplete data. Missing values are coded as `NA`.

Value

Character vector of `ncol(data)` element

See Also

`mice`

Examples

```r
make.post(nhanes2)
```
make.predictorMatrix  Creates a predictorMatrix argument

Description
This helper function creates a valid predictorMatrix. The predictorMatrix is an argument to the mice function. It specifies the target variable or block in the rows, and the predictor variables on the columns. An entry of 0 means that the column variable is NOT used to impute the row variable or block. A nonzero value indicates that it is used.

Usage
make.predictorMatrix(data, blocks = make.blocks(data))

Arguments
- data  A data.frame with the source data
- blocks  An optional specification for blocks of variables in the rows. The default assigns each variable in its own block.

Value
A matrix

See Also
make.blocks

Examples
make.predictorMatrix(nhanes)
make.predictorMatrix(nhanes, blocks = make.blocks(nhanes, "collect"))

make.visitSequence  Creates a visitSequence argument

Description
This helper function creates a valid visitSequence. The visitSequence is an argument to the mice function that specifies the sequence in which blocks are imputed.

Usage
make.visitSequence(data = NULL, blocks = NULL)
**Arguments**

- **data**
  A data frame or a matrix containing the incomplete data. Missing values are coded as NA.

- **blocks**
  List of vectors with variable names per block. List elements may be named to identify blocks. Variables within a block are imputed by a multivariate imputation method (see method argument). By default each variable is placed into its own block, which is effectively fully conditional specification (FCS) by univariate models (variable-by-variable imputation). Only variables whose names appear in blocks are imputed. The relevant columns in the where matrix are set to FALSE of variables that are not block members. A variable may appear in multiple blocks. In that case, it is effectively re-imputed each time that it is visited.

**Value**

Vector containing block names

**See Also**

- mice

**Examples**

```r
make.visitSequence(nhanes)
```

---

**Description**

This helper function creates a valid where matrix. The where matrix is an argument to the mice function. It has the same size as data and specifies which values are to be imputed (TRUE) or not (FALSE).

**Usage**

```r
make.where(data, keyword = c("missing", "all", "none", "observed"))
```

**Arguments**

- **data**
  A data frame with the source data

- **keyword**
  An optional keyword, one of "missing" (missing values are imputed), "observed" (observed values are imputed), "all" and "none". The default is keyword = "missing"

**Value**

A matrix with logical
See Also

make.blocks, make.predictorMatrix

Examples

head(make.where(nhanes), 3)

mammalsleep

Mammal sleep data

Description

Dataset from Allison and Cicchetti (1976) of 62 mammal species on the interrelationship between sleep, ecological, and constitutional variables. The dataset contains missing values on five variables.

Format

mammalsleep is a data frame with 62 rows and 11 columns:

- species Species of animal
- bw Body weight (kg)
- brw Brain weight (g)
- sws Slow wave ("nondreaming") sleep (hrs/day)
- ps Paradoxical ("dreaming") sleep (hrs/day)
- ts Total sleep (hrs/day) (sum of slow wave and paradoxical sleep)
- mls Maximum life span (years)
- gt Gestation time (days)
- pi Predation index (1-5), 1 = least likely to be preyed upon
- sei Sleep exposure index (1-5), 1 = least exposed (e.g. animal sleeps in a well-protected den), 5 = most exposed
- odi Overall danger index (1-5) based on the above two indices and other information, 1 = least danger (from other animals), 5 = most danger (from other animals)

Details

Allison and Cicchetti (1976) investigated the interrelationship between sleep, ecological, and constitutional variables. They assessed these variables for 39 mammalian species. The authors concluded that slow-wave sleep is negatively associated with a factor related to body size. This suggests that large amounts of this sleep phase are disadvantageous in large species. Also, paradoxical sleep (REM sleep) was associated with a factor related to predatory danger, suggesting that large amounts of this sleep phase are disadvantageous in prey species.

Source

matchindex

Examples

```
sleep <- data(mammalsleep)
```

matchindex

Find index of matched donor units

Description

Find index of matched donor units

Usage

`matchindex(d, t, k = 5L)`

Arguments

- `d` Numeric vector with values from donor cases.
- `t` Numeric vector with values from target cases.
- `k` Integer, number of unique donors from which a random draw is made. For `k = 1` the function returns the index in `d` corresponding to the closest unit. For multiple imputation, the advice is to set values in the range of `k = 5` to `k = 10`.

Details

For each element in `t`, the method finds the `k` nearest neighbours in `d`, randomly draws one of these neighbours, and returns its position in vector `d`.

Fast predictive mean matching algorithm in seven steps:

1. Shuffle records to remove effects of ties
2. Obtain sorting order on shuffled data
3. Calculate index on input data and sort it
4. Pre-sample vector `h` with values between 1 and `k` For each of the `n0` elements in `t`:
5. find the two adjacent neighbours
6. find the `h_i`'th nearest neighbour
7. store the index of that neighbour

Return vector of `n0` positions in `d`.

We may use the function to perform predictive mean matching under a given predictive model. To do so, specify both `d` and `t` as predictions from the same model. Suppose that `y` contains the observed outcomes of the donor cases (in the same sequence as `d`), then `y[matchindex(d, t)]` returns one matched outcome for every target case.

See https://github.com/amices/mice/issues/236. This function is a replacement for the `matcher()` function that has been in default in mice since version 2.22 (June 2014).
Value

An integer vector with length(t) elements. Each element is an index in the array d.

Author(s)

Stef van Buuren, Nasinski Maciej, Alexander Robitzsch

Examples

```r
set.seed(1)

# Inputs need not be sorted
d <- c(-5, 5, 0, 10, 12)
t <- c(-6, -4, 0, 2, 4, -2, 6)

# Index (in vector a) of closest match
idx <- matchindex(d, t, 1)
idx

# To check: show values of closest match

# Random draw among indices of the 5 closest predictors
matchindex(d, t)

# An example
train <- mtcars[1:20, ]
test <- mtcars[21:32, ]
fit <- lm(mpg ~ disp + cyl, data = train)
d <- fitted.values(fit)
t <- predict(fit, newdata = test) # note: not using mpg
idx <- matchindex(d, t)

# Borrow values from train to produce 12 synthetic values for mpg in test.
# Synthetic values are plausible values that could have been observed if
# they had been measured.
train$mpg[idx]

# Exercise: Create a distribution of 1000 plausible values for each of the
# twelve mpg entries in test, and count how many times the true value
# (which we know here) is located within the inter-quartile range of each
# distribution. Is your count anywhere close to 500? Why? Why not?
```

md.pairs

Missing data pattern by variable pairs

Description

Number of observations per variable pair.
Usage

```r
md.pairs(data)
```

Arguments

data A data frame or a matrix containing the incomplete data. Missing values are coded as NA.

Details

The four components in the output value is have the following interpretation:

- `list('rr')` response-response, both variables are observed
- `list('rm')` response-missing, row observed, column missing
- `list('mr')` missing-response, row missing, column observed
- `list('mm')` missing-missing, both variables are missing

Value

A list of four components named `rr`, `rm`, `mr` and `mm`. Each component is square numerical matrix containing the number observations within four missing data pattern.

Author(s)

Stef van Buuren, Karin Groothuis-Oudshoorn, 2009

References


Examples

```r
pat <- md.pairs(nhanes)
pat

# show that these four matrices decompose the total sample size
# for each pair
pat$rr + pat$rm + pat$mr + pat$mm

# percentage of usable cases to impute row variable from column variable
round(100 * pat$mr / (pat$mr + pat$mm))
```
**md.pattern**

*Missing data pattern*

### Description

Display missing-data patterns.

### Usage

```r
md.pattern(x, plot = TRUE, rotate.names = FALSE)
```

### Arguments

- **x**: A data frame or a matrix containing the incomplete data. Missing values are coded as NA's.
- **plot**: Should the missing data pattern be made into a plot. Default is `plot = TRUE`.
- **rotate.names**: Whether the variable names in the plot should be placed horizontally or vertically. Default is `rotate.names = FALSE`.

### Details

This function is useful for investigating any structure of missing observations in the data. In specific case, the missing data pattern could be (nearly) monotone. Monotonicity can be used to simplify the imputation model. See Schafer (1997) for details. Also, the missing pattern could suggest which variables could potentially be useful for imputation of missing entries.

### Value

A matrix with `ncol(x)+1` columns, in which each row corresponds to a missing data pattern (1=observed, 0=missing). Rows and columns are sorted in increasing amounts of missing information. The last column and row contain row and column counts, respectively.

### Author(s)

Gerko Vink, 2018, based on an earlier version of the same function by Stef van Buuren, Karin Groothuis-Oudshoorn, 2000

### References


Examples

```r
dc.pattern(nhanes)
#   age hyp bmi chl
# 13 1 1 1 1 0
#  1 1 1 0 1 1
#  3 1 1 1 0 1
#  1 1 0 0 1 2
#  7 1 0 0 0 3
#  0 8 9 10 27
```

**mdc**

*Graphical parameter for missing data plots*

Description

`mdc` returns colors used to distinguish observed, missing and combined data in plotting. `mice.theme` return a partial list of named objects that can be used as a theme in `stripplot`, `bwplot`, `densityplot` and `xyplot`.

Usage

```r
mdc(  
  r = "observed",  
  s = "symbol",  
  transparent = TRUE,  
  cso = grDevices::hcl(240, 100, 40, 0.7),  
  csi = grDevices::hcl(0, 100, 40, 0.7),  
  csc = "gray50",  
  clo = grDevices::hcl(240, 100, 40, 0.8),  
  cli = grDevices::hcl(0, 100, 40, 0.8),  
  clc = "gray50"  
)
```

Arguments

- **r** A numerical or character vector. The numbers 1-6 request colors as follows: 1=cso, 2=csi, 3=csc, 4=clo, 5=cli and 6=clc. Alternatively, r may contain the strings 'observed', 'missing', or 'both', or abbreviations thereof.
- **s** A character vector containing the strings 'symbol' or 'line', or abbreviations thereof.
- **transparent** A logical indicating whether alpha-transparency is allowed. The default is TRUE.
- **cso** The symbol color for the observed data. The default is a transparent blue.
- **csi** The symbol color for the missing or imputed data. The default is a transparent red.
- **csc** The symbol color for the combined observed and imputed data. The default is a grey color.
clo  The line color for the observed data. The default is a slightly darker transparent blue.
cli  The line color for the missing or imputed data. The default is a slightly darker transparent red.
clc  The line color for the combined observed and imputed data. The default is a grey color.

Details

This function eases consistent use of colors in plots. The default follows the Abayomi convention, which uses blue for observed data, red for missing or imputed data, and black for combined data.

Value

mdc() returns a vector containing color definitions. The length of the output vector is calculate from the length of r and s. Elements of the input vectors are repeated if needed.

Author(s)

Stef van Buuren, sept 2012.

References


See Also

hcl, rgb, xyplot.mids, xyplot, trellis.par.set

Examples

# all six colors
mdc(1:6)

# lines color for observed and missing data
mdc(c("obs", "mis"), "lin")

mice: *Multivariate Imputation by Chained Equations*

Description

The mice package implements a method to deal with missing data. The package creates multiple imputations (replacement values) for multivariate missing data. The method is based on Fully Conditional Specification, where each incomplete variable is imputed by a separate model. The MICE algorithm can impute mixes of continuous, binary, unordered categorical and ordered categorical data. In addition, MICE can impute continuous two-level data, and maintain consistency between
imputations by means of passive imputation. Many diagnostic plots are implemented to inspect the quality of the imputations.

Generates Multivariate Imputations by Chained Equations (MICE)

Usage

mice(
  data,
  m = 5,
  method = NULL,
  predictorMatrix,
  ignore = NULL,
  where = NULL,
  blocks,
  visitSequence = NULL,
  formulas,
  blots = NULL,
  post = NULL,
  defaultMethod = c("pmm", "logreg", "polyreg", "polr"),
  maxit = 5,
  printFlag = TRUE,
  seed = NA,
  data.init = NULL,
  ...
)

Arguments

data A data frame or a matrix containing the incomplete data. Missing values are coded as NA.
m Number of multiple imputations. The default is m=5.
method Can be either a single string, or a vector of strings with length length(blocks), specifying the imputation method to be used for each column in data. If specified as a single string, the same method will be used for all blocks. The default imputation method (when no argument is specified) depends on the measurement level of the target column, as regulated by the defaultMethod argument. Columns that need not be imputed have the empty method "". See details.
predictorMatrix A numeric matrix of length(blocks) rows and ncol(data) columns, containing 0/1 data specifying the set of predictors to be used for each target column. Each row corresponds to a variable block, i.e., a set of variables to be imputed. A value of 1 means that the column variable is used as a predictor for the target block (in the rows). By default, the predictorMatrix is a square matrix of ncol(data) rows and columns with all 1's, except for the diagonal. Note: For two-level imputation models (which have "2l" in their names) other codes (e.g., 2 or -2) are also allowed.
ignore A logical vector of nrow(data) elements indicating which rows are ignored when creating the imputation model. The default NULL includes all rows that
have an observed value of the variable to imputed. Rows with ignore set to TRUE do not influence the parameters of the imputation model, but are still imputed. We may use the ignore argument to split data into a training set (on which the imputation model is built) and a test set (that does not influence the imputation model estimates). Note: Multivariate imputation methods, like mice.impute.jomoImpute() or mice.impute.panImpute(), do not honour the ignore argument.

**where**
A data frame or matrix with logicals of the same dimensions as data indicating where in the data the imputations should be created. The default, where = is.na(data), specifies that the missing data should be imputed. The where argument may be used to overimpute observed data, or to skip imputations for selected missing values.

**blocks**
List of vectors with variable names per block. List elements may be named to identify blocks. Variables within a block are imputed by a multivariate imputation method (see method argument). By default each variable is placed into its own block, which is effectively fully conditional specification (FCS) by univariate models (variable-by-variable imputation). Only variables whose names appear in blocks are imputed. The relevant columns in the where matrix are set to FALSE of variables that are not block members. A variable may appear in multiple blocks. In that case, it is effectively re-imputed each time that it is visited.

**visitSequence**
A vector of block names of arbitrary length, specifying the sequence of blocks that are imputed during one iteration of the Gibbs sampler. A block is a collection of variables. All variables that are members of the same block are imputed when the block is visited. A variable that is a member of multiple blocks is re-imputed within the same iteration. The default visitSequence = "roman" visits the blocks (left to right) in the order in which they appear in blocks. One may also use one of the following keywords: "arabic" (right to left), "monotone" (ordered low to high proportion of missing data) and "revmonotone" (reverse of monotone).

**formulas**
A named list of formula's, or expressions that can be converted into formula's by as.formula. List elements correspond to blocks. The block to which the list element applies is identified by its name, so list names must correspond to block names. The formulas argument is an alternative to the predictorMatrix argument that allows for more flexibility in specifying imputation models, e.g., for specifying interaction terms.

**blots**
A named list of alist's that can be used to pass down arguments to lower level imputation function. The entries of element blots[[blockname]] are passed down to the function called for block blockname.

**post**
A vector of strings with length ncol(data) specifying expressions as strings. Each string is parsed and executed within the sampler() function to post-process imputed values during the iterations. The default is a vector of empty strings, indicating no post-processing.

**defaultMethod**
A vector of length 4 containing the default imputation methods for 1) numeric data, 2) factor data with 2 levels, 3) factor data with > 2 unordered levels, and 4) factor data with > 2 ordered levels. By default, the method uses pmm, predictive mean matching (numeric data) logreg, logistic regression imputation (binary
mice package contains functions to

- Inspect the missing data pattern
- Impute the missing data \(m\) times, resulting in \(m\) completed data sets
- Diagnose the quality of the imputed values
- Analyze each completed data set
- Pool the results of the repeated analyses
- Store and export the imputed data in various formats
- Generate simulated incomplete data
- Incorporate custom imputation methods

Generates multiple imputations for incomplete multivariate data by Gibbs sampling. Missing data can occur anywhere in the data. The algorithm imputes an incomplete column (the target column) by generating 'plausible' synthetic values given other columns in the data. Each incomplete column must act as a target column, and has its own specific set of predictors. The default set of predictors for a given target consists of all other columns in the data. For predictors that are incomplete themselves, the most recently generated imputations are used to complete the predictors prior to imputation of the target column.

A separate univariate imputation model can be specified for each column. The default imputation method depends on the measurement level of the target column. In addition to these, several other methods are provided. You can also write their own imputation functions, and call these from within the algorithm.

The data may contain categorical variables that are used in a regressions on other variables. The algorithm creates dummy variables for the categories of these variables, and imputes these from the corresponding categorical variable.

Built-in univariate imputation methods are:

- `pmm` Predictive mean matching
midastouch  any  Weighted predictive mean matching  
sample      any  Random sample from observed values  
cart        any  Classification and regression trees  
rfs         any  Random forest imputations  
mean        numeric  Unconditional mean imputation  
norm        numeric  Bayesian linear regression  
norm.nob    numeric  Linear regression ignoring model error  
norm.boot   numeric  Linear regression using bootstrap  
norm.predict numeric  Linear regression, predicted values  
quadratic   numeric  Imputation of quadratic terms  
ri          numeric  Random indicator for nonignorable data  
logreg      binary  Logistic regression  
logreg.boot binary  Logistic regression with bootstrap  
polr        ordered  Proportional odds model  
polyreg     unordered  Polytomous logistic regression  
lda         unordered  Linear discriminant analysis  
2l.norm     numeric  Level-1 normal heteroscedastic  
2l.lmer     numeric  Level-1 normal homoscedastic, lmer  
2l.pan      numeric  Level-1 normal homoscedastic, pan  
2l.bin      binary  Level-1 logistic, glmer  
2lonly.mean numeric  Level-2 class mean  
2lonly.norm numeric  Level-2 class normal  
2lonly.pmm  any   Level-2 class predictive mean matching

These corresponding functions are coded in the mice library under names mice.impute.method, where method is a string with the name of the univariate imputation method name, for example norm. The method argument specifies the methods to be used. For the j'th column, mice() calls the first occurrence of paste('mice.impute.',method[j],sep='') in the search path. The mechanism allows users to write customized imputation function, mice.impute.myfunc. To call it for all columns specify method='myfunc'. To call it only for, say, column 2 specify method=c('norm','myfunc','logreg',...).

Skipping imputation: The user may skip imputation of a column by setting its entry to the empty method: "". For complete columns without missing data mice will automatically set the empty method. Setting the empty method does not produce imputations for the column, so any missing cells remain NA. If column A contains NA's and is used as predictor in the imputation model for column B, then mice produces no imputations for the rows in B where A is missing. The imputed data for B may thus contain NA's. The remedy is to remove column A from the imputation model for the other columns in the data. This can be done by setting the entire column for variable A in the predictorMatrix equal to zero.

Passive imputation: mice() supports a special built-in method, called passive imputation. This method can be used to ensure that a data transform always depends on the most recently generated imputations. In some cases, an imputation model may need transformed data in addition to the original data (e.g. log, quadratic, recodes, interaction, sum scores, and so on). Passive imputation maintains consistency among different transformations of the same data. Passive imputation is invoked if '~' is specified as the first character of the string that specifies the univariate method. mice() interprets the entire string, including the '~' character, as the formula argument in a call to model.frame(formula,data[!r[,j]],). This provides a simple mechanism for specifying deterministic dependencies among the columns. For example, suppose that the missing entries
in variables data$height and data$weight are imputed. The body mass index (BMI) can be calculated within mice by specifying the string '~I(weight/height^2)' as the univariate imputation method for the target column data$bmi. Note that the ~ mechanism works only on those entries which have missing values in the target column. You should make sure that the combined observed and imputed parts of the target column make sense. An easy way to create consistency is by coding all entries in the target as NA, but for large data sets, this could be inefficient. Note that you may also need to adapt the default predictorMatrix to evade linear dependencies among the predictors that could cause errors like Error in solve.default() or Error: system is exactly singular. Though not strictly needed, it is often useful to specify visitSequence such that the column that is imputed by the ~ mechanism is visited each time after one of its predictors was visited. In that way, deterministic relation between columns will always be synchronized.

#'A new argument ls.meth can be parsed to the lower level .norm.draw to specify the method for generating the least squares estimates and any subsequently derived estimates. Argument ls.meth takes one of three inputs: "qr" for QR-decomposition, "svd" for singular value decomposition and "ridge" for ridge regression. ls.meth defaults to ls.meth = "qr".

Auxiliary predictors in formulas specification: For a given block, the formulas specification takes precedence over the corresponding row in the predictMatrix argument. This precedence is, however, restricted to the subset of variables specified in the terms of the block formula. Any variables not specified by formulas are imputed according to the predictMatrix specification. Variables with non-zero type values in the predictMatrix will be added as main effects to the formulas, which will act as supplementary covariates in the imputation model. It is possible to turn off this behavior by specifying the argument auxiliary = FALSE.

Value

Returns an S3 object of class mids (multiply imputed data set)

Functions

The main functions are:

- mice() Impute the missing data *m* times
- with() Analyze completed data sets
- pool() Combine parameter estimates
- complete() Export imputed data
- ampute() Generate missing data

Vignettes

There is a detailed series of six online vignettes that walk you through solving realistic inference problems with mice.

We suggest going through these vignettes in the following order

1. Ad hoc methods and the MICE algorithm
2. Convergence and pooling
3. Inspecting how the observed data and missingness are related
4. Passive imputation and post-processing
5. Imputing multilevel data
6. Sensitivity analysis with mice


Methodology

The mice software was published in the Journal of Statistical Software (Van Buuren and Groothuis-Oudshoorn, 2011). The first application of the method concerned missing blood pressure data (Van Buuren et. al., 1999). The term Fully Conditional Specification was introduced in 2006 to describe a general class of methods that specify imputations model for multivariate data as a set of conditional distributions (Van Buuren et. al., 2006). Further details on mixes of variables and applications can be found in the book Flexible Imputation of Missing Data. Second Edition. Chapman & Hall/CRC. Boca Raton, FL.

Enhanced linear algebra

Updating the BLAS can improve speed of R, sometime considerably. The details depend on the operating system. See the discussion in the "R Installation and Administration" guide for further information.

Author(s)

Stef van Buuren <stef.vanbuuren@tno.nl>, Karin Groothuis-Oudshoorn <c.g.m.oudshoorn@utwente.nl>, 2000-2010, with contributions of Alexander Robitzsch, Gerko Vink, Shahab Jolani, Roel de Jong, Jason Turner, Lisa Doove, John Fox, Frank E. Harrell, and Peter Malewski.

References


mice.impute.2l.bin


See Also

  mice, with.mids, pool, complete, ampute
  mids, with.mids, set.seed, complete

Examples

# do default multiple imputation on a numeric matrix
imp <- mice(nhanes)
imp

# list the actual imputations for BMI
imp$imp$bmi

# first completed data matrix
complete(imp)

# imputation on mixed data with a different method per column
mice(nhanes2, meth = c("sample", "pmm", "logreg", "norm"))

mice.impute.2l.bin  *Imputation by a two-level logistic model using glmer*

Description

Imputes univariate systematically and sporadically missing data using a two-level logistic model using *lme4::glmer()*. 

Usage

mice.impute.2l.bin(y, ry, x, type, wy = NULL, intercept = TRUE, ...)

Arguments

  y  Vector to be imputed
  ry Logical vector of length length(y) indicating the the subset y[ry] of elements in y to which the imputation model is fitted. The ry generally distinguishes the observed (TRUE) and missing values (FALSE) in y.
  x  Numeric design matrix with length(y) rows with predictors for y. Matrix x may have no missing values.
mice.impute.2l.bin

**type**  
Vector of length `ncol(x)` identifying random and class variables. Random variables are identified by a '2'. The class variable (only one is allowed) is coded as '-2'. Fixed effects are indicated by a '1'.

**wy**  
Logical vector of length `length(y)`. A TRUE value indicates locations in y for which imputations are created.

**intercept**  
Logical determining whether the intercept is automatically added.

**...**  
Arguments passed down to `glmer`

**Details**

Data are missing systematically if they have not been measured, e.g., in the case where we combine data from different sources. Data are missing sporadically if they have been partially observed.

**Value**

Vector with imputed data, same type as y, and of length `sum(wy)`

**Author(s)**

Shahab Jolani, 2015; adapted to mice, SvB, 2018

**References**


**See Also**

Other univariate-2l: `mice.impute.2l.lmer()`, `mice.impute.2l.norm()`, `mice.impute.2l.pan()`

**Examples**

```r
library(tidyr)
library(dplyr)
data("toenail2")
data <- tidyr::complete(toenail2, patientID, visit) %>%
  tidyr::fill(treatment) %>%
  dplyr::select(-time) %>%
  dplyr::mutate(patientID = as.integer(patientID))
## Not run:
pred <- mice(data, print = FALSE, maxit = 0, seed = 1)$pred
pred["outcome", "patientID"] <- -2
imp <- mice(data, method = "2l.bin", pred = pred, maxit = 1, m = 1, seed = 1)
## End(Not run)
```
Imputation by a two-level normal model using lmer

**Description**

Imputes univariate systematically and sporadically missing data using a two-level normal model using `lme4::lmer()`.

**Usage**

```r
mice.impute.2l.lmer(y, ry, x, type, wy = NULL, intercept = TRUE, ...)
```

**Arguments**

- **y**: Vector to be imputed
- **ry**: Logical vector of length `length(y)` indicating the subset `y[ry]` of elements in `y` to which the imputation model is fitted. The `ry` generally distinguishes the observed (TRUE) and missing values (FALSE) in `y`.
- **x**: Numeric design matrix with `length(y)` rows with predictors for `y`. Matrix `x` may have no missing values.
- **type**: Vector of length `ncol(x)` identifying random and class variables. Random variables are identified by a ’2’. The class variable (only one is allowed) is coded as ’-2’. Fixed effects are indicated by a ’1’.
- **wy**: Logical vector of length `length(y)`. A TRUE value indicates locations in `y` for which imputations are created.
- **intercept**: Logical determining whether the intercept is automatically added.
- **...**: Arguments passed down to `lmer`

**Details**

Data are missing systematically if they have not been measured, e.g., in the case where we combine data from different sources. Data are missing sporadically if they have been partially observed.

While the method is fully Bayesian, it may fix parameters of the variance-covariance matrix or the random effects to their estimated value in cases where creating draws from the posterior is not possible. The procedure throws a warning when this happens.

**Value**

Vector with imputed data, same type as `y`, and of length `sum(wy)`

**Author(s)**

Shahab Jolani, 2017
References


See Also

Other univariate-2l: `mice.impute.2l.bin()`, `mice.impute.2l.norm()`, `mice.impute.2l.pan()`

---

**mice.impute.2l.norm**

*Imputation by a two-level normal model*

Description

Imputes univariate missing data using a two-level normal model

Usage

```r
mice.impute.2l.norm(y, ry, x, type, wy = NULL, intercept = TRUE, ...)
```

Arguments

- `y` Vector to be imputed
- `ry` Logical vector of length `length(y)` indicating the the subset `y[ry]` of elements in `y` to which the imputation model is fitted. The `ry` generally distinguishes the observed (TRUE) and missing values (FALSE) in `y`.
- `x` Numeric design matrix with `length(y)` rows with predictors for `y`. Matrix `x` may have no missing values.
- `type` Vector of length `ncol(x)` identifying random and class variables. Random variables are identified by a `2`. The class variable (only one is allowed) is coded as `-2`. Random variables also include the fixed effect.
- `wy` Logical vector of length `length(y)`. A TRUE value indicates locations in `y` for which imputations are created.
- `intercept` Logical determining whether the intercept is automatically added.
- `...` Other named arguments.
Details

Implements the Gibbs sampler for the linear multilevel model with heterogeneous with-class variance (Kasim and Raudenbush, 1998). Imputations are drawn as an extra step to the algorithm. For simulation work see Van Buuren (2011).

The random intercept is automatically added in `mice.impute.2L.norm()`. A model within a random intercept can be specified by `mice(..., intercept = FALSE)`.

Value

Vector with imputed data, same type as `y`, and of length `sum(wy)`

Note

Added June 25, 2012: The currently implemented algorithm does not handle predictors that are specified as fixed effects (type=1). When using `mice.impute.2l.norm()`, the current advice is to specify all predictors as random effects (type=2).

Warning: The assumption of heterogeneous variances requires that in every class at least one observation has a response in `y`.

Author(s)

Roel de Jong, 2008

References


See Also

Other univariate-2l: `mice.impute.2l.bin()`, `mice.impute.2l.lmer()`, `mice.impute.2l.pan()`

---

**mice.impute.2l.pan**

Imputation by a two-level normal model using pan

**Description**

Imputes univariate missing data using a two-level normal model with homogeneous within group variances. Aggregated group effects (i.e. group means) can be automatically created and included as predictors in the two-level regression (see argument type). This function needs the pan package.
Usage

mice.impute.2l.pan(
  y,
  ry,
  x,
  type,
  intercept = TRUE,
  paniter = 500,
  groupcenter.slope = FALSE,
  ...
)

Arguments

y           Incomplete data vector of length n
ry          Vector of missing data pattern (FALSE=missing, TRUE=observed)
x           Matrix (n x p) of complete covariates.
type        Vector of length ncol(x) identifying random and class variables. Random effects are identified by a '2'. The group variable (only one is allowed) is coded as '-2'. Random effects also include the fixed effect. If for a covariates X1 group means shall be calculated and included as further fixed effects choose '3'. In addition to the effects in '3', specification '4' also includes random effects of X1.
intercept   Logical determining whether the intercept is automatically added.
paniter     Number of iterations in pan. Default is 500.
groupcenter.slope
            If TRUE, in case of group means (type is '3' or '4') group mean centering for these predictors are conducted before doing imputations. Default is FALSE.
...
            Other named arguments.

Details

Implements the Gibbs sampler for the linear two-level model with homogeneous within group variances which is a special case of a multivariate linear mixed effects model (Schafer & Yucel, 2002). For a two-level imputation with heterogeneous within-group variances see mice.impute.2l.norm. The random intercept is automatically added in mice.impute.2l.norm().

Value

A vector of length nmis with imputations.

Note

This function does not implement the where functionality. It always produces nmis imputation, irrespective of the where argument of the mice function.
Author(s)
Alexander Robitzsch (IPN - Leibniz Institute for Science and Mathematics Education, Kiel, Germany), <robitzsch@ipn.uni-kiel.de>

References

See Also
Other univariate-2l: mice.impute.2l.bin(), mice.impute.2l.lmer(), mice.impute.2l.norm()

Examples
# simulate some data
# two-level regression model with fixed slope

# number of groups
G <- 250
# number of persons
n <- 20
# regression parameter
beta <- .3
# intraclass correlation
rho <- .30
# correlation with missing response
rho.miss <- .10
# missing proportion
missrate <- .50
y1 <- rep(rnorm(G, sd = sqrt(rho)), each = n) + rnorm(G * n, sd = sqrt(1 - rho))
x <- rnorm(G * n)
y <- y1 + beta * x
dfr0 <- dfr <- data.frame("group" = rep(1:G, each = n), "x" = x, "y" = y)
dfr[rho.miss * x + rnorm(G * n, sd = sqrt(1 - rho.miss)) < qnorm(missrate), "y"] <- NA

# empty imputation in mice
imp0 <- mice(as.matrix(dfr), maxit = 0)
predM <- imp0$predictorMatrix
impM <- imp0$method

# specify predictor matrix and method
predM1 <- predM
predM1["y", "group"] <- -2
predM1["y", "x"] <- 1 # fixed x effects imputation
impM1 <- impM
impM1["y"] <- "21.pan"
# multilevel imputation
imp1 <- mice(as.matrix(dfr),
  m = 1, predictorMatrix = predM1,
  method = impM1, maxit = 1
)

# multilevel analysis
library(lme4)
mod <- lmer(y ~ (1 + x | group) + x, data = complete(imp1))
summary(mod)

# Examples of predictorMatrix specification

# random x effects
# predM1["y","x"] <- 2

# fixed x effects and group mean of x
# predM1["y","x"] <- 3

# random x effects and group mean of x
# predM1["y","x"] <- 4

---

mice.impute.2lonly.mean

**Imputation of most likely value within the class**

**Description**

Method 2lonly.mean replicates the most likely value within a class of a second-level variable. It works for numeric and factor data. The function is primarily useful as a quick fixup for data in which the second-level variable is inconsistent.

**Usage**

mice.impute.2lonly.mean(y, ry, x, type, wy = NULL, ...)

**Arguments**

- **y**  Vector to be imputed
- **ry** Logical vector of length length(y) indicating the the subset y[ry] of elements in y to which the imputation model is fitted. The ry generally distinguishes the observed (TRUE) and missing values (FALSE) in y.
- **x**   Numeric design matrix with length(y) rows with predictors for y. Matrix x may have no missing values.
- **type** Vector of length ncol(x) identifying random and class variables. The class variable (only one is allowed) is coded as -2.
**mice.impute.2lonly.norm**

wy Logical vector of length \( \text{length}(y) \). A TRUE value indicates locations in \( y \) for which imputations are created.

... Other named arguments.

**Details**

Observed values in \( y \) are averaged within the class, and replicated to the missing \( y \) within that class. This function is primarily useful for repairing incomplete data that are constant within the class, but vary over classes.

For numeric variables, \( \text{mice.impute.2lonly.mean()} \) imputes the class mean of \( y \). If \( y \) is a second-level variable, then conventionally all observed \( y \) will be identical within the class, and the function just provides a quick fix for any missing \( y \) by filling in the class mean.

For factor variables, \( \text{mice.impute.2lonly.mean()} \) imputes the most frequently occurring category within the class.

If there are no observed \( y \) in the class, all entries of the class are set to \( \text{NA} \). Note that this may produce problems later on in \texttt{mice} if imputation routines are called that expects predictor data to be complete. Methods designed for imputing this type of second-level variables include \( \text{mice.impute.2lonly.norm} \) and \( \text{mice.impute.2lonly.pmm} \).

**Value**

Vector with imputed data, same type as \( y \), and of length \( \text{sum(wy)} \).

**Author(s)**

Gerko Vink, Stef van Buuren, 2019

**References**


**See Also**

Other univariate-2lonly: \( \text{mice.impute.2lonly.norm()}, \text{mice.impute.2lonly.pmm}() \)

---

**Description**

Imputes univariate missing data at level 2 using Bayesian linear regression analysis. Variables are level 1 are aggregated at level 2. The group identifier at level 2 must be indicated by \( \text{type} = -2 \) in the predictorMatrix.
Usage

mice.impute.2lonly.norm(y, ry, x, type, wy = NULL, ...)

Arguments

y  Vector to be imputed
ry Logical vector of length length(y) indicating the the subset y[ry] of elements in y to which the imputation model is fitted. The ry generally distinguishes the observed (TRUE) and missing values (FALSE) in y.
x Numeric design matrix with length(y) rows with predictors for y. Matrix x may have no missing values.
type Group identifier must be specified by `'-2'`. Predictors must be specified by '1'.
wy Logical vector of length length(y). A TRUE value indicates locations in y for which imputations are created.
... Other named arguments.

Details

This function allows in combination with mice.impute.2l.pan switching regression imputation between level 1 and level 2 as described in Yucel (2008) or Gelman and Hill (2007, p. 541).

The function checks for partial missing level-2 data. Level-2 data are assumed to be constant within the same cluster. If one or more entries are missing, then the procedure aborts with an error message that identifies the cluster with incomplete level-2 data. In such cases, one may first fill in the cluster mean (or mode) by the 2lonly.mean method to remove inconsistencies.

Value

A vector of length nmis with imputations.

Note

For a more general approach, see miceadds::mice.impute.2lonly.function().

Author(s)

Alexander Robitzsch (IPN - Leibniz Institute for Science and Mathematics Education, Kiel, Germany), <robitzsch@ipn.uni-kiel.de>

References


See Also

mice.impute.norm, mice.impute.2lonly.pmm, mice.impute.2l.pan, mice.impute.2lonly.mean

Other univariate-2lonly: mice.impute.2lonly.mean(), mice.impute.2lonly.pmm()

Examples

# simulate some data
# x,y ... level 1 variables
# v,w ... level 2 variables

G <- 250 # number of groups
n <- 20 # number of persons
beta <- .3 # regression coefficient
rho <- .30 # residual intraclass correlation
rho.miss <- .10 # correlation with missing response
missrate <- .50 # missing proportion
y1 <- rep(rnorm(G, sd = sqrt(rho)), each = n) + rnorm(G * n, sd = sqrt(1 - rho))
w <- rep(round(rnorm(G), 2), each = n)
v <- rep(round(runif(G, 0, 3)), each = n)
x <- rep(round(runif(G * n), 2), each = n)
y <- y1 + beta * x + .2 * w + .1 * v

dfr0 <- dfr <- data.frame("group" = rep(1:G, each = n), "x" = x, "y" = y, "w" = w, "v" = v)
dfr[rho.miss * x + rnorm(G * n, sd = sqrt(1 - rho.miss)) < qnorm(missrate), "y"] <- NA
dfr[rep(rnorm(G), each = n) < qnorm(missrate), "w"] <- NA
dfr[rep(rnorm(G), each = n) < qnorm(missrate), "v"] <- NA

# empty mice imputation
imp0 <- mice(as.matrix(dfr), maxit = 0)
predM <- imp0$predictorMatrix
impM <- imp0$method

# multilevel imputation
predM1 <- predM
predM1[c("w", "y", "v"), "group"] <- -2
predM1["y", "x"] <- 1 # fixed x effects imputation
impM1 <- impM
impM1[c("y", "w", "v")]) <- c("2l.pan", "2lonly.norm", "2lonly.pmm")

# y ... imputation using pan
# w ... imputation at level 2 using norm
# v ... imputation at level 2 using pmm

imp1 <- mice(as.matrix(dfr),
  m = 1, predictorMatrix = predM1,
  method = impM1, maxit = 1, paniter = 500)

# Demonstration that 2lonly.norm aborts for partial missing data.
# Better use 2lonly.mean for repair.
data <- data.frame(
  patid = rep(1:4, each = 5),
  sex = rep(c(1, 2, 1, 2), each = 5),
mice.impute.2lonly.pmm

Imputation at level 2 by predictive mean matching

Description

Imputes univariate missing data at level 2 using predictive mean matching. Variables are level 1 are aggregated at level 2. The group identifier at level 2 must be indicated by type = -2 in the predictorMatrix.

Usage

mice.impute.2lonly.pmm(y, ry, x, type, wy = NULL, ...)

crp = c(
  68, 78, 93, NA, 143,
  5, 7, 9, 13, NA,
  97, NA, 56, 52, 34,
  22, 30, NA, NA, 45
)
)
pred <- make.predictorMatrix(data)
pred[, "patid"] <- -2
# only missing value (out of five) for patid == 1
data[3, "sex"] <- NA
## Not run:
# The following fails because 2lonly.norm found partially missing
# level-2 data
# imp <- mice(data, method = c("", "2lonly.norm", "2l.pan"),
# predictorMatrix = pred, maxit = 1, m = 2)
# > iter imp variable
# > 1 1 sex  crpError in .imputation.level2(y = y, ... :
# > Method 2lonly.norm found the following clusters with partially missing
# > level-2 data: 1
# > Method 2lonly.mean can fix such inconsistencies.
## End(Not run)
# In contrast, if all sex values are missing for patid == 1, it runs fine,
# except on r-patched-solaris-x86. I used dontrun to evade CRAN errors.
## Not run:
data[1:5, "sex"] <- NA
imp <- mice(data,  
  method = c("", "2lonly.norm", "2l.pan"),
  predictorMatrix = pred, maxit = 1, m = 2
)
## End(Not run)
Arguments

\textit{y}
Vector to be imputed

\textit{ry}
Logical vector of length \texttt{length(y)} indicating the subset \texttt{y[ry]} of elements in \texttt{y} to which the imputation model is fitted. The \texttt{ry} generally distinguishes the observed (TRUE) and missing values (FALSE) in \texttt{y}.

\textit{x}
Numeric design matrix with \texttt{length(y)} rows with predictors for \texttt{y}. Matrix \texttt{x} may have no missing values.

\textit{type}
Group identifier must be specified by `-2'. Predictors must be specified by `1'.

\textit{wy}
Logical vector of length \texttt{length(y)}. A TRUE value indicates locations in \texttt{y} for which imputations are created.

\textit{...}
Other named arguments.

Details

This function allows in combination with \texttt{mice.impute.2l.pan} switching regression imputation between level 1 and level 2 as described in Yucel (2008) or Gelman and Hill (2007, p. 541).

The function checks for partial missing level-2 data. Level-2 data are assumed to be constant within the same cluster. If one or more entries are missing, then the procedure aborts with an error message that identifies the cluster with incomplete level-2 data. In such cases, one may first fill in the cluster mean (or mode) by the \texttt{2lonly.mean} method to remove inconsistencies.

Value

A vector of length \texttt{nmis} with imputations.

Note

The extension to categorical variables transforms a dependent factor variable by means of the \texttt{as.integer()} function. This may make sense for categories that are approximately ordered, but less so for pure nominal measures.

For a more general approach, see \texttt{miceadds::mice.impute.2lonly.function()}. 

Author(s)

Alexander Robitzsch (IPN - Leibniz Institute for Science and Mathematics Education, Kiel, Germany), <robitzsch@ipn.uni-kiel.de>

References


See Also

mice.impute.pmm, mice.impute.2lonly.norm, mice.impute.2l.pan, mice.impute.2lonly.mean

Other univariate-2lonly: mice.impute.2lonly.mean(), mice.impute.2lonly.norm()

Examples

# simulate some data
# x,y ... level 1 variables
# v,w ... level 2 variables

G <- 250 # number of groups
n <- 20 # number of persons
beta <- .3 # regression coefficient
rho <- .30 # residual intraclass correlation
rho.miss <- .10 # correlation with missing response
missrate <- .50 # missing proportion
y1 <- rep(rnorm(G, sd = sqrt(rho)), each = n) + rnorm(G * n, sd = sqrt(1 - rho))
w <- rep(round(rnorm(G, 2), each = n))
v <- rep(round(runif(G, 0, 3)), each = n)
x <- rep(rnorm(G * n))
y <- y1 + beta * x + .2 * w + .1 * v

dfr0 <- dfr <- data.frame("group" = rep(1:G, each = n), "x" = x, "y" = y, "w" = w, "v" = v)
dfr[rho.miss * x + rnorm(G * n, sd = sqrt(1 - rho.miss)) < qnorm(missrate), "y"] <- NA
dfr[rep(rnorm(G), each = n) < qnorm(missrate), "w"] <- NA
dfr[rep(rnorm(G), each = n) < qnorm(missrate), "v"] <- NA

# empty mice imputation
imp0 <- mice(as.matrix(dfr), maxit = 0)
predM <- imp0$predictorMatrix
impM <- imp0$method

# multilevel imputation
predM1 <- predM
predM1[c("w", "y", "v"), "group"] <- -2
predM1["y", "x"] <- 1 # fixed x effects imputation
impM1 <- impM
impM1[c("y", "w", "v") <- c("2l.pan", "2lonly.norm", "2lonly.pmm")

# turn v into a categorical variable
dfr$v <- as.factor(dfr$v)
levels(dfr$v) <- LETTERS[1:4]

# y ... imputation using pan
# w ... imputation at level 2 using norm
# v ... imputation at level 2 using pmm

# skip imputation on solaris
is.solaris <- function() grepl("SunOS", Sys.info()["sysname"])
if (!is.solaris()) {
  imp <- mice(dfr,
    m = 1, predictorMatrix = predM1,
    method = impM1, maxit = 1, paniter = 500)
mice.impute.cart

Description

Imputes univariate missing data using classification and regression trees.

Usage

mice.impute.cart(y, ry, x, wy = NULL, minbucket = 5, cp = 1e-04, ...)

Arguments

- `y`: Vector to be imputed
- `ry`: Logical vector of length `length(y)` indicating the subset `y[ry]` of elements in `y` to which the imputation model is fitted. The `ry` generally distinguishes the observed (TRUE) and missing values (FALSE) in `y`.
- `x`: Numeric design matrix with `length(y)` rows with predictors for `y`. Matrix `x` may have no missing values.
- `wy`: Logical vector of length `length(y)`. A TRUE value indicates locations in `y` for which imputations are created.
- `minbucket`: The minimum number of observations in any terminal node used. See `rpart.control` for details.
- `cp`: Complexity parameter. Any split that does not decrease the overall lack of fit by a factor of `cp` is not attempted. See `rpart.control` for details.
- `...`: Other named arguments passed down to `rpart()`.

Details

Imputation of `y` by classification and regression trees. The procedure is as follows:

1. Fit a classification or regression tree by recursive partitioning;
2. For each `ymis`, find the terminal node they end up according to the fitted tree;
3. Make a random draw among the members in the node, and take the observed value from that draw as the imputation.

Value

- Vector with imputed data, same type as `y`, and of length `sum(wy)`
- Numeric vector of length `sum(!ry)` with imputations
Author(s)
Lisa Doove, Stef van Buuren, Elise Dusseldorp, 2012

References

See Also
mice, mice.impute.rf, rpart, rpart.control
Other univariate imputation functions: mice.impute.lda(), mice.impute.logreg.boot(), mice.impute.logreg(), mice.impute.mean(), mice.impute.midastouch(), mice.impute.mnar.logreg(), mice.impute.norm.boot(), mice.impute.norm.nob(), mice.impute.norm.predict(), mice.impute.norm(), mice.impute.pmm(), mice.impute.polr(), mice.impute.polyreg(), mice.impute.quadratic(), mice.impute.rf(), mice.impute.ri()

Examples

```r
require(rpart)

imp <- mice(nhanes2, meth = "cart", minbucket = 4)
plot(imp)
```

mice.impute.jomoImpute

*Multivariate multilevel imputation using jomo*

Description

This function is a wrapper around the jomoImpute function from the mitml package so that it can be called to impute blocks of variables in mice. The mitml::jomoImpute function provides an interface to the jomo package for multiple imputation of multilevel data https://CRAN.R-project.org/package=jomo. Imputations can be generated using type or formula, which offer different options for model specification.

Usage

```r
mice.impute.jomoImpute(
  data,
  formula,
  type,
)```
m = 1,
silent = TRUE,
format = "imputes",
... )

Arguments

data A data frame containing incomplete and auxiliary variables, the cluster indicator variable, and any other variables that should be present in the imputed datasets.

formula A formula specifying the role of each variable in the imputation model. The basic model is constructed by \texttt{model.matrix}, thus allowing to include derived variables in the imputation model using I(). See \texttt{jomoImpute}.

type An integer vector specifying the role of each variable in the imputation model (see \texttt{jomoImpute})

m The number of imputed data sets to generate. Default is 10.

silent (optional) Logical flag indicating if console output should be suppressed. Default is \texttt{FALSE}.

format A character vector specifying the type of object that should be returned. The default is \texttt{format = "list"}. No other formats are currently supported.

... Other named arguments: \texttt{n.burn}, \texttt{n.iter}, \texttt{group}, \texttt{prior}, \texttt{silent} and others.

Value

A list of imputations for all incomplete variables in the model, that can be stored in the the \texttt{imp} component of the \texttt{mids} object.

Note

The number of imputations \texttt{m} is set to 1, and the function is called \texttt{m} times so that it fits within the \texttt{mice} iteration scheme.

This is a multivariate imputation function using a joint model.

Author(s)

Stef van Buuren, 2018, building on work of Simon Grund, Alexander Robitzsch and Oliver Luedtke (authors of \texttt{mitml} package) and Quartagno and Carpenter (authors of \texttt{jomo} package).

References


See Also

- jomoImpute
- Other multivariate-2l: mice.impute.panImpute()

Examples

```r
# Note: Requires mitml 0.3-5.7
blocks <- list(c("bmi", "chl", "hyp"), "age")
method <- c("jomoImpute", "pmm")
ini <- mice(nhanes, blocks = blocks, method = method, maxit = 0)
pred <- ini$pred
pred["B1", "hyp"] <- -2
imp <- mice(nhanes, blocks = blocks, method = method, pred = pred, maxit = 1)
```

mice.impute.lda

**Imputation by linear discriminant analysis**

**Description**

Imputes univariate missing data using linear discriminant analysis

**Usage**

`mice.impute.lda(y, ry, x, wy = NULL, ...)`

**Arguments**

- `y` Vector to be imputed
- `ry` Logical vector of length `length(y)` indicating the subset `y[ry]` of elements in `y` to which the imputation model is fitted. The `ry` generally distinguishes the observed (TRUE) and missing values (FALSE) in `y`.
- `x` Numeric design matrix with `length(y)` rows with predictors for `y`. Matrix `x` may have no missing values.
- `wy` Logical vector of length `length(y)`. A TRUE value indicates locations in `y` for which imputations are created.
- `...` Other named arguments. Not used.

**Details**

Imputation of categorical response variables by linear discriminant analysis. This function uses the Venables/Ripley functions `lda()` and `predict.lda()` to compute posterior probabilities for each incomplete case, and draws the imputations from this posterior.

This function can be called from within the Gibbs sampler by specifying "lda" in the method argument of `mice()`. This method is usually faster and uses fewer resources than calling the function, but the statistical properties may not be as good (Brand, 1999). `mice.impute.polyreg`
Value

Vector with imputed data, of type factor, and of length \( \text{sum}(wy) \)

Warning

The function does not incorporate the variability of the discriminant weight, so it is not 'proper' in the sense of Rubin. For small samples and rare categories in the \( y \), variability of the imputed data could therefore be underestimated.

Added: SvB June 2009 Tried to include bootstrap, but disabled since bootstrapping may easily lead to constant variables within groups.

Author(s)

Stef van Buuren, Karin Groothuis-Oudshoorn, 2000

References


See Also

mice, link{mice.impute.polyreg}, lda
Other univariate imputation functions: mice.impute.cart(), mice.impute.logreg.boot(), mice.impute.logreg(), mice.impute.mean(), mice.impute.midastouch(), mice.impute.mnar.logreg(), mice.impute.norm.boot(), mice.impute.norm.nob(), mice.impute.norm.predict(), mice.impute.norm(), mice.impute.pmm(), mice.impute.polr() ,mice.impute.polyreg(), mice.impute.quadratic(), mice.impute.rf(), mice.impute.ri()
Arguments

- **y** Vector to be imputed
- **ry** Logical vector of length `length(y)` indicating the subset `y[ry]` of elements in `y` to which the imputation model is fitted. The `ry` generally distinguishes the observed (TRUE) and missing values (FALSE) in `y`.
- **x** Numeric design matrix with `length(y)` rows with predictors for `y`. Matrix `x` may have no missing values.
- **wy** Logical vector of length `length(y)`. A TRUE value indicates locations in `y` for which imputations are created.
- ... Other named arguments.

Details

Imputation for binary response variables by the Bayesian logistic regression model (Rubin 1987, p. 169-170). The Bayesian method consists of the following steps:

1. Fit a logit, and find `(bhat, V(bhat))`  
2. Draw `BETA` from `N(bhat, V(bhat))`  
3. Compute predicted scores for m.d., i.e. `logit-1(X BETA)`  
4. Compare the score to a random (0,1) deviate, and impute.

The method relies on the standard `glm.fit` function. Warnings from `glm.fit` are suppressed. Perfect prediction is handled by the data augmentation method.

Value

Vector with imputed data, same type as `y`, and of length `sum(wy)`

Author(s)

Stef van Buuren, Karin Groothuis-Oudshoorn

References


mice.impute.logreg.boot

Imputation by logistic regression using the bootstrap

Description

Imputes univariate missing data using logistic regression by a bootstrapped logistic regression model. The bootstrap method draws a simple bootstrap sample with replacement from the observed data \( y[ry] \) and \( x[ry,.] \).

Usage

```r
mice.impute.logreg.boot(y, ry, x, wy = NULL, ...)
```

Arguments

- `y` Vector to be imputed
- `ry` Logical vector of length `length(y)` indicating the the subset \( y[ry] \) of elements in \( y \) to which the imputation model is fitted. The `ry` generally distinguishes the observed (TRUE) and missing values (FALSE) in \( y \).
- `x` Numeric design matrix with `length(y)` rows with predictors for \( y \). Matrix \( x \) may have no missing values.
- `wy` Logical vector of length `length(y)`. A TRUE value indicates locations in \( y \) for which imputations are created.
- `...` Other named arguments.

Value

Vector with imputed data, same type as \( y \), and of length \( \text{sum}(wy) \)

Author(s)

Stef van Buuren, Karin Groothuis-Oudshoorn, 2000, 2011

See Also

- `mice`, `glm`, `glm.fit`
- Other univariate imputation functions: `mice.impute.cart()`, `mice.impute.lda()`, `mice.impute.logreg.boot()`, `mice.impute.mean()`, `mice.impute.midastouch()`, `mice.impute.mnar.logreg()`, `mice.impute.norm.boot()`, `mice.impute.norm.nob()`, `mice.impute.norm.predict()`, `mice.impute.norm()`, `mice.impute.pmm()`, `mice.impute.polr()`, `mice.impute.polyreg()`, `mice.impute.quadratic()`, `mice.impute.rf()`, `mice.impute.ri()`
mice.impute.mean

References

See Also

- `mice`, `glm`, `glm.fit`
- Other univariate imputation functions: `mice.impute.cart()`, `mice.impute.lda()`, `mice.impute.logreg()`, `mice.impute.mean()`, `mice.impute.midastouch()`, `mice.impute.mnar.logreg()`, `mice.impute.norm.boot()`, `mice.impute.norm.nob()`, `mice.impute.norm.predict()`, `mice.impute.norm.pmm()`, `mice.impute.polr()`, `mice.impute.polyreg()`, `mice.impute.quadratic()`, `mice.impute.rf()`, `mice.impute.ri()`

---

### Description
Imputes the arithmetic mean of the observed data

### Usage

```
mice.impute.mean(y, ry, x = NULL, wy = NULL, ...)
```

### Arguments

- **y**: Vector to be imputed
- **ry**: Logical vector of length `length(y)` indicating the subset `y[ry]` of elements in `y` to which the imputation model is fitted. The `ry` generally distinguishes the observed (TRUE) and missing values (FALSE) in `y`.
- **x**: Numeric design matrix with `length(y)` rows with predictors for `y`. Matrix `x` may have no missing values.
- **wy**: Logical vector of length `length(y)`. A TRUE value indicates locations in `y` for which imputations are created.
- **...**: Other named arguments.

### Value
Vector with imputed data, same type as `y`, and of length `sum(wy)`

### Warning
Imputing the mean of a variable is almost never appropriate. See Little and Rubin (2002, p. 61-62) or Van Buuren (2012, p. 10-11)
References


See Also

- `mice`
- `mean`

Other univariate imputation functions: `mice.impute.cart()`, `mice.impute.lda()`, `mice.impute.logreg.boot()`, `mice.impute.logreg()`, `mice.impute.midasouch()`, `mice.impute.mnarl.logreg()`, `mice.impute.norm.boot()`, `mice.impute.norm.nob()`, `mice.impute.norm.predict()`, `mice.impute.norm()`, `mice.impute.pmm()`, `mice.impute.polr()`, `mice.impute.polyreg()`, `mice.impute.quadratic()`, `mice.impute.rf()`, `mice.impute.ri()`

---

**mice.impute.midastouch**

*Imputation by predictive mean matching with distance aided donor selection*

Description

Imputes univariate missing data using predictive mean matching.

Usage

```r
mice.impute.midastouch(
  y,
  ry,
  x,
  wy = NULL,
  ridge = 1e-05,
  midas.kappa = NULL,
  output = TRUE,
  neff = NULL,
  debug = NULL,
  ...
)
```

Arguments

- `y` Vector to be imputed
**Details**

Imputation of \( y \) by predictive mean matching, based on Rubin (1987, p. 168, formulas a and b) and Siddique and Belin 2008. The procedure is as follows:

1. Draw a bootstrap sample from the donor pool.
2. Estimate a beta matrix on the bootstrap sample by the leave one out principle.
3. Compute type II predicted values for \( y_{obs} \) (nob \( s \times 1 \)) and \( y_{mis} \) (mis \( s \times \) nob \( s \)).
4. Calculate the distance between all \( y_{obs} \) and the corresponding \( y_{mis} \).
5. Convert the distances in drawing probabilities.
6. For each recipient draw a donor from the entire pool while considering the probabilities from the model.
7. Take its observed value in \( y \) as the imputation.

**Value**

Vector with imputed data, same type as \( y \), and of length \( \sum(wy) \).
Author(s)
Philipp Gaffert, Florian Meinfelder, Volker Bosch 2015

References


See Also
Other univariate imputation functions: mice.impute.cart(), mice.impute.lda(), mice.impute.logreg.boot(), mice.impute.logreg(), mice.impute.mean(), mice.impute.mnar.logreg(), mice.impute.norm.boot(), mice.impute.norm.nob(), mice.impute.norm.predict(), mice.impute.norm(), mice.impute.pmm(), mice.impute.polr(), mice.impute.polyreg(), mice.impute.quadratic(), mice.impute.rf(), mice.impute.ri()

Examples
# do default multiple imputation on a numeric matrix
imp <- mice(nhanes, method = "midastouch")
imp

# list the actual imputations for BMI
imp$imp$bmi

# first completed data matrix
complete(imp)

# imputation on mixed data with a different method per column
mice(nhanes2, method = c("sample", "midastouch", "logreg", "norm"))
mice.impute.mnar.logreg

Imputation under MNAR mechanism by NARFCS

Description

Imputes univariate data under a user-specified MNAR mechanism by linear or logistic regression and NARFCS. Sensitivity analysis under different model specifications may shed light on the impact of different MNAR assumptions on the conclusions.

Usage

mice.impute.mnar.logreg(y, ry, x, wy = NULL, ums = NULL, umx = NULL, ...)
mice.impute.mnar.norm(y, ry, x, wy = NULL, ums = NULL, umx = NULL, ...)

Arguments

y Vector to be imputed
ry Logical vector of length length(y) indicating the subset y[ry] of elements in y to which the imputation model is fitted. The ry generally distinguishes the observed (TRUE) and missing values (FALSE) in y.
x Numeric design matrix with length(y) rows with predictors for y. Matrix x may have no missing values.
wy Logical vector of length length(y). A TRUE value indicates locations in y for which imputations are created.
ums A string containing the specification of the unidentifiable part of the imputation model (the "unidentifiable model specification"), that is, the desired δ-adjustment (offset) as a function of other variables and values for the corresponding deltas (sensitivity parameters). See details.
umx An auxiliary data matrix containing variables that do not appear in the identifiable part of the imputation procedure but that have been specified via ums as being predictors in the unidentifiable part of the imputation model. See details.
...
Other named arguments.

Details

This function imputes data that are thought to be Missing Not at Random (MNAR) by the NARFCS method. The NARFCS procedure (Leacy, 2016; Tompsett et al, 2018) generalises the so-called δ-adjustment sensitivity analysis method of Van Buuren, Boshuizen & Knook (1999) to the case with multiple incomplete variables within the FCS framework. In practical terms, the NARFCS procedure shifts the imputations drawn at each iteration of mice by a user-specified quantity that can vary across subjects, to reflect systematic departures of the missing data from the data distribution imputed under MAR.
Specification of the NARFCS model is done by the `blots` argument of `mice()`. The `blots` parameter is a named list. For each variable to be imputed by `mice.impute.mnar.norm()` or `mice.impute.mnar.logreg()` the corresponding element in `blots` is a list with at least one argument `ums` and, optionally, a second argument `umx`. For example, the high-level call might like something like `mice(nhanes[,c(2,4)],method = c("pmm","mnar.norm"),blots = list(chl = list(ums = "-3+2*bmi")))`.

The `ums` parameter is required, and might look like this: ""-4+1*Y". The `ums` specification must have the following characteristics:

1. A single term corresponding to the intercept (constant) term, not multiplied by any variable name, must be included in the expression;
2. Each term in the expression (corresponding to the intercept or a predictor variable) must be separated by either a "+" or "-" sign, depending on the sign of the sensitivity parameter;
3. Within each non-intercept term, the sensitivity parameter value comes first and the predictor variable comes second, and these must be separated by a "*" sign;
4. For categorical predictors, for example a variable `Z` with K + 1 categories ("Cat0","Cat1",...,"CatK"). K category-specific terms are needed, and those not in `umx` (see below) must be specified by concatenating the variable name with the name of the category (e.g. `ZCat1`) as this is how they are named in the design matrix (argument `x`) passed to the univariate imputation function. An example is "2+1*ZCat1-3*ZCat2".

If given, the `umx` specification must have the following characteristics:

1. It contains only complete variables, with no missing values;
2. It is a numeric matrix. In particular, categorical variables must be represented as dummy indicators with names corresponding to what is used in `ums` to refer to the category-specific terms (see above);
3. It has the same number of rows as the `data` argument passed on to the main `mice` function;
4. It does not contain variables that were already predictors in the identifiable part of the model for the variable under imputation.

Limitation: The present implementation can only condition on variables that appear in the identifiable part of the imputation model (`x`) or in complete auxiliary variables passed on via the `umx` argument. It is not possible to specify models where the offset depends on incomplete auxiliary variables.

For an MNAR alternative see also `mice.impute.ri`.

Value

Vector with imputed data, same type as `y`, and of length `sum(wy)`

Author(s)

References


See Also

Other univariate imputation functions: mice.impute.cart(), mice.impute.lda(), mice.impute.logreg.boot(), mice.impute.logreg(), mice.impute.mean(), mice.impute.midastouch(), mice.impute.norm.boot(), mice.impute.norm.nob(), mice.impute.norm.predict(), mice.impute.norm(), mice.impute.pmm(), mice.impute.polr(), mice.impute.polyreg(), mice.impute.quadratic(), mice.impute.rf(), mice.impute.ri()

Examples

# 1: Example with no auxiliary data: only pass unidentifiable model specification (ums)

# Specify argument to pass on to mnar imputation functions via "blots" argument
mnar.blot <- list(X = list(ums = "-4"), Y = list(ums = "2+1*ZCat1-3*ZCat2"))

# Run NARFCS by using mnar imputation methods and passing argument via blots
impNARFCS <- mice(mnar_demo_data, 
method = c("mnar.logreg", "mnar.norm", ""), 
blots = mnar.blot, seed = 234235, print = FALSE)

# Obtain MI results: Note they coincide with those from old version at
# https://github.com/moreno-betancur/NARFCS
pool(with(impNARFCS, lm(Y ~ X + Z)))$pooled$estimate

# 2: Example passing also auxiliary data to MNAR procedure (umx)

# Assumptions:
# - Auxiliary data are complete, no missing values
# - Auxiliary data are a numeric matrix
# - Auxiliary data have same number of rows as x
# - Auxiliary data have no overlapping variable names with x

# Specify argument to pass on to mnar imputation functions via "blots" argument
aux <- matrix(0:1, nrow = nrow(mnar_demo_data))
dimnames(aux) <- list(NULL, "even")
mnar.blot <- list(
X = list(ums = "-4"),
Y = list(ums = "2+1*ZCat1-3*ZCat2+0.5*even", umx = aux))

# Run NARFCS by using mnar imputation methods and passing argument via blots
impNARFCS <- mice(mnar_demo_data,
   method = c("mnar.logreg", "mnar.norm", ""),
   blots = mnar.blot, seed = 234235, print = FALSE
)

# Obtain MI results: As expected they differ (slightly) from those
# from old version at https://github.com/moreno-betancur/NARFCS
pool(with(impNARFCS, lm(Y ~ X + Z)))$pooled$estimate

mice.impute.norm

**Imputation by Bayesian linear regression**

**Description**

Calculates imputations for univariate missing data by Bayesian linear regression, also known as the normal model.

**Usage**

mice.impute.norm(y, ry, x, wy = NULL, ...)

**Arguments**

- **y** Vector to be imputed
- **ry** Logical vector of length length(y) indicating the the subset y[ry] of elements in y to which the imputation model is fitted. The ry generally distinguishes the observed (TRUE) and missing values (FALSE) in y.
- **x** Numeric design matrix with length(y) rows with predictors for y. Matrix x may have no missing values.
- **wy** Logical vector of length length(y). A TRUE value indicates locations in y for which imputations are created.
- **...** Other named arguments.

**Details**

Imputation of y by the normal model by the method defined by Rubin (1987, p. 167). The procedure is as follows:

1. Calculate the cross-product matrix \( S = X'_{\text{obs}}X_{\text{obs}} \).
2. Calculate \( V = (S + \text{diag}(S)\kappa)^{-1} \), with some small ridge parameter \( \kappa \).
3. Calculate regression weights \( \hat{\beta} = V X'_{\text{obs}}y_{\text{obs}} \).
4. Draw a random variable \( \hat{\gamma} \sim \chi^2_\nu \) with \( \nu = n_1 - q \).
5. Calculate \( \hat{\sigma}^2 = (y_{\text{obs}} - X_{\text{obs}}\hat{\beta})'(y_{\text{obs}} - X_{\text{obs}}\hat{\beta})/\hat{\gamma} \).
6. Draw \( q \) independent \( N(0, 1) \) variates in vector \( \hat{z}_1 \).
7. Calculate \( V^{1/2} \) by Cholesky decomposition.
8. Calculate \( \hat{\beta} = \hat{\beta} + \sigma \hat{z}_1 V^{1/2}. \)
9. Draw \( n_0 \) independent \( N(0, 1) \) variates in vector \( \hat{z}_2. \)
10. Calculate the \( n_0 \) values \( y_{imp} = X_{mis} \hat{\beta} + \hat{z}_2 \sigma. \)

Using \text{mice.impute.norm} for all columns emulates Schafer’s NORM method (Schafer, 1997).

**Value**

Vector with imputed data, same type as \( y \), and of length \( \text{sum}(wy) \)

**Author(s)**

Stef van Buuren, Karin Groothuis-Oudshoorn

**References**


**See Also**

Other univariate imputation functions: \text{mice.impute.cart()}, \text{mice.impute.lda()}, \text{mice.impute.logreg.boot()}, \text{mice.impute.logreg()}, \text{mice.impute.mean()}, \text{mice.impute.midastouch()}, \text{mice.impute.mnar.logreg()}, \text{mice.impute.norm.boot()}, \text{mice.impute.norm.nob()}, \text{mice.impute.norm.predict()}, \text{mice.impute.pmm()}, \text{mice.impute.polr()}, \text{mice.impute.polyreg()}, \text{mice.impute.quadratic()}, \text{mice.impute.rf()}, \text{mice.impute.ri()}

**Description**

Imputes univariate missing data using linear regression with bootstrap

**Usage**

\text{mice.impute.norm.boot}(y, ry, x, wy = \text{NULL}, ...)

**Arguments**

\begin{itemize}
\item \textbf{y} \hspace{1cm} Vector to be imputed
\item \textbf{ry} \hspace{1cm} Logical vector of length \text{length}(y) indicating the the subset \( y[\text{ry}] \) of elements in \( y \) to which the imputation model is fitted. The \( ry \) generally distinguishes the observed (TRUE) and missing values (FALSE) in \( y \).
\item \textbf{x} \hspace{1cm} Numeric design matrix with \text{length}(y) rows with predictors for \( y \). Matrix \( x \) may have no missing values.
\end{itemize}
**mice.impute.norm.nob**

wy Logical vector of length `length(y)`. A TRUE value indicates locations in `y` for which imputations are created.

... Other named arguments.

**Details**

Draws a bootstrap sample from `x[ry,]` and `y[ry]`, calculates regression weights and imputes with normal residuals.

**Value**

Vector with imputed data, same type as `y`, and of length `sum(wy)`

**Author(s)**

Gerko Vink, Stef van Buuren, 2018

**References**


**See Also**

Other univariate imputation functions: `mice.impute.cart()`, `mice.impute.lda()`, `mice.impute.logreg.boot()`, `mice.impute.logreg()`, `mice.impute.mean()`, `mice.impute.midastouch()`, `mice.impute.mnar.logreg()`, `mice.impute.norm.nob()`, `mice.impute.norm.predict()`, `mice.impute.norm()`, `mice.impute.pmm()`, `mice.impute.polr()`, `mice.impute.polyreg()`, `mice.impute.quadratic()`, `mice.impute.rf()`, `mice.impute.ri()`

---

**Description**

Imputes univariate missing data using linear regression analysis without accounting for the uncertainty of the model parameters.

**Usage**

```r
mice.impute.norm.nob(y, ry, x, wy = NULL, ...)
```
Arguments

- **y**: Vector to be imputed
- **ry**: Logical vector of length `length(y)` indicating the the subset `y[ry]` of elements in `y` to which the imputation model is fitted. The `ry` generally distinguishes the observed (TRUE) and missing values (FALSE) in `y`.
- **x**: Numeric design matrix with `length(y)` rows with predictors for `y`. Matrix `x` may have no missing values.
- **wy**: Logical vector of length `length(y)`. A TRUE value indicates locations in `y` for which imputations are created.
- **...**: Other named arguments.

Details

This function creates imputations using the spread around the fitted linear regression line of `y` given `x`, as fitted on the observed data.

This function is provided mainly to allow comparison between proper (e.g., as implemented in `mice.impute.norm`) and improper (this function) normal imputation methods.

For large data, having many rows, differences between proper and improper methods are small, and in those cases one may opt for speed by using `mice.impute.norm.nob`.

Value

Vector with imputed data, same type as `y`, and of length `sum(wy)`

Warning

The function does not incorporate the variability of the regression weights, so it is not ‘proper’ in the sense of Rubin. For small samples, variability of the imputed data is therefore underestimated.

Author(s)

Gerko Vink, Stef van Buuren, Karin Groothuis-Oudshoorn, 2018

References


See Also

`mice`, `mice.impute.norm`

Other univariate imputation functions: `mice.impute.cart()`, `mice.impute.lda()`, `mice.impute.logreg.boot()`, `mice.impute.logreg()`, `mice.impute.mean()`, `mice.impute.midas.boot()`, `mice.impute.mnar.logreg()`, `mice.impute.norm.boot()`, `mice.impute.norm.predict()`, `mice.impute.norm()`, `mice.impute.pmm()`.
mice.impute.norm.predict

Imputation by linear regression through prediction

Description

Imputes the "best value" according to the linear regression model, also known as regression imputation.

Usage

mice.impute.norm.predict(y, ry, x, wy = NULL, ...)

Arguments

y Vector to be imputed
ry Logical vector of length length(y) indicating the the subset y[ry] of elements in y to which the imputation model is fitted. The ry generally distinguishes the observed (TRUE) and missing values (FALSE) in y.
x Numeric design matrix with length(y) rows with predictors for y. Matrix x may have no missing values.
wy Logical vector of length length(y). A TRUE value indicates locations in y for which imputations are created.
... Other named arguments.

Details

Calculates regression weights from the observed data and returns predicted values to as imputations. This method is known as regression imputation.

Value

Vector with imputed data, same type as y, and of length sum(wy)

Warning

THIS METHOD SHOULD NOT BE USED FOR DATA ANALYSIS. This method is seductive because it imputes the most likely value according to the model. However, it ignores the uncertainty of the missing values and artificially amplifies the relations between the columns of the data. Application of richer models having more parameters does not help to evade these issues. Stochastic regression methods, like mice.impute.pmm or mice.impute.norm, are generally preferred.

At best, prediction can give reasonable estimates of the mean, especially if normality assumptions are plausible. See Little and Rubin (2002, p. 62-64) or Van Buuren (2012, p. 11-13, p. 45-46) for a discussion of this method.
mice.impute.panImpute

Impute multilevel missing data using pan

Description
This function is a wrapper around the panImpute function from the mitml package so that it can be called to impute blocks of variables in mice. The mitml::panImpute function provides an interface to the pan package for multiple imputation of multilevel data (Schafer & Yucel, 2002). Imputations can be generated using type or formula, which offer different options for model specification.

Usage
mice.impute.panImpute(
  data,
  formula,
  type,
  m = 1,
  silent = TRUE,
  format = "imputes",
  ...
)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>data</td>
<td>A data frame containing incomplete and auxiliary variables, the cluster indicator variable, and any other variables that should be present in the imputed datasets.</td>
</tr>
<tr>
<td>formula</td>
<td>A formula specifying the role of each variable in the imputation model. The basic model is constructed by model.matrix, thus allowing to include derived variables in the imputation model using I(). See panImpute.</td>
</tr>
</tbody>
</table>
type  An integer vector specifying the role of each variable in the imputation model (see panImpute)
m  The number of imputed data sets to generate.
silent  (optional) Logical flag indicating if console output should be suppressed. Default is to FALSE.
format  A character vector specifying the type of object that should be returned. The default is format = "list". No other formats are currently supported.
...  Other named arguments: n.burn, n.iter, group, prior, silent and others.

Value

A list of imputations for all incomplete variables in the model, that can be stored in the imp component of the mids object.

Note

The number of imputations m is set to 1, and the function is called m times so that it fits within the mice iteration scheme.

This is a multivariate imputation function using a joint model.

Author(s)

Stef van Buuren, 2018, building on work of Simon Grund, Alexander Robitzsch and Oliver Luedtke (authors of mitml package) and Joe Schafer (author of pan package).

References


See Also

panImpute

Other multivariate-2l: mice.impute.jomoImpute()

Examples

blocks <- list(c("bmi", "chl", "hyp"), "age")
method <- c("panImpute", "pmm")
ini <- mice(nhanes, blocks = blocks, method = method, maxit = 0)
pred <- ini$pred
pred["B1", "hyp"] <- -2
imp <- mice(nhanes, blocks = blocks, method = method, pred = pred, maxit = 1)
mice.impute.passive  Passive imputation

Description

Calculate new variable during imputation

Usage

mice.impute.passive(data, func)

Arguments

data  A data frame
func  A formula specifying the transformations on data

Details

Passive imputation is a special internal imputation function. Using this facility, the user can specify, at any point in the mice Gibbs sampling algorithm, a function on the imputed data. This is useful, for example, to compute a cubic version of a variable, a transformation like \( Q = \frac{W}{H^2} \) based on two variables, or a mean variable like \( \frac{x_1+x_2+x_3}{3} \). The so derived variables might be used in other places in the imputation model. The function allows to dynamically derive virtually any function of the imputed data at virtually any time.

Value

The result of applying formula

Author(s)

Stef van Buuren, Karin Groothuis-Oudshoorn, 2000

References


See Also

mice
mice.impute.pmm

Imputation by predictive mean matching

Description

Imputation by predictive mean matching

Usage

mice.impute.pmm(
  y,
  ry,
  x,
  wy = NULL,
  donors = 5L,
  matchtype = 1L,
  ridge = 1e-05,
  use.matcher = FALSE,
  ...
)

Arguments

y Vector to be imputed

ry Logical vector of length length(y) indicating the subset y[ry] of elements in y to which the imputation model is fitted. The ry generally distinguishes the observed (TRUE) and missing values (FALSE) in y.

x Numeric design matrix with length(y) rows with predictors for y. Matrix x may have no missing values.

wy Logical vector of length length(y). A TRUE value indicates locations in y for which imputations are created.

donors The size of the donor pool among which a draw is made. The default is donors = 5L. Setting donors = 1L always selects the closest match, but is not recommended. Values between 3L and 10L provide the best results in most cases (Morris et al, 2015).

matchtype Type of matching distance. The default choice (matchtype = 1L) calculates the distance between the predicted value of yobs and the drawn values of ymis (called type-1 matching). Other choices are matchtype = 0L (distance between predicted values) and matchtype = 2L (distance between drawn values).

ridge The ridge penalty used in .norm.draw() to prevent problems with multicollinearity. The default is ridge = 1e-05, which means that 0.01 percent of the diagonal is added to the cross-product. Larger ridges may result in more biased estimates. For highly noisy data (e.g. many junk variables), set ridge = 1e-06 or even lower to reduce bias. For highly collinear data, set ridge = 1e-04 or higher.
**use.matcher** Logical. Set `use.matcher = TRUE` to specify the C function `matcher()`, the now deprecated matching function that was default in versions 2.22 (June 2014) to 3.11.7 (Oct 2020). Since version 3.12.0 `mice()` uses the much faster `matchindex` C function. Use the deprecated `matcher` function only for exact reproduction.

... Other named arguments.

**Details**

Imputation of \( y \) by predictive mean matching, based on van Buuren (2012, p. 73). The procedure is as follows:

1. Calculate the cross-product matrix \( S = X'_{\text{obs}}X_{\text{obs}} \).
2. Calculate \( V = (S + \text{diag}(S)\kappa)^{-1} \), with some small ridge parameter \( \kappa \).
3. Calculate regression weights \( \hat{\beta} = VX'_{\text{obs}}y_{\text{obs}} \).
4. Draw \( q \) independent \( N(0, 1) \) variates in vector \( \hat{z}_1 \).
5. Calculate \( V^{1/2} \) by Cholesky decomposition.
6. Calculate \( \hat{\beta} = \hat{\beta} + \hat{\sigma}\hat{z}_1V^{1/2} \).
7. Calculate \( \hat{\eta}(i,j) = |X_{\text{obs},i} - X_{\text{mis},j}| \hat{\beta} \) with \( i = 1, \ldots, n_1 \) and \( j = 1, \ldots, n_0 \).
8. Construct \( n_0 \) sets \( Z_j \), each containing \( d \) candidate donors, from \( Y_{\text{obs}} \) such that \( \sum_d \hat{\eta}(i,j) \) is minimum for all \( j = 1, \ldots, n_0 \). Break ties randomly.
9. Draw one donor \( i_j \) from \( Z_j \) randomly for \( j = 1, \ldots, n_0 \).
10. Calculate imputations \( \hat{y}_j = y_{i_j} \) for \( j = 1, \ldots, n_0 \).

The name **predictive mean matching** was proposed by Little (1988).

**Value**

Vector with imputed data, same type as \( y \), and of length \( \text{sum}(w_y) \)

**Author(s)**

Stef van Buuren, Karin Groothuis-Oudshoorn

**References**


mice.impute.polr

Imputation of ordered data by polytomous regression

Description

Imputes missing data in a categorical variable using polytomous regression.
Usage

mice.impute.polr(
    y, ry, x,
    wy = NULL,
    nnet.maxit = 100,
    nnet.trace = FALSE,
    nnet.MaxNWts = 1500,
    polr.to.loggedEvents = FALSE,
    ...
)

Arguments

y  Vector to be imputed
ry  Logical vector of length length(y) indicating the the subset y[ry] of elements in y to which the imputation model is fitted. The ry generally distinguishes the observed (TRUE) and missing values (FALSE) in y.
x  Numeric design matrix with length(y) rows with predictors for y. Matrix x may have no missing values.
wy  Logical vector of length length(y). A TRUE value indicates locations in y for which imputations are created.
nnet.maxit  Tuning parameter for nnet().
nnet.trace  Tuning parameter for nnet().
nnet.MaxNWts  Tuning parameter for nnet().
polr.to.loggedEvents  A logical indicating whether each fallback to the multinom() function should be written to loggedEvents. The default is FALSE.
...  Other named arguments.

Details

The function mice.impute.polr() imputes for ordered categorical response variables by the proportional odds logistic regression (polr) model. The function repeatedly applies logistic regression on the successive splits. The model is also known as the cumulative link model.

By default, ordered factors with more than two levels are imputed by mice.impute.polr.

The algorithm of mice.impute.polr uses the function polr() from the MASS package.

In order to avoid bias due to perfect prediction, the algorithm augment the data according to the method of White, Daniel and Royston (2010).

The call to polr might fail, usually because the data are very sparse. In that case, multinom is tried as a fallback. If the local flag polr.to.loggedEvents is set to TRUE, a record is written to the loggedEvents component of the mids object. Use mice(data,polr.to.loggedEvents = TRUE) to set the flag.
mice.impute.polyreg

Value

Vector with imputed data, same type as y, and of length \( \text{sum}(w_y) \)

Note

In December 2019 Simon White alerted that the polr could always fail silently. I can confirm this behaviour for versions mice 3.0.0 -mice 3.6.6, so any method requests for polr in these versions were in fact handled by multinom. See https://github.com/amices/mice/issues/206 for details.

Author(s)

Stef van Buuren, Karin Groothuis-Oudshoorn, 2000-2010

References


See Also

mice, multinom, polr

Other univariate imputation functions: mice.impute.cart(), mice.impute.lda(), mice.impute.logreg.boot(), mice.impute.logreg(), mice.impute.mean(), mice.impute.midastouch(), mice.impute.mnar.logreg(), mice.impute.norm.boot(), mice.impute.norm.nob(), mice.impute.norm.predict(), mice.impute.norm(), mice.impute.pmm(), mice.impute.polyreg(), mice.impute.quadratic(), mice.impute.rf(), mice.impute.pmm()

mice.impute.polyreg: Imputation of unordered data by polytomous regression

Description

Imputes missing data in a categorical variable using polytomous regression
Usage

mice.impute.polyreg(
  y,
  ry,
  x,
  wy = NULL,
  nnet.maxit = 100,
  nnet.trace = FALSE,
  nnet.MaxNWts = 1500,
  ...
)

Arguments

y  Vector to be imputed
ry Logical vector of length length(y) indicating the subset y[ry] of elements in y to which the imputation model is fitted. The ry generally distinguishes the observed (TRUE) and missing values (FALSE) in y.
x Numeric design matrix with length(y) rows with predictors for y. Matrix x may have no missing values.
wy Logical vector of length length(y). A TRUE value indicates locations in y for which imputations are created.
nnet.maxit Tuning parameter for nnet().
nnet.trace Tuning parameter for nnet().
nnet.MaxNWts Tuning parameter for nnet().
... Other named arguments.

Details

The function mice.impute.polyreg() imputes categorical response variables by the Bayesian polytomous regression model. See J.P.L. Brand (1999), Chapter 4, Appendix B.

By default, unordered factors with more than two levels are imputed by mice.impute.polyreg(). The method consists of the following steps:

1. Fit categorical response as a multinomial model
2. Compute predicted categories
3. Add appropriate noise to predictions

The algorithm of mice.impute.polyreg uses the function multinom() from the nnet package.

In order to avoid bias due to perfect prediction, the algorithm augment the data according to the method of White, Daniel and Royston (2010).

Value

Vector with imputed data, same type as y, and of length sum(wy)
**mice.impute.quadratic**

**Author(s)**

Stef van Buuren, Karin Groothuis-Oudshoorn, 2000-2010

**References**


**See Also**

`mice, multinom, polr`

Other univariate imputation functions: `mice.impute.cart()`, `mice.impute.lda()`, `mice.impute.logreg.boot()`, `mice.impute.logreg()`, `mice.impute.mean()`, `mice.impute.midastouch()`, `mice.impute.mnar.logreg()`, `mice.impute.norm.boot()`, `mice.impute.norm.nob()`, `mice.impute.norm.predict()`, `mice.impute.norm()`, `mice.impute.pmm()`, `mice.impute.polr()`, `mice.impute.quadratic()`, `mice.impute.rf()`, `mice.impute.ri()`

**Description**

Imputes incomplete variable that appears as both main effect and quadratic effect in the complete-data model.

**Usage**

`mice.impute.quadratic(y, ry, x, wy = NULL, ...)`

**Arguments**

- `y` Vector to be imputed
- `ry` Logical vector of length `length(y)` indicating the the subset `y[ry]` of elements in `y` to which the imputation model is fitted. The `ry` generally distinguishes the observed (TRUE) and missing values (FALSE) in `y`.
- `x` Numeric design matrix with `length(y)` rows with predictors for `y`. Matrix `x` may have no missing values.
- `wy` Logical vector of length `length(y)`. A TRUE value indicates locations in `y` for which imputations are created.
- `...` Other named arguments.
Details

This function implements the "polynomial combination" method. First, the polynomial combination \( Z = Y \beta_1 + Y^2 \beta_2 \) is formed. \( Z \) is imputed by predictive mean matching, followed by a decomposition of the imputed data \( Z \) into components \( Y \) and \( Y^2 \). See Van Buuren (2012, pp. 139-141) and Vink et al (2012) for more details. The method ensures that 1) the imputed data for \( Y \) and \( Y^2 \) are mutually consistent, and 2) that provides unbiased estimates of the regression weights in a complete-data linear regression that use both \( Y \) and \( Y^2 \).

Value

Vector with imputed data, same type as \( y \), and of length \( \text{sum}(w) \)

Note

There are two situations to consider. If only the linear term \( Y \) is present in the data, calculate the quadratic term \( YY \) after imputation. If both the linear term \( Y \) and the quadratic term \( YY \) are variables in the data, then first impute \( Y \) by calling \texttt{mice.impute.quadratic()} on \( Y \), and then impute \( YY \) by passive imputation as \texttt{meth["YY"] <- ~I(Y^2)}. See example section for details. Generally, we would like \( YY \) to be present in the data if we need to preserve quadratic relations between \( YY \) and any third variables in the multivariate incomplete data that we might wish to impute.

Author(s)

Gerko Vink (University of Utrecht), <g.vink@uu.nl>

See Also


Other univariate imputation functions: \texttt{mice.impute.cart()}, \texttt{mice.impute.lda()}, \texttt{mice.impute.logreg.boot()}, \texttt{mice.impute.logreg()}, \texttt{mice.impute.mean()}, \texttt{mice.impute.midastouch()}, \texttt{mice.impute.mnar.logreg()}, \texttt{mice.impute.norm.boot()}, \texttt{mice.impute.norm.nob()}, \texttt{mice.impute.norm.predict()}, \texttt{mice.impute.norm()}, \texttt{mice.impute.pmm()}, \texttt{mice.impute.polr()}, \texttt{mice.impute.polyreg()}, \texttt{mice.impute.rf()}, \texttt{mice.impute.ri()}

Examples

```r
require(lattice)

# Create Data
B1 <- .5
B2 <- .5
X <- rnorm(1000)
XX <- X^2
e <- rnorm(1000, 0, 1)
Y <- B1 * X + B2 * XX + e
dat <- data.frame(x = X, xx = XX, y = Y)
```
# Impose 25 percent MCAR Missingness
dat[0 == rbinom(1000, 1, 1 - .25), 1:2] <- NA

# Prepare data for imputation
ini <- mice(dat, maxit = 0)
meth <- c("quadratic", "-I(x^2)", "")
pred <- ini$pred
pred[, "xx"] <- 0

# Impute data
imp <- mice(dat, meth = meth, pred = pred)

# Pool results
pool(with(imp, lm(y ~ x + xx)))

# Plot results
stripplot(imp)
plot(dat$x, dat$xx, col = mdc(1), xlab = "x", ylab = "xx")
cmp <- complete(imp)
points(cmp$x[is.na(dat$x)], cmp$xx[is.na(dat$x)], col = mdc(2))

---

mice.impute.rf  
Imputation by random forests

### Description

Imputes univariate missing data using random forests.

### Usage

mice.impute.rf(y, ry, x, wy = NULL, ntree = 10, ...)

### Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>y</td>
<td>Vector to be imputed</td>
</tr>
<tr>
<td>ry</td>
<td>Logical vector of length length(y) indicating the subset y[ry] of elements in y to which the imputation model is fitted. The ry generally distinguishes the observed (TRUE) and missing values (FALSE) in y.</td>
</tr>
<tr>
<td>x</td>
<td>Numeric design matrix with length(y) rows with predictors for y. Matrix x may have no missing values.</td>
</tr>
<tr>
<td>wy</td>
<td>Logical vector of length length(y). A TRUE value indicates locations in y for which imputations are created.</td>
</tr>
<tr>
<td>ntree</td>
<td>The number of trees to grow. The default is 10.</td>
</tr>
<tr>
<td>...</td>
<td>Other named arguments passed down to mice:::install.on.demand(), randomForest::randomForest() and randomForest::randomForest.default().</td>
</tr>
</tbody>
</table>
Details

Imputation of \( y \) by random forests. The method calls \texttt{random Forrest()} which implements Breiman’s random forest algorithm (based on Breiman and Cutler’s original Fortran code) for classification and regression. See Appendix A.1 of Doove et al. (2014) for the definition of the algorithm used.

Value

Vector with imputed data, same type as \( y \), and of length \( \text{sum}(wy) \)

Note

An alternative implementation was independently developed by Shah et al (2014). This were available as functions \texttt{CALIBERrfimpute::mice.impute.rfcat} and \texttt{CALIBERrfimpute::mice.impute.rfcont} (now archived). Simulations by Shah (Feb 13, 2014) suggested that the quality of the imputation for 10 and 100 trees was identical, so mice 2.22 changed the default number of trees from \( ntree = 100 \) to \( ntree = 10 \).

Author(s)

Lisa Doove, Stef van Buuren, Elise Dusseldorp, 2012

References


See Also

\texttt{mice}, \texttt{mice.impute.cart}, \texttt{randomForest}

Other univariate imputation functions: \texttt{mice.impute.cart()}, \texttt{mice.impute.lda()}, \texttt{mice.impute.logreg.boot()}, \texttt{mice.impute.logreg()}, \texttt{mice.impute.mean()}, \texttt{mice.impute.midastouch()}, \texttt{mice.impute.mnar.logreg()}, \texttt{mice.impute.norm.boot()}, \texttt{mice.impute.norm.nob()}, \texttt{mice.impute.norm.predict()}, \texttt{mice.impute.norm()}, \texttt{mice.impute.pmm()}, \texttt{mice.impute.polr()}, \texttt{mice.impute.polyreg()}, \texttt{mice.impute.quadratic()}, \texttt{mice.impute.ri()}

Examples

```
library("lattice")

imp <- mice(nhanes2, meth = "rf", ntree = 3)
plot(imp)
```
mice.impute.ri

Imputation by the random indicator method for nonignorable data

Description

Imputes nonignorable missing data by the random indicator method.

Usage

mice.impute.ri(y, ry, x, wy = NULL, ri.maxit = 10, ...)

Arguments

y Vector to be imputed
ry Logical vector of length length(y) indicating the subset y[ry] of elements in y to which the imputation model is fitted. The ry generally distinguishes the observed (TRUE) and missing values (FALSE) in y.
x Numeric design matrix with length(y) rows with predictors for y. Matrix x may have no missing values.
wy Logical vector of length length(y). A TRUE value indicates locations in y for which imputations are created.
ri.maxit Number of inner iterations
... Other named arguments.

Details

The random indicator method estimates an offset between the distribution of the observed and missing data using an algorithm that iterates over the response and imputation models.

This routine assumes that the response model and imputation model have same predictors.

For an MNAR alternative see also mice.impute.mnar.logreg.

Value

Vector with imputed data, same type as y, and of length sum(wy)

Author(s)

Shahab Jolani (University of Utrecht)

References

mice.impute.sample

Imputation by simple random sampling

Description
Imputes a random sample from the observed y data

Usage
mice.impute.sample(y, ry, x = NULL, wy = NULL, ...)

Arguments
- y: Vector to be imputed
- ry: Logical vector of length length(y) indicating the subset y[ry] of elements in y to which the imputation model is fitted. The ry generally distinguishes the observed (TRUE) and missing values (FALSE) in y.
- x: Numeric design matrix with length(y) rows with predictors for y. Matrix x may have no missing values.
- wy: Logical vector of length length(y). A TRUE value indicates locations in y for which imputations are created.
- ...: Other named arguments.

Details
This function takes a simple random sample from the observed values in y, and returns these as imputations.

Value
Vector with imputed data, same type as y, and of length sum(wy)

Author(s)
Stef van Buuren, Karin Groothuis-Oudshoorn, 2000, 2017

References
Description

Takes a mids object, and produces a new object of class mids.

Usage

mice.mids(obj, newdata = NULL, maxit = 1, printFlag = TRUE, ...)

Arguments

- **obj**: An object of class mids, typically produces by a previous call to mice() or mice.mids()
- **newdata**: An optional data.frame for which multiple imputations are generated according to the model in obj.
- **maxit**: The number of additional Gibbs sampling iterations.
- **printFlag**: A Boolean flag. If TRUE, diagnostic information during the Gibbs sampling iterations will be written to the command window. The default is TRUE.
- **...**: Named arguments that are passed down to the univariate imputation functions.

Details

This function enables the user to split up the computations of the Gibbs sampler into smaller parts. This is useful for the following reasons:

- RAM memory may become easily exhausted if the number of iterations is large. Returning to prompt/session level may alleviate these problems.
- The user can compute customized convergence statistics at specific points, e.g. after each iteration, for monitoring convergence. For computing a 'few extra iterations'.

Note: The imputation model itself is specified in the mice() function and cannot be changed with mice.mids. The state of the random generator is saved with the mids object.

Author(s)

Stef van Buuren, Karin Groothuis-Oudshoorn, 2000

References


See Also

complete, mice, set.seed, mids
Examples

```r
imp1 <- mice(nhanes, maxit = 1, seed = 123)
imp2 <- mice.mids(imp1)

# yields the same result as
imp <- mice(nhanes, maxit = 2, seed = 123)

# verification
identical(imp$imp, imp2$imp)
```

mice.theme

Set the theme for the plotting Trellis functions

Description

The `mice.theme()` function sets default choices for Trellis plots that are built into `mice`.

Usage

```r
mice.theme(transparent = TRUE, alpha.fill = 0.3)
```

Arguments

- `transparent` A logical indicating whether alpha-transparency is allowed. The default is `TRUE`.
- `alpha.fill` A numerical values between 0 and 1 that indicates the default alpha value for fills.

Value

`mice.theme()` returns a named list that can be used as a theme in the functions in `lattice`. By default, the `mice.theme()` function sets `transparent <- TRUE` if the current device `.Device` supports semi-transparent colors.

Author(s)

Stef van Buuren 2011
**mids-class**  
*Multiply imputed data set (mids)*

**Description**

The mids object contains a multiply imputed data set. The mids object is generated by functions `mice()`, `mice.mids()`, `cbind.mids()`, `rbind.mids()` and `ibind.mids()`.

**Details**

The mids class of objects has methods for the following generic functions: `print`, `summary`, `plot`. The loggedEvents entry is a matrix with five columns containing a record of automatic removal actions. It is NULL is no action was made. At initialization the program does the following three actions:

1. A variable that contains missing values, that is not imputed and that is used as a predictor is removed.
2. A constant variable is removed.
3. A collinear variable is removed.

During iteration, the program does the following actions:

1. One or more variables that are linearly dependent are removed (for categorical data, a 'variable' corresponds to a dummy variable).
2. Proportional odds regression imputation that does not converge and is replaced by polyreg.

Explanation of elements in loggedEvents:

- `it` iteration number at which the record was added,
- `im` imputation number,
- `dep` name of the dependent variable,
- `meth` imputation method used,
- `out` a (possibly long) character vector with the names of the altered or removed predictors.

**Slots**

- `.Data`: Object of class "list" containing the following slots:
  - `data`: Original (incomplete) data set.
  - `imp`: A list of `ncol(data)` components with the generated multiple imputations. Each list components is a data.frame (nmis[j] by m) of imputed values for variable j.
  - `m`: Number of imputations.
- `where`: The where argument of the `mice()` function.
- `blocks`: The blocks argument of the `mice()` function.
- `call`: Call that created the object.
mids-class

mids: An array containing the number of missing observations per column.
method: A vector of strings of length(blocks) specifying the imputation method per block.
predictorMatrix: A numerical matrix of containing integers specifying the predictor set.
visitSequence: The sequence in which columns are visited.
formulas: A named list of formula’s, or expressions that can be converted into formula’s by as.formula. List elements correspond to blocks. The block to which the list element applies is identified by its name, so list names must correspond to block names.
post: A vector of strings of length length(blocks) with commands for post-processing.
blots: "Block dots". The blots argument to the mice() function.
ignore: A logical vector of length nrow(data) indicating the rows in data used to build the imputation model. (new in mice 3.12.0)
seed: The seed value of the solution.
iteration: Last Gibbs sampling iteration number.
lastSeedValue: The most recent seed value.
chainMean: A list of m components. Each component is a length(visitSequence) by maxit matrix containing the mean of the generated multiple imputations. The array can be used for monitoring convergence. Note that observed data are not present in this mean.
chainVar: A list with similar structure of chainMean, containing the covariances of the imputed values.
loggedEvents: A data.frame with five columns containing warnings, corrective actions, and other inside info.
version: Version number of mice package that created the object.
date: Date at which the object was created.

Note

The mice package does not use the S4 class definitions, and instead relies on the S3 list equivalent oldClass(obj) <-"mids".

Author(s)

Stef van Buuren, Karin Groothuis-Oudshoorn, 2000

References


See Also

mice, mira, mipo
Description

Converts a mids object into a format recognized by Mplus, and writes the data and the Mplus input files.

Usage

mids2mplus(
  imp,
  file.prefix = "imp",
  path = getwd(),
  sep = "\t",
  dec = ".",
  silent = FALSE
)

Arguments

imp The imp argument is an object of class mids, typically produced by the mice() function.
file.prefix A character string describing the prefix of the output data files.
path A character string containing the path of the output file. By default, files are written to the current R working directory.
sep The separator between the data fields.
dec The decimal separator for numerical data.
silent A logical flag stating whether the names of the files should be printed.

Details

This function automates most of the work needed to export a mids object to Mplus. The function writes the multiple imputation datasets, the file that contains the names of the multiple imputation data sets and an Mplus input file. The Mplus input file has the proper file names, so in principle it should run and read the data without alteration. Mplus will recognize the data set as a multiply imputed data set, and do automatic pooling in procedures where that is supported.

Value

The return value is NULL.

Author(s)

Gerko Vink, 2011.
See Also

mids, mids2spss

---

mids2spss  
*Export mids object to SPSS*

### Description

Converts a mids object into a format recognized by SPSS, and writes the data and the SPSS syntax files.

### Usage

```r
mids2spss(
  imp,
  filename = "midsdata",
  path = getwd(),
  compress = FALSE,
  silent = FALSE
)
```

### Arguments

- `imp`  
The imp argument is an object of class mids, typically produced by the `mice()` function.

- `filename`  
A character string describing the name of the output data file and its extension.

- `path`  
A character string containing the path of the output file. The value in path is appended to filedat. By default, files are written to the current R working directory. If path=NULL then no file path appending is done.

- `compress`  
A logical flag stating whether the resulting SPSS set should be a compressed .zsav file.

- `silent`  
A logical flag stating whether the location of the saved file should be printed.

### Details

This function automates most of the work needed to export a mids object to SPSS. It uses `haven::write_sav()` to facilitate the export to an SPSS .sav or .zsav file.

Below are some things to pay attention to.

The SPSS syntax file has the proper file names and separators set, so in principle it should run and read the data without alteration. SPSS is more strict than R with respect to the paths. Always use the full path, otherwise SPSS may not be able to find the data file.

Factors in R translate into categorical variables in SPSS. The internal coding of factor levels used in R is exported. This is generally acceptable for SPSS. However, when the data are to be combined with existing SPSS data, watch out for any changes in the factor levels codes.
SPSS will recognize the data set as a multiply imputed data set, and do automatic pooling in procedures where that is supported. Note however that pooling is an extra option only available to those who license the MISSING VALUES module. Without this license, SPSS will still recognize the structure of the data, but it will not pool the multiply imputed estimates into a single inference.

**Value**

The return value is NULL.

**Author(s)**

Gerko Vink, dec 2020.

**See Also**

mids

---

### mira-class

*Multiply imputed repeated analyses (mira)*

**Description**

The `mira` object is generated by the `with.mids()` function. The `as.mira()` function takes the results of repeated complete-data analysis stored as a list, and turns it into a `mira` object that can be pooled.

**Details**

In versions prior to mice 3.0 pooling required only that `coef()` and `vcov()` methods were available for fitted objects. *This feature is no longer supported.* The reason is that `vcov()` methods are inconsistent across packages, leading to buggy behaviour of the `pool()` function. Since mice 3.0+, the broom package takes care of filtering out the relevant parts of the complete-data analysis. It may happen that you’ll see the messages like No method for tidying an S3 object of class ... or Error: No glance method for objects of class .... The royal way to solve this problem is to write your own `glance()` and `tidy()` methods and add these to broom according to the specifications given in [https://broom.tidymodels.org](https://broom.tidymodels.org).

#"The mira class of objects has methods for the following generic functions: print, summary.

Many of the functions of the mice package do not use the S4 class definitions, and instead rely on the S3 list equivalent `oldClass(obj) <- "mira"`.

**Slots**

#`

Object of class "list" containing the following slots:

- `.Data`: The call that created the object.
- `.call1`: The call that created the `mids` object that was used in call.
mnar_demo_data

**mnis**: An array containing the number of missing observations per column.

**analyses**: A list of $m$ components containing the individual fit objects from each of the $m$ complete data analyses.

**Author(s)**

Stef van Buuren, Karin Groothuis-Oudshoorn, 2000

**References**


**See Also**

`with.mids`, `mids`, `mipo`

---

**mnar_demo_data** | **MNAR demo data**

**Description**

A toy example from Margarita Moreno-Betancur for checking NARFCS.

**Usage**

`mnar_demo_data`

**Format**

An object of class `data.frame` with 500 rows and 3 columns.

**Details**

A small dataset with just three columns.

**Source**

**name.blocks**

**Name imputation blocks**

### Description

This helper function names any unnamed elements in the blocks specification. This is a convenience function.

### Usage

```r
name.blocks(blocks, prefix = "B")
```

### Arguments

- **blocks**
  - List of vectors with variable names per block. List elements may be named to identify blocks. Variables within a block are imputed by a multivariate imputation method (see method argument). By default each variable is placed into its own block, which is effectively fully conditional specification (FCS) by univariate models (variable-by-variable imputation). Only variables whose names appear in blocks are imputed. The relevant columns in the where matrix are set to FALSE of variables that are not block members. A variable may appear in multiple blocks. In that case, it is effectively re-imputed each time that it is visited.

- **prefix**
  - A character vector of length 1 with the prefix to be using for naming any unnamed blocks with two or more variables.

### Details

This function will name any unnamed list elements specified in the optional argument `blocks`. Unnamed blocks consisting of just one variable will be named after this variable. Unnamed blocks containing more than one variables will be named by the `prefix` argument, padded by an integer sequence stating at 1.

### Value

A named list of character vectors with variables names.

### See Also

- `mice`

### Examples

```r
blocks <- list(c("hyp", "chl"), AGE = "age", c("bmi", "hyp"), "edu")
name.blocks(blocks)
```
name.formulas

Name formula list elements

Description

This helper function names any unnamed elements in the formula list. This is a convenience function.

Usage

name.formulas(formulas, prefix = "F")

Arguments

formulas A named list of formula's, or expressions that can be converted into formula's by as.formula. List elements correspond to blocks. The block to which the list element applies is identified by its name, so list names must correspond to block names. The formulas argument is an alternative to the predictorMatrix argument that allows for more flexibility in specifying imputation models, e.g., for specifying interaction terms.

prefix A character vector of length 1 with the prefix to be using for naming any unnamed blocks with two or more variables.

Details

This function will name any unnamed list elements specified in the optional argument formula. Unnamed formula's consisting with just one response variable will be named after this variable. Unnamed formula's containing more than one variable will be named by the prefix argument, padded by an integer sequence stating at 1.

Value

Named list of formulas

See Also

mice

Examples

# fully conditionally specified main effects model
form1 <- list(
  bmi ~ age + chl + hyp,
  hyp ~ age + bmi + chl,
  chl ~ age + bmi + hyp
)
form1 <- name.formulas(form1)
imp1 <- mice(nhanes, formulas = form1, print = FALSE, m = 1, seed = 12199)
# same model using dot notation
form2 <- list(bmi ~ ., hyp ~ ., chl ~ .)
form2 <- name.formulas(form2)
imp2 <- mice(nhanes, formulas = form2, print = FALSE, m = 1, seed = 12199)
identical(complete(imp1), complete(imp2))

# same model using repeated multivariate imputation
form3 <- name.blocks(list(all = bmi + hyp + chl ~ .))
imp3 <- mice(nhanes, formulas = form3, print = FALSE, m = 1, seed = 12199)
cmp3 <- complete(imp3)
identical(complete(imp1), complete(imp3))

# same model using predictorMatrix
imp4 <- mice(nhanes, print = FALSE, m = 1, seed = 12199, auxiliary = TRUE)
identical(complete(imp1), complete(imp4))

# different model: multivariate imputation for chl and bmi
form5 <- list(chl + bmi ~ ., hyp ~ bmi + age)
form5 <- name.formulas(form5)
imp5 <- mice(nhanes, formulas = form5, print = FALSE, m = 1, seed = 71712)

---

ncc

Number of complete cases

Description

Calculates the number of complete cases.

Usage

ncc(x)

Arguments

x

An R object. Currently supported are methods for the following classes: mids, data.frame and matrix. Also, x can be a vector.

Value

Number of elements in x with complete data.

Author(s)

Stef van Buuren, 2017

See Also

nic, cci
Examples

ncc(nhanes) # 13 complete cases

Description

Calculates the cumulative hazard rate (Nelson-Aalen estimator)

Usage

nelsonaalen(data, timevar, statusvar)

Arguments

data A data frame containing the data.
timevar The name of the time variable in data.
statusvar The name of the event variable, e.g. death in data.

Details

This function is useful for imputing variables that depend on survival time. White and Royston (2009) suggested using the cumulative hazard to the survival time $H_0(T)$ rather than $T$ or $\log(T)$ as a predictor in imputation models. See section 7.1 of Van Buuren (2012) for an example.

Value

A vector with nrow(data) elements containing the Nelson-Aalen estimates of the cumulative hazard function.

Author(s)

Stef van Buuren, 2012

References


Examples

```r
require(MASS)

leuk$status <- 1 ## no censoring occurs in leuk data (MASS)
ch <- nelsonaalen(leuk, time, status)
plot(x = leuk$time, y = ch, ylab = "Cumulative hazard", xlab = "Time")

### See example on http://www.engineeredsoftware.com/lmar/pe_cum_hazard_function.htm

time <- c(43, 67, 92, 94, 149, rep(149, 7))
status <- c(rep(1, 5), rep(0, 7))
eng <- data.frame(time, status)
ch <- nelsonaalen(eng, time, status)
plot(x = time, y = ch, ylab = "Cumulative hazard", xlab = "Time")
```

---

**nhanes**

*NHANES example - all variables numerical*

**Description**

A small data set with non-monotone missing values.

**Format**

A data frame with 25 observations on the following 4 variables.

- **age** Age group (1=20-39, 2=40-59, 3=60+)
- **bmi** Body mass index (kg/m**2**)
- **hyp** Hypertensive (1=no,2=yes)
- **chl** Total serum cholesterol (mg/dL)

**Details**

A small data set with all numerical variables. The data set nhanes2 is the same data set, but with age and hyp treated as factors.

**Source**


**See Also**

nhanes2
Examples

```r
# create 5 imputed data sets
imp <- mice(nhanes)

# print the first imputed data set
complete(imp)
```

---

nhanes2

**NHANES example - mixed numerical and discrete variables**

Description

A small data set with non-monotone missing values.

Format

A data frame with 25 observations on the following 4 variables.

- **age** Age group (1=20-39, 2=40-59, 3=60+)
- **bmi** Body mass index (kg/m**2**)  
- **hyp** Hypertensive (1=no, 2=yes)
- **chl** Total serum cholesterol (mg/dL)

Details

A small data set with missing data and mixed numerical and discrete variables. The data set nhanes is the same data set, but with all data treated as numerical.

Source


See Also

nhanes

Examples

```r
# create 5 imputed data sets
imp <- mice(nhanes2)

# print the first imputed data set
complete(imp)
```
nic  

Number of incomplete cases

Description

Calculates the number of incomplete cases.

Usage

nic(x)

Arguments

x  An R object. Currently supported are methods for the following classes: mids, data.frame and matrix. Also, x can be a vector.

Value

Number of elements in x with incomplete data.

Author(s)

Stef van Buuren, 2017

See Also

ncc, cci

Examples

nic(nhanes) # the remaining 12 rows
nic(nhanes[, c("bmi", "hyp")]) # number of cases with incomplete bmi and hyp

nimp  

Number of imputations per block

Description

Calculates the number of cells within a block for which imputation is requested.

Usage

nimp(where, blocks = make.blocks(where))
Arguments

where A data frame or matrix with logicals of the same dimensions as data indicating where in the data the imputations should be created. The default, where = is.na(data), specifies that the missing data should be imputed. The where argument may be used to overimpute observed data, or to skip imputations for selected missing values.

blocks List of vectors with variable names per block. List elements may be named to identify blocks. Variables within a block are imputed by a multivariate imputation method (see method argument). By default each variable is placed into its own block, which is effectively fully conditional specification (FCS) by univariate models (variable-by-variable imputation). Only variables whose names appear in blocks are imputed. The relevant columns in the where matrix are set to FALSE of variables that are not block members. A variable may appear in multiple blocks. In that case, it is effectively re-imputed each time that it is visited.

Value

A numeric vector of length length(blocks) containing the number of cells that need to be imputed within a block.

See Also

mice

Examples

where <- is.na(nhanes)

# standard FCS
nimp(where)

# user-defined blocks
nimp(where, blocks = name.blocks(list(c("bmi", "hyp"), "age", "chl")))

norm.draw

Draws values of beta and sigma by Bayesian linear regression

Description

This function draws random values of beta and sigma under the Bayesian linear regression model as described in Rubin (1987, p. 167). This function can be called by user-specified imputation functions.

Usage

norm.draw(y, ry, x, rank.adjust = TRUE, ...)

.norm.draw(y, ry, x, rank.adjust = TRUE, ...)
Arguments

- **y**: Incomplete data vector of length \( n \)
- **ry**: Vector of missing data pattern (FALSE=missing, TRUE=observed)
- **x**: Matrix \((n \times p)\) of complete covariates.
- **rank.adjust**: Argument that specifies whether NA’s in the coefficients need to be set to zero. Only relevant when `ls.meth = "qr"` AND the predictor matrix is rank-deficient.
- **...**: Other named arguments.

Value

A list containing components `coef` (least squares estimate), `beta` (drawn regression weights) and `sigma` (drawn value of the residual standard deviation).

Author(s)

Gerko Vink, 2018, for this version, based on earlier versions written by Stef van Buuren, Karin Groothuis-Oudshoorn, 2017

References


---

parlmice  
*Wrapper function that runs MICE in parallel*

Description

This is a wrapper function for `mice`, using multiple cores to execute `mice` in parallel. As a result, the imputation procedure can be sped up, which may be useful in general.

Usage

```r
parlmice(
  data,  
m = 5,  
seed = NA,  
cluster.seed = NA,  
n.core = NULL,  
n.imp.core = NULL,  
cl.type = "PSOCK",  
...  
)
```
Arguments

- **data**: A data frame or matrix containing the incomplete data. Similar to the first argument of `mice`.
- **m**: The number of desired imputed datasets. By default $m=5$ as with `mice`.
- **seed**: A scalar to be used as the seed value for the mice algorithm within each parallel stream. Please note that the imputations will be the same for all streams and, hence, this should be used if and only if `n.core = 1` and if it is desired to obtain the same output as under `mice`.
- **cluster.seed**: A scalar to be used as the seed value. It is recommended to put the seed value here and not outside this function, as otherwise the parallel processes will be performed with separate, random seeds.
- **n.core**: A scalar indicating the number of cores that should be used.
- **n.imp.core**: A scalar indicating the number of imputations per core.
- **cl.type**: The cluster type. Default value is "PSOCK". Posix machines (linux, Mac) generally benefit from much faster cluster computation if `type` is set to `type = "FORK"`.
- **...**: Named arguments that are passed down to function `mice` or `makeCluster`.

Details

This function relies on package `parallel`, which is a base package for R versions 2.14.0 and later. We have chosen to use parallel function `parLapply` to allow the use of `parlmice` on Mac, Linux and Windows systems. For the same reason, we use the Parallel Socket Cluster (PSOCK) type by default.

On systems other than Windows, it can be hugely beneficial to change the cluster type to `FORK`, as it generally results in improved memory handling. When memory issues arise on a Windows system, we advise to store the multiply imputed datasets, clean the memory by using `rm` and `gc` and make another run using the same settings.

This wrapper function combines the output of `parLapply` with function `ibind` in `mice`. A mids object is returned and can be used for further analyses.

Note that if a seed value is desired, the seed should be entered to this function with argument `seed`. Seed values outside the wrapper function (in an R-script or passed to `mice`) will not result to reproducible results. We refer to the manual of `parallel` for an explanation on this matter.

Value

A mids object as defined by `mids-class`

Author(s)

Gerko Vink, Rianne Schouten
pattern

References


See Also

`parallel`, `parLapply`, `makeCluster`, `mice`, `mids-class`

Examples

```r
# 150 imputations in dataset nhanes, performed by 3 cores
## Not run:
imp1 <- parlmice(data = nhanes, n.core = 3, n.imp.core = 50)
# Making use of arguments in mice.
imp2 <- parlmice(data = nhanes, method = "norm.nob", m = 100)
imp2$method
fit <- with(imp2, lm(bmi ~ hyp))
pool(fit)
## End(Not run)
```

<table>
<thead>
<tr>
<th>pattern</th>
<th>Datasets with various missing data patterns</th>
</tr>
</thead>
</table>

Description

Four simple datasets with various missing data patterns

Format

- `list("pattern1")`  Data with a univariate missing data pattern
- `list("pattern2")`  Data with a monotone missing data pattern
- `list("pattern3")`  Data with a file matching missing data pattern
- `list("pattern4")`  Data with a general missing data pattern


Details

Van Buuren (2012) uses these four artificial datasets to illustrate various missing data patterns.
Examples

```r
require(lattice)
require(MASS)

pattern4

data <- rbind(pattern1, pattern2, pattern3, pattern4)
mdpat <- cbind(expand.grid(rec = 8:1, pat = 1:4, var = 1:3), r = as.numeric(as.vector(is.na(data))))

types <- c("Univariate", "Monotone", "File matching", "General")
tp41 <- levelplot(r ~ var + rec | as.factor(pat),
data = mdpat,
as.table = TRUE, aspect = "iso",
shrink = c(0.9),
col.regions = mdc(1:2),
colorkey = FALSE,
scales = list(draw = FALSE),
xlab = "", ylab = "",
between = list(x = 1, y = 0),
strip = strip.custom(
    bg = "grey95", style = 1,
    factor.levels = types
)
)
print(tp41)

md.pattern(pattern4)
p <- md.pairs(pattern4)
p

### proportion of usable cases
p$mr / (p$mr + p$mm)

### outbound statistics
p$rm / (p$rm + p$rr)

fluxplot(pattern2)
```

---

plot.mids

*Plot the trace lines of the MICE algorithm*

Description

Trace line plots portray the value of an estimate against the iteration number. The estimate can be anything that you can calculate, but typically are chosen as parameter of scientific interest. The `plot` method for a `mids` object plots the mean and standard deviation of the imputed (not observed) values against the iteration number for each of the `$m$` replications. By default, the function plot the development of the mean and standard deviation for each incomplete variable. On convergence, the streams should intermingle and be free of any trend.
Usage

```r
## S3 method for class 'mids'
plot(
x, 
y = NULL, 
theme = mice.theme(),
layout = c(2, 3),
type = "l",
col = 1:10,
lty = 1,
...
)
```

Arguments

- **x** An object of class `mids`
- **y** A formula that specifies which variables, stream and iterations are plotted. If omitted, all streams, variables and iterations are plotted.
- **theme** The trellis theme to applied to the graphs. The default is `mice.theme()`.
- **layout** A vector of length 2 given the number of columns and rows in the plot. The default is `c(2,3)`.
- **type** Parameter `type` of `panel.xyplot`.
- **col** Parameter `col` of `panel.xyplot`.
- **lty** Parameter `lty` of `panel.xyplot`.
- **...** Extra arguments for `xyplot`.

Value

An object of class "trellis".

Author(s)

Stef van Buuren 2011

See Also

`mice`, `mids`, `xyplot`

Examples

```r
imp <- mice(nhanes, print = FALSE)
plot(imp, bmi + chl ~ .it | .ms, layout = c(2, 1))
```
**Description**

The `pool()` function combines the estimates from \( m \) repeated complete data analyses. The typical sequence of steps to do a multiple imputation analysis is:

1. Impute the missing data by the `mice` function, resulting in a multiple imputed data set (class `mids`);
2. Fit the model of interest (scientific model) on each imputed data set by the `with()` function, resulting an object of class `mira`;
3. Pool the estimates from each model into a single set of estimates and standard errors, resulting is an object of class `mipo`;
4. Optionally, compare pooled estimates from different scientific models by the `D1()` or `D3()` functions.

A common error is to reverse steps 2 and 3, i.e., to pool the multiply-imputed data instead of the estimates. Doing so may severely bias the estimates of scientific interest and yield incorrect statistical intervals and p-values. The `pool()` function will detect this case.

**Usage**

```r
pool(object, dfcom = NULL)
```

**Arguments**

- `object` An object of class `mira` (produced by `with.mids()` or `as.mira()`), or a list with model fits.
- `dfcom` A positive number representing the degrees of freedom in the complete-data analysis. Normally, this would be the number of independent observation minus the number of fitted parameters. The default (`dfcom = NULL`) extract this information in the following order: 1) the component `residual.df` returned by `glance()` if a `glance()` function is found, 2) the result of `df.residual()` applied to the first fitted model, and 3) as `999999`. In the last case, the warning "Large sample assumed" is printed. If the degrees of freedom is incorrect, specify the appropriate value manually.

**Details**

The `pool()` function averages the estimates of the complete data model, computes the total variance over the repeated analyses by Rubin’s rules (Rubin, 1987, p. 76), and computes the following diagnostic statistics per estimate:

1. Relative increase in variance due to nonresponse \( r \);
2. Residual degrees of freedom for hypothesis testing \( df \);
3. Proportion of total variance due to missingness \( \lambda \);
4. Fraction of missing information \( fmi \).

The function requires the following input from each fitted model:

1. the estimates of the model, usually obtainable by \texttt{coef()}
2. the standard error of each estimate;
3. the residual degrees of freedom of the model.

The degrees of freedom calculation for the pooled estimates uses the Barnard-Rubin adjustment for small samples (Barnard and Rubin, 1999).

The \texttt{pool()} function relies on the \texttt{broom::tidy} for extracting the parameters. Versions before \texttt{mice 3.8.5} failed when no \texttt{broom::glance()} function was found for extracting the residual degrees of freedom. The \texttt{pool()} function is now more forgiving.

In versions prior to \texttt{mice 3.0}, pooling required only that \texttt{coef()} and \texttt{vcov()} methods were available for fitted objects. This feature is no longer supported. The reason is that \texttt{vcov()} methods are inconsistent across packages, leading to buggy behaviour of the \texttt{pool()} function.

Since \texttt{mice 3.0+}, the \texttt{broom} package takes care of filtering out the relevant parts of the complete-data analysis. It may happen that you’ll see the messages like \texttt{Error: No tidy method for objects of class ...} or \texttt{Error: No glance method for objects of class ...}. The message means that your complete-data method used in \texttt{with(imp,...)} has no tidy or glance method defined in the \texttt{broom} package.

The \texttt{broom.mixed} package contains tidy and glance methods for mixed models. If you are using a mixed model, first run \texttt{library(broom.mixed)} before calling \texttt{pool()}.

If no tidy or glance methods are defined for your analysis tabulate the \( m \) parameter estimates and their variance estimates (the square of the standard errors) from the \( m \) fitted models stored in \texttt{fit$analyses}. For each parameter, run \texttt{pool.scalar} to obtain the pooled parameters estimate, its variance, the degrees of freedom, the relative increase in variance and the fraction of missing information.

An alternative is to write your own \texttt{glance()} and \texttt{tidy()} methods and add these to \texttt{broom} according to the specifications given in \texttt{https://broom.tidymodels.org}.

Value

An object of class \texttt{mipo}, which stands for 'multiple imputation pooled outcome'.

References


pool.compare

See Also


Examples

# pool using the classic MICE workflow
imp <- mice(nhanes, maxit = 2, m = 2)
fit <- with(data = imp, exp = lm(bmi ~ hyp + chl))
summary(pool(fit))

Description

This function is deprecated in V3. Use D1 or D3 instead.

Usage

pool.compare(fit1, fit0, method = c("wald", "likelihood"), data = NULL)

Arguments

fit1 An object of class 'mira', produced by with.mids().
fit0 An object of class 'mira', produced by with.mids(). The model in fit0 is a nested fit0 of fit1.
method Either "wald" or "likelihood" specifying the type of comparison. The default is "wald".
data No longer used.

details

Compares two nested models after m repeated complete data analysis

The function is based on the article of Meng and Rubin (1992). The Wald-method can be found in paragraph 2.2 and the likelihood method can be found in paragraph 3. One could use the Wald method for comparison of linear models obtained with e.g. lm (in with.mids()). The likelihood method should be used in case of logistic regression models obtained with glm() in with.mids().

The function assumes that fit1 is the larger model, and that model fit0 is fully contained in fit1. In case of method = "wald", the null hypothesis is tested that the extra parameters are all zero.
Value

A list containing several components. Component call is the call to the pool.compare function. Component call1 is the call that created fit1. Component call2 is the call that created the imputations. Component call0 is the call that created fit0. Component mnis is the number of missing entries for each variable. Component m is the number of imputations. Component call1 is a matrix, containing the estimated coefficients of the m repeated complete data analyses from fit1. Component call0 is a matrix, containing the estimated coefficients of the m repeated complete data analyses from fit0. Component call1 is the mean of the variances of fit1, formula (3.1.3), Rubin (1987). Component call0 is the mean of the variances of fit0, formula (3.1.3), Rubin (1987). Component qbar1 is the pooled estimate of fit1, formula (3.1.2) Rubin (1987). Component qbar0 is the pooled estimate of fit0, formula (3.1.2) Rubin (1987). Component Dm is the test statistic. Component rm is the relative increase in variance due to nonresponse, formula (3.1.7), Rubin (1987). Component df1: df1 = under the null hypothesis it is assumed that Dm has an F distribution with (df1,df2) degrees of freedom. Component df2: df2. Component pvalue is the P-value of testing whether the model fit1 is statistically different from the smaller fit0.

Author(s)
Karin Groothuis-Oudshoorn and Stef van Buuren, 2009

References

See Also
lm.mids, glm.mids

---

**pool.r.squared**

Pools R^2 of m models fitted to multiply-imputed data

Description

The function pools the coefficients of determination R^2 or the adjusted coefficients of determination (R^2_a) obtained with the lm modeling function. For pooling it uses the Fisher z-transformation.

Usage

```
pool.r.squared(object, adjusted = FALSE)
```
Arguments

object An object of class 'mira' or 'mipo', produced by \texttt{lm.mids}, \texttt{with.mids}, or \texttt{pool} with \texttt{lm} as modeling function.

adjusted A logical value. If \texttt{adjusted=}\texttt{TRUE} then the adjusted $R^2$ is calculated. The default value is \texttt{FALSE}.

Value

Returns a 1x4 table with components. Component \texttt{est} is the pooled $R^2$ estimate. Component \texttt{lo95} is the 95 \% lower bound of the pooled $R^2$. Component \texttt{hi95} is the 95 \% upper bound of the pooled $R^2$. Component \texttt{fmi} is the fraction of missing information due to nonresponse.

Author(s)

Karin Groothuis-Oudshoorn and Stef van Buuren, 2009

References


See Also

\texttt{pool}, \texttt{pool.scalar}

Examples

```r
imp <- mice(nhanes, print = FALSE, seed = 16117)
fit <- with(imp, lm(chl ~ age + hyp + bmi))

# input: mira object
pool.r.squared(fit)
pool.r.squared(fit, adjusted = TRUE)

# input: mipo object
est <- pool(fit)
pool.r.squared(est)
pool.r.squared(est, adjusted = TRUE)
```
Description

Pools univariate estimates of m repeated complete data analysis

Usage

pool.scalar(Q, U, n = Inf, k = 1)

Arguments

Q A vector of univariate estimates of m repeated complete data analyses.
U A vector containing the corresponding m variances of the univariate estimates.
n A number providing the sample size. If nothing is specified, an infinite sample n = Inf is assumed.
k A number indicating the number of parameters to be estimated. By default, k = 1 is assumed.

Details

The function averages the univariate estimates of the complete data model, computes the total variance over the repeated analyses, and computes the relative increase in variance due to nonresponse and the fraction of missing information.

Value

Returns a list with components.

m: Number of imputations.
qhat: The m univariate estimates of repeated complete-data analyses.
u: The corresponding m variances of the univariate estimates.
qbar: The pooled univariate estimate, formula (3.1.2) Rubin (1987).
ubar: The mean of the variances (i.e. the pooled within-imputation variance), formula (3.1.3) Rubin (1987).
t: The total variance of the pooled estimated, formula (3.1.5) Rubin (1987).
r: The relative increase in variance due to nonresponse, formula (3.1.7) Rubin (1987).
fmi: The fraction missing information due to nonresponse, formula (3.1.10) Rubin (1987).

Author(s)

Karin Groothuis-Oudshoorn and Stef van Buuren, 2009
References


See Also

pool

Examples

# example with manual and automatic pooling
imp <- mice(nhanes, maxit = 2, m = 2, print = FALSE, seed = 18210)
fit <- with(data = imp, lm(bmi ~ age))

# manual pooling
summary(fit$analyses[[1]])
summary(fit$analyses[[2]])
pool.scalar(Q = c(-1.5457, -1.428), U = c(0.9723^2, 1.041^2), n = 25, k = 2)

# automatic pooling using broom
pool(fit)

Description

Hox pupil popularity data with some missing popularity scores

Format

A data frame with 2000 rows and 7 columns:

- pupil  Pupil number within school
- school  School number
- popular  Pupil popularity with 848 missing entries
- sex  Pupil gender
- texp  Teacher experience (years)
- const  Constant intercept term
- teachpop  Teacher popularity

Details

The original, complete dataset was generated by Joop Hox as an example of well-behaved multilevel data set. The distributed data contains missing data in pupil popularity.
Source

Examples
popmis[1:3, ]

---

**pops**

*Project on preterm and small for gestational age infants (POPS)*

---

**Description**

Subset of data from the POPS study, a national, prospective study on preterm children, including all liveborn infants <32 weeks gestational age and/or <1500 g from 1983 (n = 1338).

**Format**

pops is a data frame with 959 rows and 86 columns. pops.pred is the 86 by 86 binary predictor matrix used for specifying the multiple imputation model.

**Details**

The data set concerns of subset of 959 children that survived up to the age of 19 years.

Hille et al (2005) divided the 959 survivors into three groups: Full responders (examined at an outpatient clinic and completed the questionnaires, n = 596), postal responders (only completed the mailed questionnaires, n = 109), non-responders (did not respond to any of the mailed requests or telephone calls, or could not be traced, n = 254).

Compared to the postal and non-responders, the full response group consists of more girls, contains more Dutch children, has higher educational and social economic levels and has fewer handicaps. The responders form a highly selective subgroup in the total cohort.

Multiple imputation of this data set has been described in Hille et al (2007) and Van Buuren (2012), chapter 8.

**Note**

This dataset is not part of mice.

**Source**


**Examples**

```r
pops <- data(pops)
```

**Description**

Data from Potthoff-Roy (1964) with repeated measures on dental fissures.

**Format**

tbs is a data frame with 27 rows and 6 columns:

- **id** Person number
- **sex** Sex M/F
- **d8** Distance at age 8 years
- **d10** Distance at age 10 years
- **d12** Distance at age 12 years
- **d14** Distance at age 14 years

**Details**

This data set is the famous Potthoff-Roy data, used to demonstrate MANOVA on repeated measure data. Potthoff and Roy (1964) published classic data on a study in 16 boys and 11 girls, who at ages 8, 10, 12, and 14 had the distance (mm) from the center of the pituitary gland to the pteryomaxillary fissure measured. Changes in pituitary-pteroyomaxillary distances during growth is important in orthodontic therapy. The goals of the study were to describe the distance in boys and girls as simple functions of age, and then to compare the functions for boys and girls. The data have been reanalyzed by many authors including Jennrich and Schluchter (1986), Little and Rubin (1987), Pinheiro and Bates (2000), Verbeke and Molenberghs (2000) and Molenberghs and Kenward (2007). See Chapter 9 of Van Buuren (2012) for a challenging exercise using these data.
print.mads

Source

Examples
### create missing values at age 10 as in Little and Rubin (1987)

```r
phr <- potthoffroy
idmis <- c(3, 6, 9, 10, 13, 16, 23, 24, 27)
phr[idmis, 4] <- NA
phr
md.pattern(phr)
```

---

### Description
Print a mads object

### Usage
```r
## S3 method for class 'mads'
print(x, ...)
```

### Arguments
- `x`: Object of class mads
- `...`: Other parameters passed down to `print.default()`

### Value
`NULL`

### See Also
`mads`
**Description**

Print a `mids` object
Print a `mira` object
Print a `mice.anova` object
Print a `summary.mice.anova` object

**Usage**

```r
## S3 method for class 'mids'
print(x, ...)

## S3 method for class 'mira'
print(x, ...)

## S3 method for class 'mice.anova'
print(x, ...)

## S3 method for class 'mice.anova.summary'
print(x, ...)
```

**Arguments**

- `x` Object of class `mids`, `mira` or `mipo`
- `...` Other parameters passed down to `print.default()`

**Value**

- `NULL`
- `NULL`
- `NULL`
- `NULL`
- `NULL`

**See Also**

- `mids`
- `mira`
- `mipo`
quickpred

Quick selection of predictors from the data

Description

Selects predictors according to simple statistics

Usage

quickpred(
  data,
  mincor = 0.1,
  minpuc = 0,
  include = "",
  exclude = "",
  method = "pearson"
)

Arguments

data  Matrix or data frame with incomplete data.
mincor  A scalar, numeric vector (of size ncol(data)) or numeric matrix (square, of size ncol(data)) specifying the minimum threshold(s) against which the absolute correlation in the data is compared.
minpuc  A scalar, vector (of size ncol(data)) or matrix (square, of size ncol(data)) specifying the minimum threshold(s) for the proportion of usable cases.
include  A string or a vector of strings containing one or more variable names from names(data). Variables specified are always included as a predictor.
exclude  A string or a vector of strings containing one or more variable names from names(data). Variables specified are always excluded as a predictor.
method  A string specifying the type of correlation. Use 'pearson' (default), 'kendall' or 'spearman'. Can be abbreviated.

Details

This function creates a predictor matrix using the variable selection procedure described in Van Buuren et al. (1999, p. 687–688). The function is designed to aid in setting up a good imputation model for data with many variables.

Basic workings: The procedure calculates for each variable pair (i.e. target-predictor pair) two correlations using all available cases per pair. The first correlation uses the values of the target and the predictor directly. The second correlation uses the (binary) response indicator of the target and the values of the predictor. If the largest (in absolute value) of these correlations exceeds mincor, the predictor will be added to the imputation set. The default value for mincor is 0.1.

In addition, the procedure eliminates predictors whose proportion of usable cases fails to meet the minimum specified by minpuc. The default value is 0, so predictors are retained even if they have no usable case.
Finally, the procedure includes any predictors named in the `include` argument (which is useful for background variables like age and sex) and eliminates any predictor named in the `exclude` argument. If a variable is listed in both `include` and `exclude` arguments, the `include` argument takes precedence.

Advanced topic: `mincor` and `minpuc` are typically specified as scalars, but vectors and squares matrices of appropriate size will also work. Each element of the vector corresponds to a row of the predictor matrix, so the procedure can effectively differentiate between different target variables. Setting a high value for `mincor` can be useful for auxiliary, less important, variables. The set of predictor for those variables can remain relatively small. Using a square matrix extends the idea to the columns, so that one can also apply cellwise thresholds.

**Value**

A square binary matrix of size `ncol(data)`.

**Note**

`quickpred()` uses `data.matrix` to convert factors to numbers through their internal codes. Especially for unordered factors the resulting quantification may not make sense.

**Author(s)**

Stef van Buuren, Aug 2009

**References**


**See Also**

`mice`, `mids`

**Examples**

```r
# default: include all predictors with absolute correlation over 0.1
quickpred(nhanes)

# all predictors with absolute correlation over 0.4
quickpred(nhanes, mincor = 0.4)

# include age and bmi, exclude chl
quickpred(nhanes, mincor = 0.4, inc = c("age", "bmi"), exc = "chl")

# only include predictors with at least 30% usable cases
quickpred(nhanes, minpuc = 0.3)
```
# use low threshold for bmi, and high thresholds for hyp and chl
pred <- quickpred(nhanes, mincor = c(0, 0.1, 0.5, 0.5))
pred

# use it directly from mice
imp <- mice(nhanes, pred = quickpred(nhanes, minpuc = 0.25, include = "age"))

### rbind.mids

#### Combine mids objects by rows

**Description**

This function combines two mids objects rowwise into a single mids object, or combines a mids object with a vector, matrix, factor or dataframe rowwise into a mids object.

**Usage**

```r
rbind.mids(x, y = NULL, ...)
```

**Arguments**

- `x` A mids object.
- `y` A mids object, or a data.frame, matrix, factor or vector.
- `...` Additional data.frame, matrix, vector or factor. These can be given as named arguments.

**Details**

If `y` is a mids object, then `rbind` requires that the number of multiple imputations in `x` and `y` is identical. Also, columns of `x$data` and `y$data` should match.

If `y` is not a mids object, the columns of `x$data` and `y` should match. The `where` matrix for `y` is set to `FALSE`, signaling that any missing values in `y` were not imputed. The `ignore` vector for `y` is set to `FALSE`, elements of `y` will therefore influence the parameters of the imputation model in future iterations.

**Value**

An S3 object of class `mids`

**Note**

The function construct the elements of the new mids object as follows:

- `data` Rowwise combination of the (incomplete) data in `x` and `y`
- `imp` Equals `rbind(x$imp[[j]], y$imp[[j]])` if `y` is mids object; otherwise the data of `y` will be copied
- `m` Equals `x$m`
- `where` Rowwise combination of `where` arguments
blocks
Equals x$blocks

call
Vector, call[1] creates x, call[2] is call to rbind.mids

nmis
x$nmis + y$nmis

method
Taken from x$method

predictorMatrix
Taken from x$predictorMatrix

visitSequence
Taken from x$visitSequence

formulas
Taken from x$formulas

post
Taken from x$post

blots
Taken from x$blots

ignore
Concatenate x$ignore and y$ignore

seed
Taken from x$seed

iteration
Taken from x$iteration

lastSeedValue
Taken from x$lastSeedValue

chainMean
Set to NA

chainVar
Set to NA

loggedEvents
Taken from x$loggedEvents

version
Taken from x$version

date
Taken from x$date

Author(s)
Karin Groothuis-Oudshoorn, Stef van Buuren

References

See Also
cbind.mids, ibind.mids

Examples

imp1 <- mice(nhanes[1:13, ], m = 2, maxit = 1, print = FALSE)
imp5 <- mice(nhanes[1:13, ], m = 2, maxit = 2, print = FALSE)
mylist <- list(age = NA, bmi = NA, hyp = NA, chl = NA)
nrow(complete(rbind(imp1, imp5)))
nrow(complete(rbind(imp1, mylist)))

nrow(complete(rbind(imp1, data.frame(mylist))))
nrow(complete(rbind(imp1, complete(imp5)))))
Description

Dataset containing height and weight data (measured, self-reported) from two studies.

Format

A data frame with 2060 rows and 15 variables:

- **src**: Study, either krul or mgg (factor)
- **id**: Person identification number
- **pop**: Population, all NL (factor)
- **age**: Age of respondent in years
- **sex**: Sex of respondent (factor)
- **hm**: Height measured (cm)
- **wm**: Weight measured (kg)
- **hr**: Height reported (cm)
- **wr**: Weight reported (kg)
- **prg**: Pregnancy (factor), all Not pregnant
- **edu**: Educational level (factor)
- **etn**: Ethnicity (factor)
- **web**: Obtained through web survey (factor)
- **bm**: BMI measured (kg/m2)
- **br**: BMI reported (kg/m2)

Details

This dataset combines two datasets: krul data (Kril, 2010) (1257 persons) and the mgg data (Van Keulen 2011; Van der Klauw 2011) (803 persons). The krul dataset contains height and weight (both measures and self-reported) from 1257 Dutch adults, whereas the mgg dataset contains self-reported height and weight for 803 Dutch adults. Section 7.3 in Van Buuren (2012) shows how the missing measured data can be imputed in the mgg data, so corrected prevalence estimates can be calculated.

Source

Examples

```r
md.pattern(selfreport[, c("age", "sex", "hm", "hr", "wm", "wr")])

### FIMD Section 7.3.5 Application

bmi <- function(h, w) {
  return(w / (h / 100)^2)
}
init <- mice(selfreport, maxit = 0)
meth <- init$meth
meth["bm"] <- "-bmi(hm,wm)"
pred <- init$pred
pred[, c("src", "id", "web", "bm", "br")] <- 0
imp <- mice(selfreport, pred = pred, meth = meth, seed = 66573, maxit = 2, m = 1)
## imp <- mice(selfreport, pred=pred, meth=meth, seed=66573, maxit=20, m=10)

### Like FIMD Figure 7.6

cd <- complete(imp, 1)
xy <- xy.coords(cd$bm, cd$br - cd$bm)
plot(xy,
     col = mdc(2), xlab = "Measured BMI", ylab = "Reported - Measured BMI",
     xlim = c(17, 45), ylim = c(-5, 5), type = "n", lwd = 0.7)
polygon(x = c(30, 20, 30), y = c(0, 10, 10), col = "grey95", border = NA)
polygon(x = c(30, 40, 30), y = c(0, -10, -10), col = "grey95", border = NA)
abline(0, 0, lty = 2, lwd = 0.7)

idx <- cd$src == "krul"
xyc <- xy
xyc$x <- xy$x[idx]
xyc$y <- xy$y[idx]

xys <- xy
xys$x <- xy$x[!idx]
xys$y <- xy$y[!idx]
points(xyc, col = mdc(1), cex = 0.7)
points(xys, col = mdc(2), cex = 0.7)
lines(lowess(xyc), col = mdc(4), lwd = 2)
lines(lowess(xys), col = mdc(5), lwd = 2)
text(1:4, x = c(40, 28, 20, 32), y = c(4, 4, -4, -4), cex = 3)
box(lwd = 1)
```
**squeeze**

*Squeeze the imputed values to be within specified boundaries.*

**Description**

This function replaces any values in x that are lower than bounds[1] by bounds[1], and replaces any values higher than bounds[2] by bounds[2].

**Usage**

```r
squeeze(x, bounds = c(min(x[r]), max(x[r])), r = rep.int(TRUE, length(x)))
```

**Arguments**

- **x**: A numerical vector with values
- **bounds**: A numerical vector of length 2 containing the lower and upper bounds. By default, the bounds are to the minimum and maximum values in x.
- **r**: A logical vector of length length(x) that is used to select a subset in x before calculating automatic bounds.

**Value**

A vector of length length(x).

**Author(s)**

Stef van Buuren, 2011.

---

**stripplot.mids**

*Stripplot of observed and imputed data*

**Description**

Plotting methods for imputed data using lattice. stripplot produces one-dimensional scatterplots. The function automatically separates the observed and imputed data. The functions extend the usual features of lattice.
Usage

```r
## S3 method for class 'mids'
stripplot(
  x,
  data,
  na.groups = NULL,
  groups = NULL,
  as.table = TRUE,
  theme = mice.theme(),
  allow.multiple = TRUE,
  outer = TRUE,
  drop.unused.levels = lattice::lattice.getOption("drop.unused.levels"),
  panel = lattice::lattice.getOption("panel.stripplot"),
  default.prepanel = lattice::lattice.getOption("prepanel.default.stripplot"),
  jitter.data = TRUE,
  horizontal = FALSE,
  ...
)
```

Arguments

- `x`: A `mids` object, typically created by `mice()` or `mice.mids()`.
- `data`: Formula that selects the data to be plotted. This argument follows the `lattice` rules for formulas, describing the primary variables (used for the per-panel display) and the optional conditioning variables (which define the subsets plotted in different panels) to be used in the plot.

The formula is evaluated on the complete data set in the long form. Legal variable names for the formula include `names(x$data)` plus the two administrative factors `.imp` and `.id`.

**Extended formula interface:** The primary variable terms (both the LHS `y` and RHS `x`) may consist of multiple terms separated by a ‘+’ sign, e.g., `y1 + y2 ~ x | a * b`. This formula would be taken to mean that the user wants to plot both `y1 ~ x | a * b` and `y2 ~ x | a * b`, but with the `y1 ~ x` and `y2 ~ x` in separate panels. This behavior differs from standard `lattice`. Only combine terms of the same type, i.e. only factors or only numerical variables. Mixing numerical and categorical data occasionally produces odds labeling of vertical axis.

For convenience, in `stripplot()` and `bwplot` the formula `y~.imp` may be abbreviated as `y`. This applies only to a single `y`, and does not (yet) work for `y1+y2~.imp`.

- `na.groups`: An expression evaluating to a logical vector indicating which two groups are distinguished (e.g. using different colors) in the display. The environment in which this expression is evaluated is the response indicator `is.na(x$data)`.

The default `na.group = NULL` contrasts the observed and missing data in the LHS `y` variable of the display, i.e. groups created by `is.na(y)`. The expression `y` creates the groups according to `is.na(y)`. The expression `y1 & y2` creates
groups by is.na(y1) & is.na(y2), and y1 | y2 creates groups as is.na(y1) | is.na(y2), and so on.

This is the usual groups arguments in lattice. It differs from na.groups because it evaluates in the completed data data.frame(complete(x,"long",inc=TRUE)) (as usual), whereas na.groups evaluates in the response indicator. See xyplot for more details. When both na.groups and groups are specified, na.groups takes precedence, and groups is ignored.

as.table
A named list containing the graphical parameters. The default function mice.theme produces a short list of default colors, line width, and so on. The extensive list may be obtained from trellis.par.get(). Global graphical parameters like col or cex in high-level calls are still honored, so first experiment with the global parameters. Many setting consists of a pair. For example, mice.theme defines two symbol colors. The first is for the observed data, the second for the imputed data. The theme settings only exist during the call, and do not affect the trellis graphical parameters.

allow.multiple
See xyplot.

outer
See xyplot.

drop.unused.levels
See xyplot.

panel
See xyplot.

default.prepanel
See xyplot.

jitter.data
See panel.xyplot.

horizontal
See xyplot.

...
Further arguments, usually not directly processed by the high-level functions documented here, but instead passed on to other functions.

subscripts
See xyplot.

subset
See xyplot.

Details

The argument na.groups may be used to specify (combinations of) missingness in any of the variables. The argument groups can be used to specify groups based on the variable values themselves. Only one of both may be active at the same time. When both are specified, na.groups takes precedence over groups.

Use the subset and na.groups together to plots parts of the data. For example, select the first imputed data set by by subset=.imp==1.

Graphical parameters like col, pch and cex can be specified in the arguments list to alter the plotting symbols. If length(col)==2, the color specification to define the observed and missing groups. col[1] is the color of the 'observed' data, col[2] is the color of the missing or imputed data. A convenient color choice is col=mdc(1:2), a transparent blue color for the observed data, and a transparent red color for the imputed data. A good choice is col=mdc(1:2),pch=20,cex=1.5. These choices can be set for the duration of the session by running mice.theme().
Value

The high-level functions documented here, as well as other high-level Lattice functions, return an object of class "trellis". The update method can be used to subsequently update components of the object, and the print method (usually called by default) will plot it on an appropriate plotting device.

Note

The first two arguments (x and data) are reversed compared to the standard Trellis syntax implemented in lattice. This reversal was necessary in order to benefit from automatic method dispatch.

In mice the argument x is always a mids object, whereas in lattice the argument x is always a formula.

In mice the argument data is always a formula object, whereas in lattice the argument data is usually a data frame.

All other arguments have identical interpretation.

Author(s)

Stef van Buuren

References


See Also

mice, xyplot, densityplot, bwplot, lattice for an overview of the package, as well as stripplot, panel.stripplot, print.trellis, trellis.par.set

Examples

imp <- mice(boys, maxit = 1)

### stripplot, all numerical variables
## Not run:
stripplot(imp)
## End(Not run)

### same, but with improved display
## Not run:
stripplot(imp, col = c("grey", mdc(2)), pch = c(1, 20))
## End(Not run)

### distribution per imputation of height, weight and bmi
### labeled by their own missingness

```r
Not run:
stripplot(imp, hgt + wgt + bmi ~ .imp,
       cex = c(2, 4), pch = c(1, 20), jitter = FALSE,
       layout = c(3, 1))
```

### same, but labeled with the missingness of wgt (just four cases)

```r
Not run:
stripplot(imp, hgt + wgt + bmi ~ .imp,
       na = wgt, cex = c(2, 4), pch = c(1, 20), jitter = FALSE,
       layout = c(3, 1))
```

### distribution of age and height, labeled by missingness in height
### most height values are missing for those around
### the age of two years
### some additional missings occur in region WEST

```r
Not run:
stripplot(imp, age + hgt ~ .imp | reg, hgt,
       col = c(grDevices::hcl(0, 0, 40, 0.2), mdc(2)), pch = c(1, 20))
```

### heavily jitted relation between two categorical variables
### labeled by missingness of gen
### aggregated over all imputed data sets

```r
Not run:
stripplot(imp, gen ~ phb, factor = 2, cex = c(8, 1), hor = TRUE)
```

### circle fun

```r
stripplot(imp, gen ~ .imp,
       na = wgt, factor = 2, cex = c(8.6),
       hor = FALSE, outer = TRUE, scales = "free", pch = c(1, 19))
```

---

**Summary.mira**  
*Summary of a mira object*

---

**Description**

Summary of a mira object

Summary of a mids object
Summary of a mads object

Print a mice.anova object

Usage

```r
## S3 method for class 'mira'
summary(object, type = c("tidy", "glance", "summary"), ...)

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

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

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

Arguments

- `object`: A mira object
- `type`: A length-1 character vector indicating the type of summary. There are three choices: type = "tidy" return the parameters estimates of each analyses as a data frame. type = "glance" return the fit statistics of each analysis as a data frame. type = "summary" returns a list of length m with the analysis results. The default is "tidy".
- `...`: Other parameters passed down to `print()` and `summary()`

Value

NULL

NULL

NULL

NULL

See Also

- mira
- mids
- mads
- mipo
supports.transparent

**Description**

This function is used by mdc() to find out whether the current device supports semi-transparent foreground colors.

**Usage**

```r
supports.transparent()
```

**Details**

The function calls the function `dev.capabilities()` from the package `grDevices`. The function return FALSE if the status of the current device is unknown.

**Value**

TRUE or FALSE

**See Also**

`mdc dev.capabilities`

**Examples**

```r
supports.transparent()
```

tbc

**Terneuzen birth cohort**

**Description**

Data of subset of the Terneuzen Birth Cohort data on child growth.

**Format**

tbs is a data frame with 3951 rows and 11 columns:

- id  Person number
- occ Occasion number
- nocc Number of occasions
- first Is this the first record for this person? (TRUE/FALSE)
**typ**  Type of data (all observed)

**age**  Age (years)

**sex**  Sex 1=M, 2=F

**hgt.z**  Height Z-score

**wgt.z**  Weight Z-score

**bmi.z**  BMI Z-score

**ao**  Adult overweight (0=no, 1=yes)

**tbc.target** is a data frame with 2612 rows and 3 columns:

**id**  Person number

**ao**  Adult overweight (0=no, 1=yes)

**bmi.z.jv**  BMI Z-score as young adult (18-29 years)

### Details

This tbc data set is a random subset of persons from a much larger collection of data from the Terneuzen Birth Cohort. The total cohort comprises of 2604 unique persons, whereas the subset in tbc covers 306 persons. The tbc.target is an auxiliary data set containing two outcomes at adult age. For more details, see De Kroon et al (2008, 2010, 2011). The imputation methodology is explained in Chapter 9 of Van Buuren (2012).

### Source


### Examples

```r
data <- tbc
dm.pattern(data)
```
Description

The toenail data come from a Multicenter study comparing two oral treatments for toenail infection. Patients were evaluated for the degree of separation of the nail. Patients were randomized into two treatments and were followed over seven visits - four in the first year and yearly thereafter. The patients have not been treated prior to the first visit so this should be regarded as the baseline.

Format

A data frame with 1908 observations on the following 5 variables:

- ID: a numeric vector giving the ID of patient
- outcome: a numeric vector giving the response (0=none or mild separation, 1=moderate or severe)
- treatment: a numeric vector giving the treatment group
- month: a numeric vector giving the time of the visit (not exactly monthly intervals hence not round numbers)
- visit: a numeric vector giving the number of the visit

Details

This dataset was copied from the DPpackage, which is scheduled to be discontinued from CRAN in August 2019.

Source


References


See Also
toenail2
Toenail data

Description

The toenail data come from a Multicenter study comparing two oral treatments for toenail infection. Patients were evaluated for the degree of separation of the nail. Patients were randomized into two treatments and were followed over seven visits - four in the first year and yearly thereafter. The patients have not been treated prior to the first visit so this should be regarded as the baseline.

Format

A data frame with 1908 observations on the following 5 variables:

- patientID a numeric vector giving the ID of patient
- outcome a factor with 2 levels giving the response
- treatment a factor with 2 levels giving the treatment group
- time a numeric vector giving the time of the visit (not exactly monthly intervals hence not round numbers)
- visit an integer giving the number of the visit

Details

Apart from formatting, this dataset is identical to toenail. The formatting is taken identical to `data("toenail",package = "HSAUR3")`.

Source


References


See Also

toenail
version

Echoes the package version number

Description

Echoes the package version number

Usage

version(pkg = "mice")

Arguments

pkg A character vector with the package name.

Value

A character vector containing the package name, version number and installed directory.

Author(s)

Stef van Buuren, Oct 2010

Examples

version()
version("base")

walking

Walking disability data

Description

Two items YA and YB measuring walking disability in samples A, B and E.

Format

A data frame with 890 rows on the following 5 variables:

sex Sex of respondent (factor)
age Age of respondent
YA Item administered in samples A and E (factor)
YB Item administered in samples B and E (factor)
src Source: Sample A, B or E (factor)
Details

Example dataset to demonstrate imputation of two items (YA and YB). Item YA is administered to sample A and sample E, item YB is administered to sample B and sample E, so sample E acts as a bridge study. Imputation using a bridge study is better than simple equating or than imputation under independence.

Item YA corresponds to the HAQ8 item, and item YB corresponds to the GAR9 items from Van Buuren et al (2005). Sample E (as well as sample B) is the Euridiss study (n=292), sample A is the ERGOPLUS study (n=306).


References


Examples

```r
md.pattern(walking)

micemill <- function(n) {
  for (i in 1:n) {
    imp <<- mice.mids(imp) # global assignment
    cors <- with(imp, cor(as.numeric(YA),
      as.numeric(YB),
      method = "kendall"
    ))
    tau <<- rbind(tau, getfit(cors, s = TRUE)) # global assignment
  }
}

plotit <- function() {
  matplot(
    x = 1:nrow(tau), y = tau,
    ylab = expression(paste("Kendall's ", tau)),
    xlab = "Iteration", type = "l", lwd = 1,
    lty = 1:10, col = "black"
  )
}

tau <- NULL
imp <- mice(walking, max = 0, m = 10, seed = 92786)
pred <- imp$pred
pred[, c("src", "age", "sex")] <- 0
imp <- mice(walking, max = 0, m = 3, seed = 92786, pred = pred)
micemill(5)
plotit()

### to get figure 9.8 van Buuren (2018) use m=10 and micemill(20)
```
Description

Subset of Irish wind speed data

Format

A data frame with 433 rows and 6 columns containing the daily average wind speeds within the period 1961-1978 at meteorological stations in the Republic of Ireland. The data are a random sample from a larger data set.

RochePt Roche Point
Rosslare Rosslare
Shannon Shannon
Dublin Dublin
Clones Clones
MalinHead Malin Head

Details

The original data set is much larger and was analyzed in detail by Haslett and Raftery (1989). Van Buuren et al (2006) used this subset to investigate the influence of extreme MAR mechanisms on the quality of imputation.

References


Examples

windspeed[1:3, ]
Evaluate an expression in multiple imputed datasets

Description

Performs a computation of each of imputed datasets in data.

Usage

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

Arguments

- `data`: An object of type `mids`, which stands for 'multiply imputed data set', typically created by a call to function `mice()`.
- `expr`: An expression to evaluate for each imputed data set. Formula's containing a dot (notation for "all other variables") do not work.
- `...`: Not used

Value

An object of S3 class `mira`

Note

Version 3.11.10 changed to tidy evaluation on a quosure. This change should not affect any code that worked on previous versions. It turned out that the latter statement was not true (#292). Version 3.12.2 reverts to the old `with()` function.

Author(s)

Karin Oudshoorn, Stef van Buuren 2009, 2012, 2020

References


See Also

`mids, mira, pool.D1, D3, pool.r.squared`
Examples

imp <- mice(nhanes2, m = 2, print = FALSE, seed = 14221)

# descriptive statistics
getfit(with(imp, table(hyp, age)))

# model fitting and testing
fit1 <- with(imp, lm(bmi ~ age + hyp + chl))
fit2 <- with(imp, glm(hyp ~ age + chl, family = binomial))
fit3 <- with(imp, anova(lm(bmi ~ age + chl)))

xyplot.mads Scatterplot of amputed and non-amputed data against weighted sum scores

Description

Plotting method to investigate relation between amputed data and the weighted sum scores. Based on lattice. xyplot produces scatterplots. The function plots the variables against the weighted sum scores. The function automatically separates the amputed and non-amputed data to see the relation between the amputation and the weighted sum scores.

Usage

## S3 method for class 'mads'
xyplot(
x, data, which.pat = NULL, standardized = TRUE, layout = NULL, colors = mdc(1:2), ...
)

Arguments

x A mads object, typically created by ampute.
data A string or vector of variable names that needs to be plotted. As a default, all variables will be plotted.
which.pat A scalar or vector indicating which patterns need to be plotted. As a default, all patterns are plotted.
standardized Logical. Whether the scatterplots need to be created from standardized data or not. Default is TRUE.
layout
A vector of two values indicating how the scatterplots of one pattern should be divided over the plot. For example, \(c(2,3)\) indicates that the scatterplots of six variables need to be placed on 3 rows and 2 columns. There are several defaults for different #variables. Note that for more than 9 variables, multiple plots will be created automatically.

colors
A vector of two RGB values defining the colors of the non-amputed and amputed data respectively. RGB values can be obtained with \texttt{hcl}.

Value
A list containing the scatterplots. Note that a new pattern will always be shown in a new plot.

Note
The \texttt{mads} object contains all the information you need to make any desired plots. Check \texttt{mads-class} or the vignette \textit{Multivariate Amputation using Ampute} to understand the contents of class object \texttt{mads}.

Author(s)
Rianne Schouten, 2016

See Also
\texttt{ampute, bwplot, Lattice} for an overview of the package, \texttt{mads-class}

---

\texttt{xyplot.mids} \hspace{1cm} \textit{Scatterplot of observed and imputed data}

Description
Plotting methods for imputed data using \texttt{lattice}. \texttt{xyplot()} produces a conditional scatterplots. The function automatically separates the observed (blue) and imputed (red) data. The function extends the usual features of \texttt{lattice}.

Usage
\begin{verbatim}
## S3 method for class 'mids'
xyplot()
  x,
  data,
  na.groups = NULL,
  groups = NULL,
  as.table = TRUE,
  theme = mice.theme(),
  allow.multiple = TRUE,
\end{verbatim}
outer = TRUE,
drop.unused.levels = lattice::lattice.getOption("drop.unused.levels"),
...
subscripts = TRUE,
subset = TRUE
)

Arguments

x
A mids object, typically created by mice() or mice.mids().
data
Formula that selects the data to be plotted. This argument follows the lattice rules for formulas, describing the primary variables (used for the per-panel display) and the optional conditioning variables (which define the subsets plotted in different panels) to be used in the plot.

The formula is evaluated on the complete data set in the long form. Legal variable names for the formula include names(x$data) plus the two administrative factors .imp and .id.

Extended formula interface: The primary variable terms (both the LHS y and RHS x) may consist of multiple terms separated by a `+` sign, e.g., y1 + y2 ~ x | a * b. This formula would be taken to mean that the user wants to plot both y1 ~ x | a * b and y2 ~ x | a * b, but with the y1 ~ x and y2 ~ x in separate panels. This behavior differs from standard lattice. Only combine terms of the same type, i.e. only factors or only numerical variables. Mixing numerical and categorical data occasionally produces odds labeling of vertical axis.

na.groups
An expression evaluating to a logical vector indicating which two groups are distinguished (e.g. using different colors) in the display. The environment in which this expression is evaluated in the response indicator is.na(x$data).

The default na.group = NULL contrasts the observed and missing data in the LHS y variable of the display, i.e. groups created by is.na(y). The expression y creates the groups according to is.na(y). The expression y1 & y2 creates groups by is.na(y1) & is.na(y2), and y1 | y2 creates groups as is.na(y1) | is.na(y2), and so on.

groups
This is the usual groups arguments in lattice. It differs from na.groups because it evaluates in the completed data.frame(complete(x,"long",inc=TRUE)) (as usual), whereas na.groups evaluates in the response indicator. See xyplot for more details. When both na.groups and groups are specified, na.groups takes precedence, and groups is ignored.

as.table
See xyplot.

theme
A named list containing the graphical parameters. The default function mice.theme produces a short list of default colors, line width, and so on. The extensive list may be obtained from trellis.par.get(). Global graphical parameters like col or cex in high-level calls are still honored, so first experiment with the global parameters. Many setting consists of a pair. For example, mice.theme defines two symbol colors. The first is for the observed data, the second for the imputed data. The theme settings only exist during the call, and do not affect the trellis graphical parameters.

allow.multiple
See xyplot.
outer
   See \texttt{xyplot}.

\texttt{drop.unused.levels}
   See \texttt{xyplot}.

... Further arguments, usually not directly processed by the high-level functions documented here, but instead passed on to other functions.

\texttt{subscripts}
   See \texttt{xyplot}.

\texttt{subset}
   See \texttt{xyplot}.

\subsection*{Details}
The argument \texttt{na.groups} may be used to specify (combinations of) missingness in any of the variables. The argument \texttt{groups} can be used to specify groups based on the variable values themselves. Only one of both may be active at the same time. When both are specified, \texttt{na.groups} takes precedence over \texttt{groups}.

Use the \texttt{subset} and \texttt{na.groups} together to plots parts of the data. For example, select the first imputed data set by by \texttt{subset=.imp==1}.

Graphical parameters like \texttt{col}, \texttt{pch} and \texttt{cex} can be specified in the arguments list to alter the plotting symbols. If \texttt{length(col)==2}, the color specification to define the observed and missing groups. \texttt{col[1]} is the color of the ‘observed’ data, \texttt{col[2]} is the color of the missing or imputed data. A convenient color choice is \texttt{col=mdc(1:2)}, a transparent blue color for the observed data, and a transparent red color for the imputed data. A good choice is \texttt{col=mdc(1:2),pch=20,cex=1.5}. These choices can be set for the duration of the session by running \texttt{mice.theme()}. 

\subsection*{Value}
The high-level functions documented here, as well as other high-level Lattice functions, return an object of class \texttt{"trellis"}. The \texttt{update} method can be used to subsequently update components of the object, and the \texttt{print} method (usually called by default) will plot it on an appropriate plotting device.

\subsection*{Note}
The first two arguments (\texttt{x} and \texttt{data}) are reversed compared to the standard Trellis syntax implemented in \texttt{lattice}. This reversal was necessary in order to benefit from automatic method dispatch.

In \texttt{mice} the argument \texttt{x} is always a \texttt{mids} object, whereas in \texttt{lattice} the argument \texttt{x} is always a formula.

In \texttt{mice} the argument \texttt{data} is always a formula object, whereas in \texttt{lattice} the argument \texttt{data} is usually a data frame.

All other arguments have identical interpretation.

\subsection*{Author(s)}
Stef van Buuren
References


See Also

*mice, stripplot, densityplot, bwplot, lattice* for an overview of the package, as well as *xyplot, panel.xyplot, print.trellis, trellis.par.set*

Examples

```r
imp <- mice(boys, maxit = 1)

# xyplot: scatterplot by imputation number
# observe the erroneous outlying imputed values
# (caused by imputing hgt from bmi)
xyplot(imp, hgt ~ age | .imp, pch = c(1, 20), cex = c(1, 1.5))

# same, but label with missingness of wgt (four cases)
xyplot(imp, hgt ~ age | .imp, na.group = wgt, pch = c(1, 20), cex = c(1, 1.5))
```
Index

* classes
  - mids-class, 129
  - mira-class, 133

* datagen
  - mice.impute.2l.bin, 79
  - mice.impute.2l.1mer, 81
  - mice.impute.2l.norm, 82
  - mice.impute.2lonly.mean, 86
  - mice.impute.cart, 93
  - mice.impute.jomoImpute, 94
  - mice.impute.lda, 96
  - mice.impute.logreg, 97
  - mice.impute.logreg.boot, 99
  - mice.impute.mean, 100
  - mice.impute.midastouch, 101
  - mice.impute.mnar.logreg, 104
  - mice.impute.norm, 107
  - mice.impute.norm.boot, 108
  - mice.impute.norm.nob, 109
  - mice.impute.norm.predict, 111
  - mice.impute.panImpute, 112
  - mice.impute.passive, 114
  - mice.impute.pmm, 115
  - mice.impute.polr, 117
  - mice.impute.polyreg, 119
  - mice.impute.quadratic, 121
  - mice.impute.rf, 123
  - mice.impute.ri, 125
  - mice.impute.sample, 126

* datasets
  - boys, 15
  - brandsma, 16
  - employee, 35
  - fdd, 38
  - fdgs, 40
  - leiden85, 56
  - mammalsleep, 66
  - mnar_demo_data, 134
  - nhanes, 139
  - nhanes2, 140
  - pattern, 145
  - popmis, 154
  - pops, 155
  - potthoffroy, 156
  - selfreport, 163
  - tbc, 171
  - toenail, 173
  - toenail2, 174
  - walking, 175
  - windspeed, 177

* hplot
  - bwplot.mids, 19
  - densityplot.mids, 32
  - mdc, 71
  - stripplot.mids, 165
  - supports.transparent, 171
  - xyplot.mids, 180

* htest
  - pool.compare, 150
  - pool.r.squared, 151

* iteration
  - mice, 72
  - mice.mids, 127

* manip
  - cbind.mids, 22
  - complete.mids, 26
  - filter.mids, 42
  - getfit, 48
  - ibind, 51
  - mids2mplus, 131
  - mids2spss, 132
  - rbind.mids, 161

* mids
  - as.mids, 11

* misc
  - fico, 41
  - flux, 45
  - fluxplot, 46
nelsonaalen, 138
quickpred, 159
version, 175

* multivariate-2l
  mice.impute.jomoImpute, 94
  mice.impute.panImpute, 112

* multivariate
  glm.mids, 50
  lm.mids, 56
  with.mids, 178

* univariate imputation functions
  mice.impute.cart, 93
  mice.impute.lda, 96
  mice.impute.logreg, 97
  mice.impute.logreg.boot, 99
  mice.impute.mean, 100
  mice.impute.mnar.logreg, 104
  mice.impute.norm, 107
  mice.impute.norm.boot, 108
  mice.impute.norm.nob, 109
  mice.impute.norm.predict, 111
  mice.impute.pmm, 115
  mice.impute.polr, 117
  mice.impute.polyreg, 119
  mice.impute.quadratic, 121
  mice.impute.rf, 123
  mice.impute.ri, 125

* univariate-2lonly
  mice.impute.2lonly.mean, 86
  mice.impute.2lonly.norm, 87
  mice.impute.2lonly.pmm, 90

* univariate-2l
  mice.impute.2l.bin, 79
  mice.impute.2l.lmer, 81
  mice.impute.2l.norm, 82
  mice.impute.2l.pan, 83

* univar
  cc, 24
  cci, 25
  ic, 52
  ici, 53
  md.pairs, 68
  md.pattern, 70
  .norm.draw (norm.draw), 142
  .pmm.match, 5
  2l.pan (mice.impute.2l.pan), 83
  2lonly.mean (mice.impute.2lonly.mean), 86
  2lonly.norm (mice.impute.2lonly.norm), 87
  2lonly.pmm (mice.impute.2lonly.pmm), 90
  ampute, 6, 18, 19, 58, 79, 179, 180
  ampute.continuous, 7
  ampute.default.freq, 7
  ampute.default.odds, 7
  ampute.default.patterns, 7
  ampute.default.type, 7
  ampute.discrete, 7
  anova.mira, 10
  appendbreak, 11
  as.mids, 11
  as.mira, 13, 150
  as.mitml.result, 14
  boys, 15
  brandsma, 16
  bwplot, 10, 19, 22, 35, 168, 180, 183
  bwplot (bwplot.mids), 19
  bwplot.mads, 18
  bwplot.mids, 19
  cart (mice.impute.cart), 93
  cbind, 23
  cbind.mids, 22, 51, 162
  cc, 24, 25, 52
  cci, 25, 25, 53, 137, 141
  complete, 79, 127
  complete (complete.mids), 26
  complete.cases, 25
  complete.mids, 26
  construct.blocks, 27
  D1, 29, 150, 178
  D2, 30
  D3, 31, 150, 178
  data.enders.employee, 36
  data.matrix, 160
  densityplot, 22, 35, 168, 183
  densityplot (densityplot.mids), 32
  densityplot.mids, 32
  dev.capabilities, 171
  employee, 35
  estimice, 36
extractBS, 37
fdd, 38
fdgs, 40
fico, 41, 46, 48
filter, 43
filter.mids, 42
fix.coef, 32, 44
flux, 42, 45, 48
fluxplot, 42, 46, 46
formula, 50, 57
gc, 144
getfit, 48
getqbar, 49
glance, 150
glm, 50, 99, 100
glm.fit, 99, 100
glm.mids, 50, 151
hazard (nelsonaalen), 138
hcl, 72, 180
ibind, 23, 51, 144, 162
ic, 52, 53
ici, 24, 25, 52, 53
ici, data.frame-method (ici), 53
ici, matrix-method (ici), 53
ici, mids-method (ici), 53
is.mads, 53
is.mids, 54
is.mipo, 54
is.mira, 55
is.mitml.result, 55
jomoImpute, 95, 96
Lattice, 19, 180
lattice, 22, 35, 168, 179, 183
lda, 97
leiden85, 56
lm, 50, 57
lm.mids, 56, 151
mads, 157, 170
mads-class, 57
make.blocks, 28, 59, 60, 61, 64, 66
make.blots, 60
make.formulas, 61
make.method, 62
make.post, 63
make.predictorMatrix, 61, 64, 66
make.visitSequence, 64
make.where, 65
makeCluster, 144, 145
mammalsleep, 66
matchindex, 67
md.pairs, 68
md.pattern, 7, 42, 46, 48, 70
mdc, 71, 171
mean, 101
mice.impute.2l.bin, 79, 82, 83, 85
mice.impute.2l.lmer, 80, 81, 83, 85
mice.impute.2l.norm, 80, 82, 84, 85
mice.impute.2l.pan, 80, 82, 83, 88, 89, 91, 92
mice.impute.2lonly.mean, 86, 89, 92
mice.impute.2lonly.norm, 87, 89, 92
mice.impute.2lonly.pmm, 87, 89, 90
mice.impute.jomoImpute, 94, 113
mice.impute.mean, 94, 96, 97, 99, 100, 100, 103, 106, 108–110, 112, 117, 119, 121, 122, 124, 126
mice.impute.mnar.norm (mice.impute.mnar.logreg), 104
INDEX

mice.impute.panImpute, 96, 112
mice.impute.sample, 126
mice.mids, 127
mice.theme, 128
mids (mids-class), 129
mids-class, 129
mids2plus, 131
mids2spss, 132, 132
mipo, 130, 134, 158, 170
mira, 14, 49, 50, 57, 130, 158, 170, 178
mira (mira-class), 133
mira-class, 133
mnar.logreg (mice.impute.mnar.logreg), 104
mnar.norm (mice.impute.mnar.logreg), 104
mnar.demo.data, 134
multinom, 119, 121
na.omit, 25
name.blocks, 28, 135
name.formulas, 136
ncc, 137, 141
nelsnaalen, 138
nhanes, 139, 140
nhanes2, 139, 140
nic, 137, 141
nimp, 141
norm (mice.impute.norm), 107
norm.boot (mice.impute.norm.boot), 108
norm.draw, 142
norm.nob (mice.impute.norm.nob), 109
norm.predict (mice.impute.norm.predict), 111
panel.bwplot, 22
panel.densityplot, 35
panel.stripplot, 168
panel.xyplot, 147, 167, 183
parlmice, 112, 113
parallel, 144, 145
parLapply, 144, 145
parlmice, 143
pattern, 145
pattern1 (pattern), 145
pattern2 (pattern), 145
pattern3 (pattern), 145
pattern4 (pattern), 145
plot.mids, 146
pmm (mice.impute.pmm), 115
polr, 119, 121
pool, 79, 148, 152, 154, 178
pool.compare, 150
pool.r.squared, 151, 178
pool.scalar, 149, 150, 152, 153
poppmis, 154
pops, 155
potthoffroy, 156
print, 21, 34, 168, 182
print.mads, 157
print.mice.anova (print.mids), 158
print.mids, 158
print.mira (print.mids), 158
print.trellis, 22, 35, 168, 183
quadratic (mice.impute.quadratic), 121
quickpred, 159
randomForest, 124
rbind.mids, 23, 51, 161
rgb, 72
ri (mice.impute.ri), 125
rm, 144
rpart, 94
rpart.control, 93, 94
selfreport, 163
set.seed, 79, 127
sleep (mammalsleep), 66
squeeze, 165
stripplot, 22, 35, 168, 183
stripplot (stripplot.mids), 165
stripplot.mids, 165
summary.mads (summary.mira), 169
summary.mice.anova (summary.mira), 169
summary.mids (summary.mira), 169
summary.mira, 169
supports.transparent, 171
tb, 171
tenneuzen (tbc), 171
testModels, 29, 30
tidy, 150
toenail, 173, 174
toenail2, 173, 174
transparent (supports.transparent), 171
trellis.par.set, 22, 35, 72, 168, 183
update, 21, 34, 168, 182
version, 175
walking, 175
windspeed, 177
with.mids, 49, 50, 57, 79, 134, 150, 178
with.mitml.list, 14
xyplot, 10, 20–22, 33–35, 72, 147, 167, 168, 181–183
xyplot (xyplot.mids), 180
xyplot.mads, 179
xyplot.mids, 72, 180