

Package ‘mice’

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boys

Growth of Dutch boys

Description

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

Usage

`data(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

Fredriks, A.M., van Buuren, S., Burgmeijer, R.J., Meulmeester JF, Beuker, R.J., Brugman, E., Roede, M.J., Verloove-Vanhorick, S.P., Wit, J.M. (2000) Continuing positive secular growth change in The Netherlands 1955-1997. *Pediatric Research*, **47**, 316-323. <http://www.stefvanbuuren.nl/publications/Continuingsecular-PedRes2000.pdf>

Fredriks, A.M., van Buuren, S., Wit, J.M., Verloove-Vanhorick, S.P. (2000). Body index measurements in 1996-7 compared with 1980. *Archives of Disease in Childhood*, **82**, 107-112. <http://www.stefvanbuuren.nl/publications/Bodyindex-ADC2000.pdf>

Examples

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

# create imputations for age <8yrs
plot(z$age, z$gen, col=c("blue", "red")[1+is.na(boys$gen)])

# figure to show that the default imputation method does not impute BMI
# consistently
plot(z$bmi, z$wgt/(z$hgt/100)^2, col=c("blue", "red")[1+is.na(boys$bmi)],
     ylab="Calculated BMI")

# also, BMI distributions are somewhat different
oldpar <- par(mfrow=c(1,2))
truehist(z$bmi[!is.na(boys$bmi)], h=1, xlim=c(10, 30), ymax=0.25,
         col="blue", xlab="BMI observed")
truehist(z$bmi[is.na(boys$bmi)], h=1, xlim=c(10, 30), ymax=0.25,
         col="red", 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=2, meth=meth, pred=pred)
z2 <- complete(imp2, 1)

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

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

```

cbind.mids

Combine a Multiply Imputed Data Set with other mids object or dataframe

Description

Columnwise combination of mids objects

Usage

```
cbind.mids(x, y, ...)
```

Arguments

<code>x</code>	A mids object.
<code>y</code>	A mids object or a dataframe, matrix, factor or vector.
<code>...</code>	Dataframes, matrices, vectors or factors. These can be given as named arguments.

Details

This function combines two mids objects columnwise into a single object of class mids, or combines a mids object with a vector, matrix, factor or dataframe columnwise into an object of class mids. The number of rows in the (incomplete) data `x$data` and `y` (or `y$data` if `y` is a mids object) should be equal. If `y` is a mids object then the number of imputations in `x` and `y` should be equal. Note: If `y` is a vector or factor its original name is lost and it will be denoted with `y` in the mids object.

Value

call	A vector, with first argument the <code>mice()</code> statement that created <code>x</code> and second argument the call to <code>cbind.mids()</code> .
data	The <code>cbind</code> of the (incomplete) data in <code>x\$data</code> and <code>y\$data</code> .
m	The number of imputations.
nmis	An array containing the number of missing observations per column.
imp	A list of <code>nvar</code> components with the generated multiple imputations. Each part of the list is a <code>nmis[j]</code> by <code>m</code> matrix of imputed values for variable <code>j</code> . The original data of <code>y</code> will be copied into this list, including the missing values of <code>y</code> then <code>y</code> is not imputed.
method	A vector of strings of length(<code>nvar</code>) specifying the elementary imputation method per column. If <code>y</code> is a <code>mids</code> object this vector is a combination of <code>x\$method</code> and <code>y\$method</code> , otherwise this vector is <code>x\$method</code> and for the columns of <code>y</code> the method is set to <code>" "</code> .
predictorMatrix	A square matrix of size <code>ncol(data)</code> containing code 0/1 data specifying the predictor set. If <code>x</code> and <code>y</code> are <code>mids</code> objects then the predictor matrices of <code>x</code> and <code>y</code> are combined with zero matrices on the off diagonal blocks. Otherwise the variables in <code>y</code> are included in the predictor matrix of <code>x</code> such that <code>y</code> is not used as predictor(s) and not imputed as well.
visitSequence	The sequence in which columns are visited. The same as <code>x\$visitSequence</code> .
seed	The seed value of the solution, <code>x\$seed</code> .
iteration	Last Gibbs sampling iteration number, <code>x\$iteration</code> .
lastSeedValue	The most recent seed value, <code>x\$lastSeedValue</code>
chainMean	Combination of <code>x\$chainMean</code> and <code>y\$chainMean</code> . If <code>y\$chainMean</code> does not exist this element equals <code>x\$chainMean</code> .
chainVar	Combination of <code>x\$chainVar</code> and <code>y\$chainVar</code> . If <code>y\$chainVar</code> does not exist this element equals <code>x\$chainVar</code> .
pad	A list containing various settings of the padded imputation model, i.e. the imputation model after creating dummy variables. This list is defined by combining <code>x\$pad</code> and <code>y\$pad</code> if <code>y</code> is a <code>mids</code> object. Otherwise, it is defined by the settings of <code>x</code> and the combination of the data <code>x\$data</code> and <code>y</code> .

Remark that if a column of `y` is categorical this is ignored in the padded model since that column is not used as predictor for another column.

Author(s)

Karin Groothuis-Oudshoorn, Stef van Buuren, 2009

See Also

[rbind.mids](#), [ibind](#), [mids](#)

Examples

```

# append 'forgotten' variable bmi to imp
temp <- boys[,c(1:3,5:9)]
imp <- mice(temp,maxit=1)
imp2 <- cbind.mids(imp, data.frame(bmi=boys$bmi))

# append maturation score to imp (numerical)
mat <- (as.integer(temp$gen) + as.integer(temp$phb)
  + as.integer(cut(temp$tv,breaks=c(0,3,6,10,15,20,25))))
imp2 <- cbind.mids(imp, as.data.frame(mat))

# append maturation score to imp (factor)
# known issue: new column name is 'y', not 'mat'
mat <- as.factor(mat)
imp2 <- cbind.mids(imp, mat)

# append data frame with two columns to imp
temp2 <- data.frame(bmi=boys$bmi,mat=as.factor(mat))
imp2 <- cbind.mids(imp, temp2)

# combine two mids objects
impa <- mice(temp, maxit=2)
impb <- mice(temp2, maxit=3)

# first a then b
impab <- cbind.mids(impa, impb)

# first b then a
impba <- cbind.mids(impb, impa)

```

complete

*Creates a Complete Flat File from a Multiply Imputed Data Set***Description**

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

Usage

```
complete(x, action=1, include=FALSE)
```

Arguments

`x` An object of class `mids` as created by the function `mice()`.

`action` If `action` is a scalar between 1 and `x$m`, the function returns the data with imputation number `action` filled in. Thus, `action=1` returns the first completed data set, `action=2` returns the second completed data set, and so on. The value of `action` can also be one of the following strings: "long", "broad", "repeated". See 'Details' for the interpretation.

`include` Flag to indicate whether the original data with the missing values should be included. This requires that `action` is specified as "long", "broad" or "repeated".

Details

The argument `action` can also be a string, which is partially matched as follows:

"long" produces a long data frame of vertically stacked imputed data sets with `nrow(x$data)` * `x$m` rows and `ncol(x$data)+2` columns. The two additional columns are labeled `.id` containing the row names of `x$data`, and `.imp` containing the imputation number. If `include=TRUE` then `nrow(x$data)` additional rows with the original data are appended with `.imp` set equal to 0.

"broad" produces a broad data frame with `nrow(x$data)` rows and `ncol(x$data) * x$m` columns. Columns are ordered such that the first `ncol(x$data)` columns corresponds to the first imputed data matrix. The imputation number is appended to each column name. If `include=TRUE` then `ncol(x$data)` additional columns with the original data are appended. The number `.0` is appended to the column names.

"repeated" produces a broad data frame with `nrow(x$data)` rows and `ncol(x$data) * x$m` columns. Columns are ordered such that the first `x$m` columns correspond to the `x$m` imputed versions of the first column in `x$data`. The imputation number is appended to each column name. If `include=TRUE` then `ncol(x$data)` additional columns with the original data are appended. The number `.0` is appended to the column names.

Value

A data frame with the imputed values filled in. Optionally, the original data are appended.

Author(s)

Stef van Buuren, Karin Groothuis-Oudshoorn, 2009

See Also

[mice](#), [mids](#)

Examples

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

# obtain first imputed matrix
mat <- complete(imp)

# fill in the third imputation
mat <- complete(imp, 3)

# long matrix with stacked complete data
mat <- complete(imp, "long")
```

```
# long matrix with stacked complete data, including the original data
mat <- complete(imp, "long", inc=TRUE)

# repeated matrix with complete data
mat <- complete(imp, "r")

# for numeric data, produces a blocked correlation matrix, where
# each block contains of the same variable pair over different
# multiple imputations.
cor(mat)
```

glm.mids

Generalized Linear Model for Multiply Imputed Data

Description

Applies `glm()` to a multiply imputed data set

Usage

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

Arguments

formula	a formula expression as for other regression models, of the form <code>response ~ predictors</code> . See the documentation of <code>lm</code> and <code>formula</code> for details.
data	An object of type <code>mids</code> , which stands for 'multiply imputed data set', typically created by function <code>mice()</code> .
...	Additional parameters passed to <code>glm</code> .

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 `glm.objects`, plus some descriptive information.

Author(s)

Stef van Buuren, Karin Groothuis-Oudshoorn, 2000

References

Van Buuren, S., Groothuis-Oudshoorn, C.G.M. (2000) *Multivariate Imputation by Chained Equations: MICE V1.0 User's manual*. Leiden: TNO Quality of Life. <http://www.stefvanbuuren.nl/publications/MICEV1.0ManualTNO000382000.pdf>

See Also

[with.mids](#), [glm](#), [mids](#), [mira](#)

Examples

```
imp <- mice(nhanes)
glm.mids((hyp==2)~bmi+chl, data=imp)
# fit
# $call:
# glm.mids(formula = (hyp == 2) ~ bmi + chl, data = imp)
#
# $call1:
# mice(data = nhanes)
#
# $nmis:
#   age bmi hyp chl
#    0   9   8  10
#
# $analyses:
# $analyses[[1]]:
# Call:
# glm(formula = formula, data = data.i)
#
# Coefficients:
# (Intercept)          bmi          chl
# -0.4746337 -0.01565534  0.005417846
#
# Degrees of Freedom: 25 Total; 22 Residual
# Residual Deviance: 2.323886
#
# $analyses[[2]]:
# Call:
# glm(formula = formula, data = data.i)
#
# Coefficients:
# (Intercept)          bmi          chl
# -0.1184695 -0.02885779  0.006090282
#
# Degrees of Freedom: 25 Total; 22 Residual
# Residual Deviance: 3.647927
#
```

 ibind

 Combine imputations fitted to the same data

Description

Combine imputations fitted to the same data

Usage

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

Arguments

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

Details

This function combines two `mids` objects `x` and `y` into a single `mids` object. The two `mids` objects should have the same underlying multiple imputation model and should be fitted on exactly the same dataset. If the number of imputations in `x` is $m(x)$ and in `y` is $m(y)$ then the combination of both objects contains $m(x) + m(y)$ imputations.

Value

`call` A vector, with first argument the `mice` statement that created `x` and second argument the call to `ibind()`.

`data` The incomplete data in `x` and `y`.

`m` Defined as $x\$m + y\m , the total number of imputations from `x` and `y`.

`nmis` Defined as `x$nmis`, an array containing the number of missing observations per column of `x$data`.

`imp` A combination of `x$imp` and `y$imp`.

`method` Defined as `x$method`.

`predictorMatrix`
 Defined as `x$predictorMatrix`.

`visitSequence`
 `x$visitSequence`

`seed` Defined as `x$seed`.

`iteration` Last Gibbs sampling iteration number, `x$iteration`.

`lastSeedValue`
 Defined as `x$lastSeedValue`.

`chainMean` Combination of `x$chainMean` and `y$chainMean`.

`chainVar` Combination of `x$chainVar` and `y$chainVar`.

`pad` Defined as `x$pad` (which should equal `y$pad`).

Author(s)

Karin Groothuis-Oudshoorn, Stef van Buuren, 2009

See Also

[rbind.mids](#), [cbind.mids](#), [mids](#)

lm.mids

Linear Regression on Multiply Imputed Data

Description

Applies `lm()` to multiply imputed data set

Usage

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

Arguments

<code>formula</code>	a formula object, with the response on the left of a <code>~</code> operator, and the terms, separated by <code>+</code> operators, on the right. See the documentation of lm and formula for details.
<code>data</code>	An object of type 'mids', which stands for 'multiply imputed data set', typically created by a call to function <code>mice()</code> .
<code>...</code>	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 Oudshoorn, 2000

References

Van Buuren, S., Groothuis-Oudshoorn, C.G.M. (2000). *Multivariate Imputation by Chained Equations: MICE V1.0 User's manual*. Leiden: TNO Quality of Life. <http://www.stefvanbuuren.nl/publications/MICEV1.0ManualTNO000382000.pdf>

See Also

[lm](#), [mids](#), [mira](#)

Examples

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

md.pairs

Missing data pattern by variable pairs

Description

Number of observations per variable pair.

Usage

```
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:

rr response-response, both variables are observed
rm response-missing, row observed, column missing
mr missing -response, row missing, column observed
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 Oudshoorn, 2009

References

Van Buuren, S., Groothuis-Oudshoorn, K. (2009) MICE: Multivariate Imputation by Chained Equations in R. *Journal of Statistical Software*, forthcoming. <http://www.stefvanbuuren.nl/publications/MICEinR-Draft.pdf>

Examples

```
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

```
md.pattern(x)
```

Arguments

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

Details

This function is useful for investigating any structure of missing observation 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)

Stef van Buuren, Karin Oudshoorn, 2000

References

Schafer, J.L. (1997), Analysis of multivariate incomplete data. London: Chapman&Hall.

Van Buuren, S., Groothuis-Oudshoorn, K. (2009) MICE: Multivariate Imputation by Chained Equations in R. *Journal of Statistical Software*, forthcoming. <http://www.stefvanbuuren.nl/publications/MICEinR-Draft.pdf>

Examples

```
md.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
```

mice

Multivariate Imputation by Chained Equations (MICE)

Description

Generates Multivariate Imputations by Chained Equations (MICE)

Usage

```
mice(data, m = 5,
      method = vector("character", length=ncol(data)),
      predictorMatrix = (1 - diag(1, ncol(data))),
      visitSequence = (1:ncol(data))[apply(is.na(data), 2, any)],
      post = vector("character", length = ncol(data)),
      defaultMethod = c("pmm", "logreg", "polyreg"),
      maxit = 5,
      diagnostics = TRUE,
      printFlag = TRUE,
      seed = NA,
      imputationMethod = NULL,
      defaultImputationMethod = 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.

<code>method</code>	Can be either a single string, or a vector of strings with length <code>ncol(data)</code> , specifying the elementary imputation method to be used for each column in data. If specified as a single string, the same method will be used for all columns. The default imputation method (when no argument is specified) depends on the measurement level of the target column and are specified by the <code>defaultMethod</code> argument. Columns that need not be imputed have the empty method <code>"</code> . See details for more information.
<code>predictorMatrix</code>	A square matrix of size <code>ncol(data)</code> containing 0/1 data specifying the set of predictors to be used for each target column. Rows correspond to target variables (i.e. variables to be imputed), in the sequence as they appear in data. A value of '1' means that the column variable is used as a predictor for the target variable (in the rows). The diagonal of <code>predictorMatrix</code> must be zero. The default for <code>predictorMatrix</code> is that all other columns are used as predictors (sometimes called massive imputation). Note: For two-level imputation codes '2' and '-2' are also allowed.
<code>visitSequence</code>	A vector of integers of arbitrary length, specifying the column indices of the visiting sequence. The visiting sequence is the column order that is used to impute the data during one pass through the data. A column may be visited more than once. All incomplete columns that are used as predictors should be visited, or else the function will stop with an error. The default sequence <code>1:ncol(data)</code> implies that columns are imputed from left to right. It is possible to specify one of the keywords "roman" (left to right), "arabic" (right to left), "monotone" (sorted in increasing amount of missingness) and "revmonotone" (reverse of monotone). The keyword should be supplied as a string and may be abbreviated.
<code>post</code>	A vector of strings with length <code>ncol(data)</code> , specifying expressions. Each string is parsed and executed within the <code>sampler()</code> function to postprocess imputed values. The default is to do nothing, indicated by a vector of empty strings <code>"</code> .
<code>defaultMethod</code>	A vector of three strings containing the default imputation methods for numerical columns, factor columns with 2 levels, and factor columns with more than two levels, respectively. If nothing is specified, the following defaults will be used: <code>pmm</code> , predictive mean matching (numeric data) <code>logreg</code> , logistic regression imputation (binary data, factor with 2 levels) <code>polyreg</code> , polytomous regression imputation categorical data (factor ≥ 2 levels)
<code>maxit</code>	A scalar giving the number of iterations. The default is 5.
<code>diagnostics</code>	A Boolean flag. If <code>TRUE</code> , diagnostic information will be appended to the value of the function. If <code>FALSE</code> , only the imputed data are saved. The default is <code>TRUE</code> .
<code>printFlag</code>	If <code>TRUE</code> , <code>mice</code> will print history on console. Use <code>print=FALSE</code> for silent computation.
<code>seed</code>	An integer that is used as argument by the <code>set.seed()</code> for offsetting the random number generator. Default is to leave the random number generator alone.

`imputationMethod`

Same as `method` argument. Included for backwards compatibility.

`defaultImputationMethod`

Same as `defaultMethod` argument. Included for backwards compatibility.

Details

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. The extended model containing the dummy variables is called the padded model. Its structure is stored in the list component `pad`.

Built-in elementary imputation methods are:

pmm Predictive mean matching (numeric)

norm Bayesian linear regression (numeric)

norm.nob Linear regression ignoring model error (numeric)

mean Unconditional mean imputation (numeric)

2l.norm Two-level normal imputation (numeric)

logreg Logistic regression (factor, 2 categories)

polyreg Polytomous logistic regression (factor, ≥ 2 categories)

lda Linear discriminant analysis (factor, ≥ 2 categories)

sample Random sample from the observed values (any)

These corresponding functions are coded in the `mice` library under names `mice.impute.method`, where `method` is a string with the name of the elementary 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", ...)`.

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 elementary 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 elementary 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.

Value

Returns an object of class `mids` (multiply imputed data set) with components

<code>call</code>	The call that created the object
<code>data</code>	A copy of the incomplete data set
<code>m</code>	The number of imputations
<code>nmis</code>	An array of length <code>ncol(data)</code> containing the number of missing observations per column
<code>imp</code>	A list of <code>ncol(data)</code> components with the generated multiple imputations. Each part of the list is a <code>nmis[j]</code> by <code>m</code> matrix of imputed values for variable <code>data[,j]</code> . The component equals <code>NULL</code> for columns without missing data.
<code>method</code>	A vector of strings of length <code>ncol(data)</code> specifying the elementary imputation method per column
<code>predictorMatrix</code>	A square matrix of size <code>ncol(data)</code> containing 0/1 data specifying the predictor set
<code>visitSequence</code>	The sequence in which columns are visited
<code>post</code>	A vector of strings of length <code>ncol(data)</code> with commands for post-processing
<code>seed</code>	The seed value of the solution
<code>iteration</code>	Last Gibbs sampling iteration number
<code>lastSeedValue</code>	The most recent seed value
<code>chainMean</code>	An array containing the mean of the generated multiple imputations. The array can be used for monitoring convergence. Factors are replaced by their numerical representation using <code>as.integer()</code> . Note that observed data are not present in this mean.

<code>chainVar</code>	An array with similar structure of <code>chainMean</code> , containing the variances of the imputed values.
<code>pad</code>	A list containing various settings of the padded imputation model, i.e. the imputation model after creating dummy variables. Normally, this list is only useful for error checking. List members are <code>pad\$data</code> (data padded with columns for factors), <code>pad\$predictorMatrix</code> (predictor matrix for the padded data), <code>pad\$method</code> (imputation methods applied to the padded data), the vector <code>pad\$visitSequence</code> (the visit sequence applied to the padded data), <code>pad\$post</code> (post-processing commands for padded data) and <code>categories</code> (a matrix containing descriptive information about the padding operation).

Author(s)

Stef van Buuren (stef.vanbuuren@tno.nl), Karin Groothuis-Oudshoorn (k.groothuis@rrd.nl) (2000-2009) with contributions of Roel de Jong, Jason Turner, John Fox, Frank E. Harrell, and Peter Malewski.

References

Van Buuren, S., Groothuis-Oudshoorn, K. (2009) MICE: Multivariate Imputation by Chained Equations in R. *Journal of Statistical Software*, forthcoming. <http://www.stefvanbuuren.nl/publications/MICEinR-Draft.pdf>

Van Buuren, S., Brand, J.P.L., Groothuis-Oudshoorn C.G.M., Rubin, D.B. (2006) Fully conditional specification in multivariate imputation. *Journal of Statistical Computation and Simulation*, **76**, 12, 1049–1064. <http://www.stefvanbuuren.nl/publications/FCSinmultivariateimputation-JSCS2.pdf>

Van Buuren, S. (2007) Multiple imputation of discrete and continuous data by fully conditional specification. *Statistical Methods in Medical Research*, **16**, 3, 219–242. <http://www.stefvanbuuren.nl/publications/MIbyFCS-SMMR2007.pdf>

Van Buuren, S., Boshuizen, H.C., Knook, D.L. (1999) Multiple imputation of missing blood pressure covariates in survival analysis. *Statistics in Medicine*, **18**, 681–694. <http://www.stefvanbuuren.nl/publications/Multipleimputation-StatMed1999.pdf>

Brand, J.P.L. (1999) *Development, implementation and evaluation of multiple imputation strategies for the statistical analysis of incomplete data sets*. Dissertation. Rotterdam: Erasmus University.

See Also

[complete](#), [mids](#), [with.mids](#), [set.seed](#)

Examples

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

# list the actual imputations for BMI
imp$imputations$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.norm
```

Imputation by a Two-Level Normal Model

Description

Imputes univariate missing data using a two-level normal model

Usage

```
mice.impute.2l.norm(y, ry, x, type)
```

Arguments

<code>y</code>	Incomplete data vector of length <code>n</code>
<code>ry</code>	Vector of missing data pattern (FALSE=missing, TRUE=observed)
<code>x</code>	Matrix (<code>n</code> x <code>p</code>) of complete covariates.
<code>type</code>	Vector of length <code>ncol(x)</code> identifying random and class variables. Random variables are identified by a '2'. The class variable (only one is allow) is code as '-2'. Random variables always include the fixed effect.

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 statistical properties see Van Buuren (2010).

Value

A vector of length `nmis` with imputations.

Author(s)

Roel de Jong, 2008

References

Kasim RM, Raudenbush SW. (1998). Application of Gibbs sampling to nested variance components models with heterogeneous within-group variance. *Journal of Educational and Behavioral Statistics*, 23(2), 93–116.

Van Buuren, S., Groothuis-Oudshoorn, K. (2009) MICE: Multivariate Imputation by Chained Equations in R. *Journal of Statistical Software*, forthcoming. <http://www.stefvanbuuren.nl/publications/MICEinR-Draft.pdf>

Van Buuren, S. (2010) Multiple imputation of multilevel data. In Hox, J.J. and Roberts, K. (Eds.), *The Handbook of Advanced Multilevel Analysis*, Milton Park, UK: Routledge.

mice.impute.lda *Imputation by Linear Discriminant Analysis*

Description

Imputes univariate missing data using linear discriminant analysis

Usage

```
mice.impute.lda(y, ry, x)
```

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.

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.

Value

A vector of length `nmiss` with imputations.

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 somewhat underestimated.

Note

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 `mice.impute.polyreg`.

Author(s)

Stef van Buuren, Karin Groothuis-Oudshoorn, 2000

References

Van Buuren, S., Groothuis-Oudshoorn, K. (2009) MICE: Multivariate Imputation by Chained Equations in R. *Journal of Statistical Software*, forthcoming. <http://www.stefvanbuuren.nl/publications/MICEinR-Draft.pdf>

Brand, J.P.L. (1999). Development, Implementation and Evaluation of Multiple Imputation Strategies for the Statistical Analysis of Incomplete Data Sets. Ph.D. Thesis, TNO Prevention and Health/Erasmus University Rotterdam. ISBN 90-74479-08-1.

Venables, W.N. & Ripley, B.D. (1997). Modern applied statistics with S-PLUS (2nd ed). Springer, Berlin.

See Also

`mice`, `link{mice.impute.polyreg}`, `lda`

`mice.impute.logreg` *Imputation by Logistic Regression*

Description

Imputes univariate missing data using logistic regression.

Usage

```
mice.impute.logreg(y, ry, x)
```

Arguments

<code>y</code>	Incomplete data vector of length <code>n</code>
<code>ry</code>	Vector of missing data pattern of length <code>n</code> (FALSE=missing, TRUE=observed)
<code>x</code>	Matrix (<code>n</code> x <code>p</code>) of complete covariates.

Details

Imputation for binary response variables by the Bayesian logistic regression model. See Rubin (1987, p. 169-170) for a description of the method. The 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. $\text{logit}^{-1}(X \text{ BETA})$
4. Compare the score to a random (0,1) deviate, and impute.

The method relies on the standard `glm.fit` function.

Value

`imp` A vector of length `nmis` with imputations (0 or 1).

Author(s)

Stef van Buuren, Karin Groothuis-Oudshoorn, 2000

References

Van Buuren, S., Groothuis-Oudshoorn, K. (2009) MICE: Multivariate Imputation by Chained Equations in R. *Journal of Statistical Software*, forthcoming. <http://www.stefvanbuuren.nl/publications/MICEinR-Draft.pdf>

Brand, J.P.L. (1999). Development, Implementation and Evaluation of Multiple Imputation Strategies for the Statistical Analysis of Incomplete Data Sets. Ph.D. Thesis, TNO Prevention and Health/Erasmus University Rotterdam. ISBN 90-74479-08-1.

Venables, W.N. & Ripley, B.D. (1997). Modern applied statistics with S-Plus (2nd ed). Springer, Berlin.

See Also

[mice](#), [glm](#), [glm.fit](#)

`mice.impute.mean` *Imputation by the Mean*

Description

Imputes the arithmetic mean of the observed data

Usage

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

Arguments

<code>y</code>	Incomplete data vector of length <code>n</code>
<code>ry</code>	Vector of missing data pattern (FALSE=missing, TRUE=observed)
<code>x</code>	Matrix (<code>n x p</code>) of complete covariates.

Value

A vector of length `nmiss` with imputations.

Warning

Imputing the mean of a variable is almost never appropriate. See Little and Rubin (1987).

Author(s)

Stef van Buuren, Karin Oudshoorn, 2000

References

Van Buuren, S., Groothuis-Oudshoorn, K. (2009) MICE: Multivariate Imputation by Chained Equations in R. *Journal of Statistical Software*, forthcoming. <http://www.stefvanbuuren.nl/publications/MICEinR-Draft.pdf>

Little, R.J.A. and Rubin, D.B. (1987). *Statistical Analysis with Missing Data*. New York: John Wiley and Sons.

See Also

[mice, mean](#)

`mice.impute.norm` *Imputation by Bayesian Linear Regression*

Description

Imputes univariate missing data using Bayesian linear regression analysis

Usage

```
mice.impute.norm(y, ry, x)
```

Arguments

<code>y</code>	Incomplete data vector of length <code>n</code>
<code>ry</code>	Vector of missing data pattern (FALSE=missing, TRUE=observed)
<code>x</code>	Matrix (<code>n x p</code>) of complete covariates.

Details

Draws values of `beta` and `sigma` for Bayesian linear regression imputation of `y` given `x` according to Rubin p. 167.

Value

A vector of length `nmiss` with imputations.

Note

Using `mice.impute.norm` for all columns is similar to Schafer's NORM method (Schafer, 1997).

Author(s)

Stef van Buuren, Karin Groothuis-Oudshoorn, 2000

References

Van Buuren, S., Groothuis-Oudshoorn, K. (2009) MICE: Multivariate Imputation by Chained Equations in R. *Journal of Statistical Software*, forthcoming. <http://www.stefvanbuuren.nl/publications/MICEinR-Draft.pdf>

Brand, J.P.L. (1999) *Development, implementation and evaluation of multiple imputation strategies for the statistical analysis of incomplete data sets*. Dissertation. Rotterdam: Erasmus University.

Schafer, J.L. (1997). *Analysis of incomplete multivariate data*. London: Chapman & Hall.

`mice.impute.norm.nob`

Imputation by Linear Regression (non Bayesian)

Description

Imputes univariate missing data using linear regression analysis (non Bayesian version)

Usage

```
mice.impute.norm.nob(y, ry, x)
```

Arguments

<code>y</code>	Incomplete data vector of length <code>n</code>
<code>ry</code>	Vector of missing data pattern (FALSE=missing, TRUE=observed)
<code>x</code>	Matrix (<code>n x p</code>) of complete covariates.

Details

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

Value

A vector of length `nmi.s` with imputations.

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.

Note

This function is provided mainly to allow comparison between proper and improper norm methods. Also, it may be useful to impute large data containing many rows.

Author(s)

Stef van Buuren, Karin Groothuis-Oudshoorn, 2000

References

Van Buuren, S., Groothuis-Oudshoorn, K. (2009) MICE: Multivariate Imputation by Chained Equations in R. *Journal of Statistical Software*, forthcoming. <http://www.stefvanbuuren.nl/publications/MICEinR-Draft.pdf>

Brand, J.P.L. (1999). Development, Implementation and Evaluation of Multiple Imputation Strategies for the Statistical Analysis of Incomplete Data Sets. Ph.D. Thesis, TNO Prevention and Health/Erasmus University Rotterdam.

See Also

[mice](#), [mice.impute.norm](#)

`mice.impute.passive`

Passive Imputation

Description

Derive a new variable based on the imputed data

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 $Q = W/H^2$ based on two variables, or a mean variable like $(x_1+x_2+x_3)/3$. 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

t	The transformed data
---	----------------------

Author(s)

Stef van Buuren, Karin Groothuis-Oudshoorn, 2000

References

Van Buuren, S., Groothuis-Oudshoorn, K. (2009) MICE: Multivariate Imputation by Chained Equations in R. *Journal of Statistical Software*, forthcoming. <http://www.stefvanbuuren.nl/publications/MICEinR-Draft.pdf>

See Also

[mice](#)

mice.impute.pmm *Imputation by Predictive Mean Matching*

Description

Imputes univariate missing data using predictive mean matching

Usage

```
mice.impute.pmm(y, ry, x)
```

Arguments

y	Numeric vector with incomplete data
ry	Response pattern of y (TRUE=observed, FALSE=missing)
x	Design matrix with length(y) rows and p columns containing complete covariates

Details

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

1. Draw beta and sigma from the proper posterior
2. Compute predicted values for y_{obs} and y_{mis}
3. For each y_{mis} , find the observation with closest predicted value, and take its observed value in y as the imputation.
4. If there is more than one candidate, make a random draw among them. Note: The matching is done on predicted y , NOT on observed y .

Value

`imp` Numeric vector of length `sum(!ry)` with imputations

Author(s)

Stef van Buuren, Karin Groothuis-Oudshoorn, 2000

References

Little, R.J.A. (1988), Missing data adjustments in large surveys (with discussion), *Journal of Business Economics and Statistics*, 6, 287–301.

Rubin, D.B. (1987). *Multiple imputation for nonresponse in surveys*. New York: Wiley.

Van Buuren, S., Brand, J.P.L., Groothuis-Oudshoorn C.G.M., Rubin, D.B. (2006) Fully conditional specification in multivariate imputation. *Journal of Statistical Computation and Simulation*, 76, 12, 1049–1064. <http://www.stefvanbuuren.nl/publications/FCSinmultivariateimputation-JSCS2.pdf>

Van Buuren, S., Groothuis-Oudshoorn, K. (2009) MICE: Multivariate Imputation by Chained Equations in R. *Journal of Statistical Software*, forthcoming. <http://www.stefvanbuuren.nl/publications/MICEinR-Draft.pdf>

`mice.impute.polyreg`

Imputation by Polytomous Regression

Description

Imputes missing data in a categorical variable using polytomous regression

Usage

`mice.impute.polyreg(y, ry, x)`

Arguments

<code>y</code>	Incomplete data vector of length <code>n</code>
<code>ry</code>	Vector of missing data pattern (<code>FALSE</code> =missing, <code>TRUE</code> =observed)
<code>x</code>	Matrix (<code>n x p</code>) of complete covariates.

Details

Imputation for categorical response variables by the Bayesian polytomous regression model. See J.P.L. Brand (1999), Chapter 4, Appendix B.

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.

This algorithm uses the function `multinom()` from the libraries `nnet` (Venables and Ripley).

Value

A vector of length `nmiss` with imputations.

Author(s)

Stef van Buuren, Karin Groothuis-Oudshoorn, 2000

References

Van Buuren, S., Groothuis-Oudshoorn, K. (2009) MICE: Multivariate Imputation by Chained Equations in R. *Journal of Statistical Software*, forthcoming. <http://www.stefvanbuuren.nl/publications/MICEinR-Draft.pdf>

Brand, J.P.L. (1999) *Development, implementation and evaluation of multiple imputation strategies for the statistical analysis of incomplete data sets*. Dissertation. Rotterdam: Erasmus University.

Venables, W.N. & Ripley, B.D. (1997). *Modern applied statistics with S-Plus* (2nd ed). Springer, Berlin.

See Also

[mice](#), [multinom](#)

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)
```

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.

Details

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

Value

A vector of length n with imputations.

Author(s)

Stef van Buuren, Karin Groothuis-Oudshoorn, 2000

References

Van Buuren, S., Groothuis-Oudshoorn, K. (2009) MICE: Multivariate Imputation by Chained Equations in R. *Journal of Statistical Software*, forthcoming. <http://www.stefvanbuuren.nl/publications/MICEinR-Draft.pdf>

`mice.mids`*Multivariate Imputation by Chained Equations (Iteration Step)*

Description

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

Usage

```
## S3 method for class 'mids':  
mice(obj, maxit=1, diagnostics=TRUE, printFlag=TRUE)
```

Arguments

<code>obj</code>	An object of class <code>mids</code> , typically produced by a previous call to <code>mice()</code> or <code>mice.mids()</code>
<code>maxit</code>	The number of additional Gibbs sampling iterations.
<code>diagnostics</code>	A Boolean flag. If <code>TRUE</code> , diagnostic information will be appended to the value of the function. If <code>FALSE</code> , only the imputed data are saved. The default is <code>TRUE</code> .
<code>printFlag</code>	A Boolean flag. If <code>TRUE</code> , diagnostic information during the Gibbs sampling iterations will be written to the command window. The default is <code>TRUE</code> .

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

Van Buuren, S., Groothuis-Oudshoorn, K. (2009) MICE: Multivariate Imputation by Chained Equations in R. *Journal of Statistical Software*, forthcoming. <http://www.stefvanbuuren.nl/publications/MICEinR-Draft.pdf>

See Also

[complete](#), [mice](#), [set.seed](#)

Examples

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

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

# for example:
#
# > imp$imp$bmi[1,]
#   1   2   3   4   5
# 1 30.1 35.3 33.2 35.3 27.5
# > imp2$imp$bmi[1,]
#   1   2   3   4   5
# 1 30.1 35.3 33.2 35.3 27.5
#
```

mids

Multiply Imputed Data Set

Description

An object containing a multiply imputed data set. The `mids` object is generated by the `mice` and `mice.mids` functions. The `mids` class of objects has methods for the following generic functions: `print`, `summary`, `plot`.

Usage

```
## S3 method for class 'mids':
print(x, ...)
## S3 method for class 'mids':
summary(object, ...)
## S3 method for class 'mids':
plot(x, layoutplot = c(3, 2), askplot = TRUE, ...)
```

Arguments

<code>x</code> , object	A <code>mids</code> object.
<code>layoutplot</code>	Vector of two integers specifying the number of panel per row and column respectively.
<code>askplot</code>	TRUE if the user needs to be asked before drawing a new page
...	Currently not used.

Value

<code>call</code>	The call that created the object.
<code>data</code>	A copy of the incomplete data set.
<code>m</code>	The number of imputations.
<code>nmis</code>	An array containing the number of missing observations per column.
<code>imp</code>	A list of <code>nvar</code> components with the generated multiple imputations. Each part of the list is a <code>nmis[j]</code> by <code>m</code> matrix of imputed values for variable <code>j</code> .
<code>method</code>	A vector of strings of length(<code>nvar</code>) specifying the elementary imputation method per column.
<code>predictorMatrix</code>	A square matrix of size <code>ncol(data)</code> containing code 0/1 data specifying the predictor set.
<code>visitSequence</code>	The sequence in which columns are visited.
<code>post</code>	A vector of strings of length <code>ncol(data)</code> with commands for post-processing
<code>seed</code>	The seed value of the solution.
<code>iteration</code>	Last Gibbs sampling iteration number.
<code>lastSeedValue</code>	The most recent seed value.
<code>chainMean</code>	A list of <code>m</code> components. Each component is a <code>length(visitSequence)</code> by <code>maxit</code> 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.
<code>chainVar</code>	A list with similar structure of <code>chainMean</code> , containing the covariances of the imputed values.
<code>pad</code>	A list containing various settings of the padded imputation model, i.e. the imputation model after creating dummy variables. Normally, this array is only useful for error checking.

Author(s)

Stef van Buuren, Karin Groothuis-Oudshoorn, 2000

References

Van Buuren, S., Groothuis-Oudshoorn, K. (2009) MICE: Multivariate Imputation by Chained Equations in R. *Journal of Statistical Software*, forthcoming. <http://www.stefvanbuuren.nl/publications/MICEinR-Draft.pdf>

See Also

[mice](#), [mira](#), [mipo](#)

mipo

Multiply Imputed Pooled Analysis

Description

The `mipo` object is generated by the `pool` function from a `link{mira}` object. The `mipo` class of objects has methods for the following generic functions: `print`, `summary`.

Usage

```
## S3 method for class 'mipo':
print(x, ...)
## S3 method for class 'mipo':
summary(object, ...)
```

Arguments

<code>x</code> , <code>object</code>	An object of class <code>mira</code> containing the <code>m</code> fit objects of a complete data analysis, plus some additional information.
<code>...</code>	not used.

Value

<code>call</code>	The call that created the <code>mipo</code> object.
<code>call1</code>	The call that created the <code>mira</code> object that was used in <code>call</code> .
<code>call2</code>	The call that created the <code>mids</code> object that was used in <code>call1</code> .
<code>nmis</code>	An array containing the number of missing observations per column.
<code>m</code>	Number of multiple imputations.
<code>qhat</code>	An <code>m</code> by <code>npar</code> matrix containing the complete data estimates for the <code>npar</code> parameters of the <code>m</code> complete data analyses.
<code>u</code>	An <code>m</code> by <code>npar</code> by <code>npar</code> array containing the variance-covariance matrices of the <code>m</code> complete data analyses.
<code>qbar</code>	The average of complete data estimates.
<code>ubar</code>	The average of the variance-covariance matrix of the complete data estimates.
<code>b</code>	The between imputation variance-covariance matrix.
<code>t</code>	The total variance-covariance matrix.
<code>r</code>	Relative increases in variance due to missing data
<code>df</code>	Degrees of freedom associated with the t-statistics.
<code>f</code>	Fraction of missing information.

Author(s)

Stef van Buuren, Karin Groothuis-Oudshoorn, 2000

References

Van Buuren, S., Groothuis-Oudshoorn, K. (2009) MICE: Multivariate Imputation by Chained Equations in R. *Journal of Statistical Software*, forthcoming. <http://www.stefvanbuuren.nl/publications/MICEinR-Draft.pdf>

See Also

[pool](#), [mids](#), [mira](#)

mira

Multiply Imputed Repeated Analyses

Description

The `mira` object is generated by the `with.mids()`, `lm.mids()` and `glm.mids()` functions. The `mira` class of objects has methods for the following generic functions: `print`, `summary`.

Usage

```
## S3 method for class 'mira':
print(x, ...)
## S3 method for class 'mira':
summary(object, correlation, ...)
```

Arguments

<code>x</code> , <code>object</code>	An object containing the <code>m</code> fit objects of a complete data analysis, plus some additional information.
<code>correlation</code>	
<code>...</code>	not used

Value

<code>call</code>	The call that created the object.
<code>call1</code>	The call that created the <code>mids</code> object that was used in <code>call</code> .
<code>nmis</code>	An array containing the number of missing observations per column.
<code>analyses</code>	A list of <code>m</code> components containing the individual fit objects from each of the <code>m</code> complete data analyses.

Author(s)

Stef van Buuren, Karin Groothuis-Oudshoorn, 2000

References

Van Buuren, S., Groothuis-Oudshoorn, K. (2009) MICE: Multivariate Imputation by Chained Equations in R. *Journal of Statistical Software*, forthcoming. <http://www.stefvanbuuren.nl/publications/MICEinR-Draft.pdf>

See Also

[with.mids](#), [mids](#), [mipo](#)

nhanes

NHANES example - all variables numerical

Description

A small data set with non-monotone missing values.

Usage

```
data(nhanes)
```

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)

ch1 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

Schafer, J.L. (1997). *Analysis of Incomplete Multivariate Data*. London: Chapman & Hall. Table 6.14.

See Also

[nhanes2](#)

Examples

```
imp <- mice(nhanes)      # create 5 imputed data sets
complete(imp)           # print the first imputed data set
```

`nhanes2`*NHANES example - mixed numerical and discrete variables*

Description

A small data set with non-monotone missing values.

Usage

```
data(nhanes2)
```

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)

ch1 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

Schafer, J.L. (1997). *Analysis of Incomplete Multivariate Data*. London: Chapman & Hall. Table 6.14.

See Also

[nhanes](#)

Examples

```
imp <- mice(nhanes2)      # create 5 imputed data sets
complete(imp)           # print the first imputed data set
```

 pool

Multiple Imputation Pooling

Description

Pools the results of m repeated complete data analysis

Usage

```
pool(object, method="smallsample")
```

Arguments

object	An object of class <code>mira</code> , produced by <code>with.mids()</code> .
method	A string describing the method to compute the degrees of freedom. The default value is "smallsample", which specifies the is Barnard-Rubin adjusted degrees of freedom (Barnard and Rubin, 1999) for small samples. Specifying a different string produces the conventional degrees of freedom as in Rubin (1987).

Details

The function averages the 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. The function relies on the availability of

1. the estimates of the model, typically present as 'coefficients' in the fit object
2. an appropriate estimate of the variance-covariance matrix of the estimates per analyses (estimated by `vcov`).

The function pools also estimates obtained with `lme()` and `lmer()`, BUT only the fixed part of the model.

Value

An object of class `mipo`, which stands for 'multiple imputation pooled outcome'. The object is a list containing the following items:

call	The call to the pool function.
call1	The original call how the <code>mira</code> object was calculated.
call2	The original call to the <code>mice</code> function to calculate the underlying <code>midsobject</code> .
formula	The formula that is used in <code>call1</code> .
nmis	The number of missing entries for each variable.
m	The number of imputations
qhat	A matrix, containing the estimated coefficients of the m repeated complete data analyses

u	The corresponding m variance matrices of the estimates in an three dimensional array.
qbar	The pooled estimate, formula (3.1.2) Rubin (1987).
ubar	The mean of the variances, formula (3.1.3), Rubin (1987).
b	The within imputation variance, formula (3.1.4), Rubin (1987).
t	Total variance of the pooled estimates, formula (3.1.5), Rubin (1987).
r	Relative increase in variance due to nonresponse, formula (3.1.7), Rubin (1987).
df	Degrees of freedom for t reference distribution, calculated according to the article of Barnard and Rubin (1999).
f	Fraction missing information due to nonresponse, formula (3.1.10), Rubin (1987).

Author(s)

Stef van Buuren, Karin Groothuis-Oudshoorn, 2009

References

Barnard, J. and Rubin, D.B. (1999). Small sample degrees of freedom with multiple imputation. *Biometrika*, 86, 948-955.

Rubin, D.B. (1987). *Multiple Imputation for Nonresponse in Surveys*. New York: John Wiley and Sons.

Van Buuren, S., Groothuis-Oudshoorn, K. (2009) MICE: Multivariate Imputation by Chained Equations in R. *Journal of Statistical Software*, forthcoming. <http://www.stefvanbuuren.nl/publications/MICEinR-Draft.pdf>

Pinheiro, J.C. and Bates, D.M. (2000). *Mixed-Effects Models in S and S-PLUS*. Berlin: Springer.

See Also

[with.mids](#), [vcov](#), [print.mipo](#), [summary.mipo](#)

Examples

```
# which vcov methods can R find
methods(vcov)

#
imp <- mice(nhanes)
fit <- with(data=imp, exp=lm(bmi~hyp+chl))
pool(fit)

#Call: pool(object = fit)
#
#Pooled coefficients:
#(Intercept)      hyp      chl
# 22.01313    -1.45578    0.03459
#
#Fraction of information about the coefficients missing due to nonresponse:
#(Intercept)      hyp      chl
```

```

#      0.29571      0.05639      0.38759
#> summary(pool(fit))
#              est          se          t          df Pr(>|t|)      lo 95      hi 95 missing
#(Intercept) 22.01313  4.94086  4.4553 12.016 0.000783 11.24954 32.77673      NA
#hyp         -1.45578  2.26789 -0.6419 20.613 0.528006 -6.17752  3.26596      8
#chl         0.03459  0.02829  1.2228  9.347 0.251332 -0.02904  0.09822     10
#              fmi
#(Intercept) 0.29571
#hyp         0.05639
#chl         0.38759
#

```

pool.compare	<i>Compare two nested models fitted to imputed data</i>
--------------	---

Description

Compares two nested models after *m* repeated complete data analysis

Usage

```
pool.compare(fit1, fit0, data=NULL, method="Wald")
```

Arguments

fit1	An object of class 'mira', produced by <code>with.mids()</code> .
fit0	An object of class 'mira', produced by <code>with.mids()</code> . The model in <code>fit0</code> should be a submodel of <code>fit1</code> . Moreover, the variables of the submodel should be the first variables of the larger model and in the same order as in the submodel.
data	In case of method "likelihood" it is necessary to pass also the original <code>mids</code> object to the <code>data</code> argument. Default value is <code>NULL</code> , in case of <code>method="Wald"</code> .
method	A string describing the method to compare the two models. Two kind of comparisons are included so far: "Wald" and "likelihood".

Details

The function is based on the article of Meng and Rubin (1992). The Wald-method can be found in paragraph 2.2 and the likelihoodmethod 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()`. It is assumed that `fit1` contains the larger model and the model in `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 the elements:

call	The call to the <code>pool.compare</code> function
call11	The call that created <code>fit1</code>
call12	The call that created the imputations.
call01	The call that created <code>fit0</code>
call02	The call that created the imputations.
method	The method used to compare two models: "Wald" or "likelihood"
nmis	The number of missing entries for each variable.
m	The number of imputations
qhat1	A matrix, containing the estimated coefficients of the m repeated complete data analyses from <code>fit1</code>
qhat0	A matrix, containing the estimated coefficients of the m repeated complete data analyses from <code>fit0</code>
ubar1	The mean of the variances of <code>object1</code> , formula (3.1.3), Rubin (1987).
ubar0	The mean of the variances of <code>object0</code> , formula (3.1.3), Rubin (1987).
qbar1	The pooled estimate of <code>object1</code> , formula (3.1.2) Rubin (1987).
qbar0	The pooled estimate of <code>object0</code> , formula (3.1.2) Rubin (1987).
Dm	The test statistic
rm	Relative increase in variance due to nonresponse, formula (3.1.7), Rubin (1987).
df1	df1; Under the null hypothesis it is assumed that D_m has an F distribution with (df1,df2) degrees of freedom.
df2	df2
pvalue	P-value of testing whether the larger model is statistically different from the smaller submodel.

Author(s)

Karin Groothuis-Oudshoorn and Stef van Buuren, 2009

References

- Li, K.H., Meng, X.L., Raghunathan, T.E. and Rubin, D. B. (1991). Significance levels from repeated p-values with multiply-imputed data. *Statistica Sinica*, 1, 65-92.
- Meng, X.L. and Rubin, D.B. (1992). Performing likelihood ratio tests with multiple-imputed data sets. *Biometrika*, 79, 103-111.
- Van Buuren, S., Groothuis-Oudshoorn, K. (2009) MICE: Multivariate Imputation by Chained Equations in R. *Journal of Statistical Software*, forthcoming. <http://www.stefvanbuuren.nl/publications/MICEinR-Draft.pdf>

See Also

[lm.mids](#), [glm.mids](#), [vcov](#), [print.mira](#), [summary.mira](#)

Examples

```
### To compare two linear models:
imp <- mice(nhanes2)
mi1 <- with(data=imp, expr=lm(bmi~age+hyp+chl))
mi0 <- with(data=imp, expr=lm(bmi~age+hyp))
pc <- pool.compare(mi1, mi0, method="Wald")
pc$spvalue
#           [,1]
#[1,] 0.000293631
#

### Comparison of two general linear models (logistic regression).
imp <- mice(boys, maxit=2)

fit0 <- with(imp, glm(gen>levels(gen)[1] ~ hgt+hc, family=binomial))
fit1 <- with(imp, glm(gen>levels(gen)[1] ~ hgt+hc+reg, family=binomial))
pool.compare(fit1, fit0, method="likelihood", data=imp)
```

pool.r.squared *Pooling: R squared*

Description

Pools R^2 of m repeated complete data models.

Usage

```
pool.r.squared(object, adjusted=FALSE)
```

Arguments

object	An object of class 'mira', produced by <code>lm.mids</code> or <code>with.mids</code> with <code>lm</code> as modelling function.
adjusted	A logical value. If <code>adjusted=TRUE</code> then the adjusted R^2 is calculated. The default value is <code>FALSE</code> .

Details

The function pools the coefficients of determination R^2 or the adjusted coefficients of determination (R^2_a) obtained with the `lm` modelling function. For pooling it uses the Fisher z -transformation.

Value

Returns a 1x4 table with elements:

est	The pooled R^2 estimate
lo95	The 95 % lower bound of the pooled R^2 .

hi95 The 95 % upper bound of the pooled R².
 fmi The fraction of missing information due to nonresponse.

Author(s)

Karin Groothuis-Oudshoorn and Stef van Buuren, 2009

References

Harel, O (2009). The estimation of R² and adjusted R² in incomplete data sets using multiple imputation, *Journal of Applied Statistics* (to appear).

Rubin, D.B. (1987). *Multiple Imputation for Nonresponse in Surveys*. New York: John Wiley and Sons.

Van Buuren, S., Groothuis-Oudshoorn, K. (2009) MICE: Multivariate Imputation by Chained Equations in R. *Journal of Statistical Software*, forthcoming. <http://www.stefvanbuuren.nl/publications/MICEinR-Draft.pdf>

See Also

[pool, pool.scalar](#)

Examples

```
imp<-mice(nhanes)

fit<-lm.mids(chl~age+hyp+bmi, imp)
pool.r.squared(fit)
pool.r.squared(fit, adjusted=TRUE)

#fit<-lm.mids(chl~age+hyp+bmi, imp)
#
#> pool.r.squared(fit)
#      est      lo 95      hi 95      fmi
#R^2  0.5108041 0.1479687 0.7791927 0.3024413
#
#> pool.r.squared(fit, adjusted=TRUE)
#      est      lo 95      hi 95      fmi
#adj R^2 0.4398066 0.08251427 0.743172 0.3404165
#
```

pool.scalar

Multiple Imputation Pooling: Univariate version

Description

Pools univariate estimates of m repeated complete data analysis

Usage

```
pool.scalar(Q, U)
```

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.

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 The 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, formula (3.1.3) Rubin (1987).
b The within imputation variance, formula (3.1.4) Rubin (1987).
t Total variance of the pooled estimated, formula (3.1.5) Rubin (1987).
r Relative increase in variance due to nonresponse, formula (3.1.7) Rubin (1987).
df Degrees of freedom for t reference distribution, formula (3.1.6) Rubin (1987).
f Fraction missing information due to nonresponse, formula (3.1.10) Rubin (1987).

Author(s)

Karin Groothuis-Oudshoorn and Stef van Buuren, 2009

References

Rubin, D.B. (1987). Multiple Imputation for Nonresponse in Surveys. New York: John Wiley and Sons.

See Also

[pool](#)

Examples

```

imp <- mice(nhanes)
m <- imp$m
Q <- rep(NA,m)
U <- rep(NA,m)
for (i in 1:m) {
  Q[i] <- mean(complete(imp,i)$bmi)
  U[i] <- var(complete(imp,i)$bmi)
}
pool.scalar(Q,U)

#pool.scalar(Q,U)
#$m
#[1] 5
#
#$qhat
#[1] 26.764 26.748 27.024 27.340 26.436
#
#$u
#[1] 17.85490 19.11677 20.61440 21.05750 15.16990
#
#$qbar
#[1] 26.8624
#
#$ubar
#[1] 18.76269
#
#$b
#[1] 0.1147008
#
#$t
#[1] 18.90033
#
#$r
#[1] 0.007335885
#
#$df
#[1] 75422.96
#
#$f
#[1] 0.007308785
#

```

 popmis

Hox pupil popularity data with missing popularity scores

Description

Hox pupil popularity data with some missing popularity scores

Usage

```
data (popmis)
```

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
teexp 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

Hox, J. J. (2002) *Multilevel analysis. Techniques and applications*. Mahwah, NJ: Lawrence Erlbaum.

Examples

```
popmis[1:3, ]
```

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

<code>data</code>	Matrix or data frame with incomplete data.
<code>mincor</code>	A scalar, numeric vector (of size <code>ncol(data)</code>) or numeric matrix (square, of size <code>ncol(data)</code>) specifying the minimum threshold(s) against which the absolute correlation in the data is compared.
<code>minpuc</code>	A scalar, vector (of size <code>ncol(data)</code>) or matrix (square, of size <code>ncol(data)</code>) specifying the minimum threshold(s) for the proportion of usable cases.
<code>include</code>	A string or a vector of strings containing one or more variable names from <code>names(data)</code> . Variables specified are always included as a predictor.
<code>exclude</code>	A string or a vector of strings containing one or more variable names from <code>names(data)</code> . Variables specified are always excluded as a predictor.
<code>method</code>	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 values for 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)`.

Author(s)

Stef van Buuren, Aug 2009

References

Van Buuren, S., Groothuis-Oudshoorn, K. (2009) MICE: Multivariate Imputation by Chained Equations in R. *Journal of Statistical Software*, forthcoming. <http://www.stefvanbuuren.nl/publications/MICEinR-Draft.pdf>

See Also

[mice](#), [mids](#)

Examples

```
# 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
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	<i>Combine a Multiply Imputed Data Set with other mids object or dataframe</i>
------------	--

Description

Append mids objects by rows

Usage

```
rbind.mids(x, y, ...)
```

Arguments

x	A mids object.
y	A mids object or a dataframe, matrix, factor or vector.
...	Dataframes, matrices, vectors or factors. These can be given as named arguments.

Details

This function combines two `mids` objects rowwise into a single `mids` object or combines a `mids` object and a vector, matrix, factor or dataframe rowwise into a `mids` object. The number of columns in the (incomplete) data `x$data` and `y` (or `y$data` if `y` is a `mids` object) should be equal. If `y` is a `mids` object then the number of imputations in `x` and `y` should be equal.

Value

<code>call</code>	A vector, with first argument the <code>mice()</code> statement that created <code>x</code> and second argument the call to <code>rbind.mids()</code>
<code>data</code>	The rowwise combination of the (incomplete) data in <code>x</code> and <code>y</code> .
<code>m</code>	<code>x\$m</code>
<code>nmis</code>	An array containing the number of missing observations per column, defined as <code>x\$nmis + y\$nmis</code>
<code>imp</code>	A list of <code>nvar</code> components with the generated multiple imputations. Each part of the list is a <code>nmis[j]</code> by <code>m</code> matrix of imputed values for variable <code>j</code> . If <code>y</code> is a <code>mids</code> object then <code>imp[[j]]</code> equals <code>rbind(x\$imp[[j]], y\$imp[[j]])</code> ; otherwise the original data of <code>y</code> will be copied into this list, including the missing values of <code>y</code> then <code>y</code> is not imputed.
<code>method</code>	A vector of strings of length <code>nvar</code> specifying the elementary imputation method per column defined as <code>x\$method</code>
<code>predictorMatrix</code>	A square matrix of size <code>ncol(data)</code> containing code 0/1 data specifying the predictor set defined as <code>x\$predictorMatrix</code>
<code>visitSequence</code>	The sequence in which columns are visited, defined as <code>x\$visitSequence</code> .
<code>seed</code>	The seed value of the solution, <code>x\$seed</code>
<code>iteration</code>	Last Gibbs sampling iteration number, <code>x\$iteration</code>
<code>lastSeedValue</code>	The most recent seed value, <code>x\$lastSeedValue</code>
<code>chainMean</code>	Set to NA
<code>chainVar</code>	Set to NA
<code>pad</code>	<code>x\$pad</code> , a list containing various settings of the padded imputation model, i.e. the imputation model after creating dummy variables

Author(s)

Karin Groothuis-Oudshoorn, Stef van Buuren, 2009

References

Van Buuren, S., Groothuis-Oudshoorn, K. (2009) MICE: Multivariate Imputation by Chained Equations in R. *Journal of Statistical Software*, forthcoming. <http://www.stefvanbuuren.nl/publications/MICEinR-Draft.pdf>

See Also

[cbind.mids](#), [ibind](#), [mids](#)

windspeed

Subset of Irish wind speed data

Description

Subset of Irish wind speed data

Usage

```
data(windspeed)
```

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

Haslett, J. and Raftery, A. E. (1989). *Space-time Modelling with Long-memory Dependence: Assessing Ireland's Wind Power Resource (with Discussion)*. Applied Statistics 38, 1-50. <http://lib.stat.cmu.edu/datasets/wind.desc><http://lib.stat.cmu.edu/datasets/wind.data>

Van Buuren, S., Brand, J.P.L., Groothuis-Oudshoorn C.G.M., Rubin, D.B. (2006) Fully conditional specification in multivariate imputation. *Journal of Statistical Computation and Simulation*, **76**, 12, 1049–1064. <http://www.stefvanbuuren.nl/publications/FCSinmultivariateimputation-JSCS2.pdf>

Examples

```
windspeed[1:3,]
```

with.mids

*Evaluate an expression in multiple imputed datasets***Description**

Performs a computation of each of imputed datasets in data.

Usage

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

Arguments

data	An object of type <code>mids</code> , which stands for 'multiply imputed data set', typically created by a call to function <code>mice()</code> .
expr	An expression with a formula object, with the response on the left of a <code>~</code> operator, and the terms, separated by <code>+</code> operators, on the right. See the documentation of <code>lm</code> and <code>formula</code> for details.
...	Additional parameters passed to <code>expr</code>

Value

call	The call that created the object.
call1	The call that created the <code>mids</code> object that was used in <code>call</code> .
nmis	An array containing the number of missing observations per column.
analyses	A list of <code>m</code> components containing the individual fit objects from each of the <code>m</code> complete data analyses.
formula	The formula of the call that created the object.

Author(s)

Karin Oudshoorn, 2009

References

Van Buuren, S., Groothuis-Oudshoorn, K. (2009) MICE: Multivariate Imputation by Chained Equations in R. *Journal of Statistical Software*, forthcoming. <http://www.stefvanbuuren.nl/publications/MICEinR-Draft.pdf>

See Also

[lm.mids](#), [glm.mids](#), [mids](#), [mira](#), [pool](#), [pool.compare](#), [pool.r.squared](#)

Examples

```
imp <- mice(nhanes2)
fit1 <- with(data=imp, exp=lm(bmi~age+hyp+chl))
fit2 <- with(data=imp, exp=glm(hyp~age+bmi+chl, family=binomial))
anova.imp <- with(data=imp, exp=anova(lm(bmi~age+hyp+chl)))
```

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