

Package ‘micemd’

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Type Package

Title Multiple Imputation by Chained Equations with Multilevel Data

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Description

Addons for the 'mice' package to perform multiple imputation using chained equations with two-level data. Includes imputation methods dedicated to sporadically and systematically missing values. Imputation of continuous, binary or count variables are available. Following the recommendations of Audigier, V. et al (2018) <[doi:10.1214/18-STS646](https://doi.org/10.1214/18-STS646)>, the choice of the imputation method for each variable can be facilitated by a default choice tuned according to the structure of the incomplete dataset. Allows parallel calculation and overimputation for 'mice'.

License GPL-2 | GPL-3

Depends R (>= 3.5.0), mice (>= 2.42)

Imports Matrix, graphics, utils, stats, MASS, parallel, nlme, lme4, mvmeta (>= 0.4.7), jomo (>= 2.6-3), mvtnorm, digest, abind, GJRM, mgcv, mixmeta, pbivnorm, ggplot2

Suggests VIM

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NeedsCompilation no

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micemd-package	<i>Multiple Imputation by Chained Equations with Multilevel Data</i>
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Description

Addons for the mice package to perform multiple imputation using chained equations with two-level data. Includes imputation methods specifically handling sporadically and systematically missing values (Resche-Rigon et al. 2013). Imputation of continuous, binary or count variables are available. Following the recommendations of Audigier, V. et al (2018), the choice of the imputation method for each variable can be facilitated by a default choice tuned according to the structure of the incomplete dataset. Allows parallel calculation for mice.

Author(s)

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References

Audigier, V., White, I., Jolani, S., Debray, T., Quartagno, M., Carpenter, J., van Buuren, S. and Resche-Rigon, M. Multiple imputation for multilevel data with continuous and binary variables (2018). *Statistical Science*. <doi:10.1214/18-STS646>.

Jolani, S., Debray, T. P. A., Koffijberg, H., van Buuren, S., and Moons, K. G. M. (2015). Imputation of systematically missing predictors in an individual participant data meta-analysis: a generalized approach using MICE. *Statistics in Medicine*, 34(11):1841-1863. <doi:10.1002/sim.6451>

Quartagno, M. and Carpenter, J. R. (2016). jomo: A package for Multilevel Joint Modelling Multiple Imputation.

Quartagno, M. and Carpenter, J. R. (2016). Multiple imputation for IPD meta-analysis: allowing for heterogeneity and studies with missing covariates. *Statistics in Medicine*, 35(17):2938-2954. <doi:10.1002/sim.6837>

Resche-Rigon, M. and White, I. R. (2016). Multiple imputation by chained equations for systematically and sporadically missing multilevel data. *Statistical Methods in Medical Research*. To appear. <doi:10.1177/0962280216666564>

Resche-Rigon, M., White, I. R., Bartlett, J., Peters, S., Thompson, S., and on behalf of the PROG-IMT Study Group (2013). Multiple imputation for handling systematically missing confounders in meta-analysis of individual participant data. *Statistics in Medicine*, 32(28):48904905. <doi:10.1002/sim.5894>

Van Buuren, S., Groothuis-Oudshoorn, K. (2011). mice: Multivariate Imputation by Chained Equations in R. *Journal of Statistical Software*, 45(3), 1-67. <doi:10.18637/jss.v045.i03> <http://www.jstatsoft.org/v45/i03/>

See Also

[mice](#)

Examples

```
require(lme4)
data(CHEM97Na)

ind.clust<-1#index for the cluster variable

#initialisation of the argument predictorMatrix
predictor.matrix<-mice(CHEM97Na,m=1,maxit=0)$pred
predictor.matrix[ind.clust,ind.clust]<-0
predictor.matrix[-ind.clust,ind.clust]<- -2
predictor.matrix[predictor.matrix==1]<-2

#initialisation of the argument method
method<-find.defaultMethod(CHEM97Na,ind.clust)

#multiple imputation by chained equations (parallel calculation) [time consuming]
#res.mice<-mice.par(CHEM97Na,predictorMatrix = predictor.matrix,method=method)

#check convergence
#plot(res.mice)

#analysis (apply a generalized linear mixed effects model to each imputed dataset)
#ana<-with(res.mice,expr=glmer(Score~Sex+GSC+(1|School),
#                             family="poisson",
#                             control=glmerControl(optimizer = "bobyqa")))

#check the number of generated tables
#plot(ana)

#pooling
#res.pool<-pool(ana)
#summary(res.pool)
```

CHEM97Na

An incomplete two-level dataset which consists of A/AS-level examination data from England

Description

This dataset is an extract of the CHEM97 dataset (Fielding, A. et al, 2003) dealing with point scores of 31,022 pupils grouped in 2,280 schools. CHEM97Na reports point score for Schools with more than 70 pupils only, i.e. 1681 pupils grouped in 18 schools. Systematically missing values and sporadically missing values have been added according to a missing completely at random (MCAR) mechanism (Little R.J.A. and Rubin D.B., 2002). Systematically missing values are values that are missing for all pupils of a same school, while sporadically missing values are values which are missing for an individual only (Resche-Rigon, et al 2013).

Usage

```
data("CHEM97Na")
```

Format

A data frame with 1681 observations on the following 5 variables.

School a numeric indexing the School

Sex a factor with levels M F

Age a numeric indicating the age in months

GSCE a numeric vector indicating the point score at the General Certificate of Secondary Education

Score a numeric vector indicating the point score on A-level Chemistry in 1997

Details

For more details, see Fielding, A. et al (2003).

Source

Fielding, A., Yang, M., and Goldstein, H. (2003). Multilevel ordinal models for examination grades. *Statistical Modelling*, 3 (2): 127-153.

Available at <http://www.bristol.ac.uk/cmm/learning/mmssoftware/data-rev.html#chem97>

References

Fielding, A., Yang, M., and Goldstein, H. (2003). Multilevel ordinal models for examination grades. *Statistical Modelling*, 3 (2): 127-153. <doi:10.1191/1471082X03st052oa>

Resche-Rigon, M., White, I. R., Bartlett, J., Peters, S., Thompson, S., and on behalf of the PROG-IMT Study Group (2013). Multiple imputation for handling systematically missing confounders in meta-analysis of individual participant data. *Statistics in Medicine*, 32(28):48904905. <doi:10.1002/sim.5894>

Little R.J.A., Rubin D.B. (2002) *Statistical Analysis with Missing Data*. Wiley series in probability and statistics, New-York

See Also[matrixplot](#)**Examples**

```
data(CHEM97Na)

#summary
summary(CHEM97Na)

#summary per School
by(CHEM97Na, CHEM97Na$School, summary)
```

`data_heckman`*A two-level incomplete dataset based on an online obesity survey*

Description

The dataset used here was based on data collected from 2111 individuals in an online obesity survey in different locations. The data were simplified and grouped into five clusters.

The values and observability of the weight variable were defined according to Heckman's model in a hierarchical model, and a systematic loss of this variable was assumed in one cluster.

Additionally, the predictor variables Age, Height and FAVC follow a MAR missing mechanism. Response time (Time) was used as an exclusion restriction variable.

Format

A dataframe with 2111 observations with the following variables:

Gender	a factor value with two levels: 1 ("Female"), 0 ("Male").
Age	a numeric value indicating age of subject in years.
Height	a numeric value with Height in meters.
FAVC	a factor value describing the frequent consumption of high caloric food (FAVC) with two levels: 1("Yes"), 0("Mal")
Weight	a numeric value with Weight in Kilograms.
Time	a numeric value indicating time in responding the questions in minutes.
Cluster	a numeric indexing the cluster.

Details

Simulation data code on [gen_dataObs.R](#) github repository

Source

Dataset obtained from "https://www.kaggle.com/datasets/fabinmndez/obesitydata?select=ObesityDataSet_raw_and_data_sin

References

Palechor, F. M., & de la Hoz Manotas, A. (2019). Dataset for estimation of obesity levels based on eating habits and physical condition in individuals from Colombia, Peru and Mexico. Data in brief, 25, 104344.

Examples

```
require(mice)
require(ggplot2)

data(data_heckman)
summary(data_heckman)

# missing data pattern
md.pattern(data_heckman)

# Count missingness per group
by(data_heckman,
    INDICES = data_heckman$Cluster,
    FUN=md.pattern)

# Plot weight
ggplot(data_heckman, aes(x = Weight, group=as.factor(Cluster))) +
  geom_histogram(aes(color = as.factor(Cluster), fill= as.factor(Cluster)),
    position = "identity", bins = 30)+facet_grid(Cluster~.)
```

find.defaultMethod	<i>Suggestion of conditional imputation models to use accordingly to the incomplete dataset</i>
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Description

Provides conditionnal imputation models to use for each column of the incomplete dataset according to the number of clusters, the number of individuals per cluster and the class of the variables.

Usage

```
find.defaultMethod(don.na, ind.clust, I.small = 7, ni.small = 100, prop.small = 0.4)
```

Arguments

don.na	An incomplete data frame.
ind.clust	A scalar indexes the variable corresponding to the cluster indicator.
I.small	A scalar that is used as threshold to consider the number of observed clusters (fully observed or partially observed) as small. Default is I.small=7.
ni.small	A scalar that is used as threshold to consider the number individuals per clusters (with observed values) as small. Default is ni.small=100.
prop.small	A scalar that is used as threshold to consider the number of small clusters as small. Default is prop.small=0.4.

Details

Provides conditionnal imputation models to use for each column of the incomplete dataset according to the number of clusters, the number of individuals per cluster and the class of the variable (Audigier, V. et al 2017). Returned methods can be: 2l.stage.bin (binary), 2l.stage.norm (continuous), 2l.stage.pois (integer), 2l.glm.bin (binary), 2l.glm.norm (continuous), 2l.glm.pois (integer), 2l.jomo (continuous or binary). For a given variable, the method retained is chosen according to the following decision tree:

Few observed clusters		
Few observed values per cluster		Many observed values per cluster
continuous	2l.glm.norm	2l.stage.norm
binary	2l.glm.bin	2l.stage.bin
integer	2l.glm.pois	2l.stage.pois
Many observed clusters		
Few observed values per cluster		Many observed values per cluster
continuous	2l.glm.norm	2l.stage.norm
binary	2l.jomo	2l.jomo
integer	2l.glm.pois	2l.stage.pois

For instance, with few observed clusters (i.e. less than `I.small`), and many observed values per cluster (i.e. less than `prop.small` clusters with less than `ni.small` observed values), imputation of a continuous variable according to the method `2l.stage.norm` will be suggested.

Value

A vector of strings with length `ncol(data)`.

Author(s)

Vincent Audigier <vincent.audigier@cnam.fr>

References

Audigier, V., White, I., Jolani, S., Debray, T., Quartagno, M., Carpenter, J., van Buuren, S. and Resche-Rigon, M. Multiple imputation for multilevel data with continuous and binary variables (2018). *Statistical Science*. <doi:10.1214/18-STS646>.

Jolani, S., Debray, T. P. A., Koffijberg, H., van Buuren, S., and Moons, K. G. M. (2015). Imputation of systematically missing predictors in an individual participant data meta-analysis: a generalized approach using MICE. *Statistics in Medicine*, 34(11):1841-1863. <doi:10.1002/sim.6451>

Quartagno, M. and Carpenter, J. R. (2016). Multiple imputation for IPD meta-analysis: allowing for heterogeneity and studies with missing covariates. *Statistics in Medicine*, 35(17):2938-2954. <doi:10.1002/sim.6837>

Resche-Rigon, M. and White, I. R. (2016). Multiple imputation by chained equations for systematically and sporadically missing multilevel data. *Statistical Methods in Medical Research*. To appear. <doi:10.1177/0962280216666564>

See Also

[mice](#), [mice.par](#)

Examples

```
data(CHEM97Na)

ind.clust<-1#index for the cluster variable

#initialisation of the argument predictorMatrix
predictor.matrix<-mice(CHEM97Na,m=1,maxit=0)$pred
predictor.matrix[ind.clust,ind.clust]<-0
predictor.matrix[-ind.clust,ind.clust]<- -2
predictor.matrix[predictor.matrix==1]<-2

#initialisation of the argument method
method<-find.defaultMethod(CHEM97Na,ind.clust)
print(method)

#multiple imputation by chained equations (parallel calculation)
#res.mice<-mice.par(CHEM97Na, m = 3, predictorMatrix = predictor.matrix, method = method)
```

IPDNa

A simulated Individual Patient Data (IPD) meta-analysis with missing values.

Description

This dataset is a simulated version of an IPD meta-analysis consisting of 28 studies focusing on risk factors in acute heart failure (GREAT, 2013). Each study includes a list of patient characteristics and potential risk factors. Each of them is incomplete, leading to sporadically missing values (Resche-Rigon, et al 2013). In addition, some variables have been collected on some studies only, leading to systematically missing values. More details on the original dataset are provided in Audigier et al. (2018). To mimic the real data, a general location model has been fitted on each study (Schafer, 1997). Then, each study has been generated according to the estimated parameters. Finally, missing values have been allocated similarly to the original dataset.

Usage

```
data("IPDNa")
```

Format

A data frame with 11685 observations on the following 10 variables.

centre a numeric indexing the center where the study is conducted

gender a factor with levels 0 1

bmi a numeric vector indicating the body mass index

age a numeric vector indicating the age

sbp a numeric vector indicating the systolic blood pressure

dbp a numeric vector indicating the diastolic blood pressure

hr a numeric vector indicating the heart rate

lvef a numeric vector indicating the ventricular ejection fraction

bnp a numeric vector indicating the level of the brain natriuretic peptide biomarker

afib a factor with levels 0 1 indicating the atrial fibrillation

Details

For more details, see Audigier et al. (2018)

Source

GREAT Network (2013). Managing acute heart failure in the ed - case studies from the acute heart failure academy. <http://www.greatnetwork.org>

References

Audigier, V., White, I. , Jolani ,S. Debray, T., Quartagno, M., Carpenter, J., van Buuren, S. and Resche-Rigon, M. Multiple imputation for multilevel data with continuous and binary variables (2018). *Statistical Science*. <doi:10.1214/18-STS646>.

Resche-Rigon, M., White, I. R., Bartlett, J., Peters, S., Thompson, S., and on behalf of the PROG-IMT Study Group (2013). Multiple imputation for handling systematically missing confounders in meta-analysis of individual participant data. *Statistics in Medicine*, 32(28):48904905. <doi:10.1002/sim.5894>

Schafer, J. L. (1997) *Analysis of Incomplete Multivariate Data*. Chapman & Hall, Chapter 9.

Examples

```
data(IPDNa)
```

```
#summary  
summary(IPDNa)
```

```
#summary per study  
by(IPDNa, IPDNa$centre, summary)
```

```
mice.impute.2l.2stage.bin
```

Imputation by a two-level logistic model based on a two-stage estimator

Description

Imputes univariate two-level binary variable from a logistic model. The imputation method is based on a two-stage estimator: at step 1, a logistic regression model is fitted to each observed cluster; at step 2, estimates obtained from each cluster are combined according to a linear random effect model.

Usage

```
mice.impute.2l.2stage.bin(y, ry, x, type, method_est = "mm", ...)
```

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 × 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 allowed) is coded as '-2'. Random variables also include the fixed effect.
<code>method_est</code>	Vector of string given the version of the estimator to used. Choose <code>method_est="reml"</code> for restricted maximum likelihood estimator or <code>method_est="mm"</code> for the method of moments. By default <code>method_est="mm"</code> .
<code>...</code>	Other named arguments.

Details

Imputes univariate two-level continuous variable from a heteroscedastic normal model. The imputation method is based on a two-stage estimator: at step 1, a linear regression model is fitted to each observed cluster; at step 2, estimates obtained from each cluster are combined according to a linear random effect model. Two possibilities are available to combine estimates at stage 2: by default, parameters of the linear random effect model are estimated according to the method of moments (MM), otherwise, parameters of the linear random effect model can be estimated according to the restricted maximum likelihood estimator (REML). The variability on the parameters of the imputation is propagated according to an asymptotic strategy requiring a large number of clusters. Compared to the REML version, the MM version is quicker to perform, but it provides less theoretical guarantees. Nevertheless, simulation studies show that both versions lead to similar inferences (Audigier et al, 2018; Resche-Rigon, M. and White, I. R., 2016).

Value

A vector of length `nmi`s with imputations.

Author(s)

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References

Audigier, V., White, I., Jolani, S., Debray, T., Quartagno, M., Carpenter, J., van Buuren, S. and Resche-Rigon, M. Multiple imputation for multilevel data with continuous and binary variables (2018). *Statistical Science*. <doi:10.1214/18-STS646>.

Resche-Rigon, M. and White, I. R. (2016). Multiple imputation by chained equations for systematically and sporadically missing multilevel data. *Statistical Methods in Medical Research*. To appear. <doi:10.1177/0962280216666564>

See Also

[mice](#), [mice.impute.2l.glm.bin](#), [mice.impute.2l.jomo](#)

mice.impute.2l.2stage.heckman

Imputation based on Heckman model for multilevel data.

Description

Imputes outcome and predictor variables that follow an MNAR mechanism according to Heckman's model and come from a multilevel database such as individual participant data with systematically and sporadically missing values.

Usage

```
mice.impute.2l.2stage.heckman(y, ry, x, wy = NULL, type,
pmm = FALSE, ypmm = NULL, meta_method = "reml", ...)
```

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.
type	Type of the variable in the prediction model 0: No predictor, 1: Predictor in both the outcome and selection, -2: Cluster id (study id), -3: Predictor only in the selection model, -4: Predictor only in the outcome model.

pmm	Predictive mean matching can be applied only for missing continuous variables: "TRUE", "FALSE".
ypmm	Continuous vector of donor values of y to perform the predictive mean matching, in case ypmm is not provided, the observable values of y are used.
meta_method	Meta_analysis estimation method for random effects: "ml" (maximum likelihood), "reml" (restricted maximum likelihood) or "mm" method of moments.
...	Other named arguments. Not used.

Details

Imputes systematically and sporadically missing binary and continuous univariate variables that follow a MNAR mechanism according to the Heckman selection model and come from a clustered dataset. The imputation method uses a two-stage approach in which the Heckman model parameters at the cluster level are estimated using the copula method.

Value

Vector with imputed data, of type binary or continuous

Note

Missing binary variables should be included as two-level factor type variables in the incomplete dataset. Cluster variable should be included as numeric variable in the dataset, and defined as -2 in the predictor matrix. When the cluster variable is not specified, the imputation method is based on a simple Heckman model, i.e. without taking into account the hierarchical structure. In case the Heckman model cannot be estimated at the cluster level, the imputation method will be based on the simple Heckman model.

Author(s)

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References

Munoz J, Hufstедler H, Gustafson P, Barnighausen T, De Jong V, Debray T. Dealing with missing data using the Heckman selection model: methods primer for epidemiologists. *IJE*, December 2022. DOI: 10.1093/ije/dyac237.

Munoz J, Egger M, Efthimiou O, Audigier V, De Jong V, Debray T. Multiple imputation of incomplete multilevel data using Heckman selection models, Jan 2023, <https://doi.org/10.48550/arXiv.2301.05043>.

See Also

[mice](#)

Examples

```

require(mice)
data(data_heckman)

#####
# Initialisation
#####

# define imputation methods for each incomplete variables
ini <- mice(data_heckman, maxit = 0)
meth <- ini$method
meth[c("Age", "Height")] <- c("2l.norm", "2l.norm")
meth[c("FAVC")] <- "2l.glm.bin"
meth["Weight"] <- "2l.2stage.heckman"

# set type of predictor variable, here Weight variable is assumed an MNAR variable
# as Age and Gender are predictors in both selection and outcome model are set as 1

pred <- ini$predictorMatrix
pred[, "Cluster"] <- -2 # Cluster variable
pred[, "Weight", "Time"] <- -3 # Variable only affects the selection model (Exclusion restriction)
pred[, "Weight", c("Height", "FAVC")] <- -4 # Variables only affect the outcome model

#####
# multiple imputation
#####
#imp <- mice(data = data_heckman, meth = meth, pred = pred, seed = 123)

#-----
# Summary weight
#-----

#summary(complete(imp, "long")$Weight)

#-----
# Model weight
#-----

#library(broom.mixed)
#model_MNAR <- with(imp, lmer(Weight~Gender+Age+Height+FAVC+(1|Cluster)))
#summary(pool(model_MNAR))

#####
# multiple imputation with pmm
#####

#imp_pmm <- mice(data = data_heckman, meth = meth, pred = pred,
#pmm=TRUE, ypmm=seq(35,180,0.1), seed = 123)
#model_MNAR_pmm <- with(imp_pmm, lmer(Weight~Gender+Age+Height+FAVC+(1|Cluster)))
#summary(pool(model_MNAR_pmm))

```

mice.impute.2l.2stage.norm

Imputation by a two-level heteroscedastic normal model based on a two-stage estimator

Description

Imputes univariate two-level continuous variable from a heteroscedastic normal model. The imputation method is based on a two-stage estimator: at step 1, a linear regression model is fitted to each observed cluster; at step 2, estimates obtained from each cluster are combined according to a linear random effect model.

Usage

```
mice.impute.2l.2stage.norm(y, ry, x, type, method_est = "mm", ...)
```

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 variables are identified by a '2'. The class variable (only one is allowed) is coded as '-2'. Random variables also include the fixed effect.
method_est	Vector of string given the version of the estimator to used. Choose method_est="reml" for restricted maximum likelihood estimator or method_est="mm" for the method of moments. By default method_est="mm".
...	Other named arguments.

Details

Imputes univariate two-level continuous variable from a heteroscedastic normal model. The imputation method is based on a two-stage estimator: at step 1, a linear regression model is fitted to each observed cluster; at step 2, estimates obtained from each cluster are combined according to a linear random effect model. Two possibilities are available to combine estimates at stage 2: by default, parameters of the linear random effect model are estimated according to the method of moments (MM), otherwise, parameters of the linear random effect model can be estimated according to the restricted maximum likelihood estimator (REML). The variability on the parameters of the imputation is propagated according to an asymptotic strategy requiring a large number of clusters. Compared to the REML version, the MM version is quicker to perform, but it provides less theoretical guarantees. Nevertheless, simulation studies show that both versions lead to similar inferences (Resche-Rigon, M. and White, I. R. (2016)).

Value

A vector of length nmi s with imputations.

Author(s)

Vincent Audigier <vincent.audigier@cnam.fr>

References

Resche-Rigon, M. and White, I. R. (2016). Multiple imputation by chained equations for systematically and sporadically missing multilevel data. *Statistical Methods in Medical Research*. To appear. <doi:10.1177/0962280216666564>

Audigier, V., White, I. , Jolani ,S. Debray, T., Quartagno, M., Carpenter, J., van Buuren, S. and Resche-Rigon, M. Multiple imputation for multilevel data with continuous and binary variables (2018). *Statistical Science*. <doi:10.1214/18-STS646>.

See Also

[mice](#), [mice.impute.2l.2stage.pmm](#), [mice.impute.2l.glm.norm](#), [mice.impute.2l.jomo](#)

mice.impute.2l.2stage.pmm

Predictive mean matching imputation for two-level variable

Description

Similarly to `mice.impute.2l.stage.norm`, this function imputes univariate two-level continuous variable from a heteroscedastic normal model. The difference consists in replacing missing values by observed values instead of adding a parametric noise to the prediction of a linear model with random effects (as done in `mice.impute.2l.stage.norm.mm` and `mice.impute.2l.stage.norm.reml`).

Usage

```
mice.impute.2l.2stage.pmm(y, ry, x, type,
                          method_est = "mm",
                          incluster = FALSE,
                          kpmm = 5, ...)
```

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 allowed) is coded as '-2'. Random variables also include the fixed effect.
<code>method_est</code>	Vector of string given the version of the estimator to used. Choose <code>method_est="reml"</code> for restricted maximum likelihood estimator or <code>method_est="mm"</code> for the method of moments. By default <code>method_est="mm"</code> .

<code>incluster</code>	Boolean indicating if the imputed values are drawn from the cluster or from the full dataset. By default imputed values are drawn from all available clusters <code>incluster=FALSE</code> .
<code>kpmm</code>	The size of the donor pool among which a draw is made. The default is <code>k = 5</code> .
<code>...</code>	Other named arguments.

Details

Imputes univariate two-level continuous variable from observed values. The imputation method is based on a two-stage estimator: at step 1, a linear regression model is fitted to each observed cluster; at step 2, estimates obtained from each cluster are combined according to a linear random effect model. To combine estimates at stage 2, parameters of the linear random effect model are estimated according to the method of moments or according to the restricted maximum likelihood estimator. The variability on the parameters of the imputation is propagated according to an asymptotic strategy requiring a large number of clusters. The sample variability is reflected by using a predictive mean matching approach, meaning that missing values are imputed by a draw from observed values. The pool of `k` donors is defined according to the Manhattan distance between the prediction of the observation which is imputed and the predictions of other available observations (matching of type 2). The pool can be restricted to the cluster of the individual that is imputed or from all clusters. By drawing values inside the cluster, the heteroscedasticity assumption is preserved. Otherwise, the sample variability of imputed values is the same for all clusters, which strengthen the homoscedasticity assumption. Among the pool of `k` donors, the selected one is drawn at random.

Value

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

Note

This method is experimental.

Author(s)

Vincent Audigier <vincent.audigier@cnam.fr>

References

- Rubin, D.B. (1987). Multiple imputation for nonresponse in surveys. New York: Wiley.
- Resche-Rigon, M. and White, I. R. (2016). Multiple imputation by chained equations for systematically and sporadically missing multilevel data. *Statistical Methods in Medical Research*. To appear. <[doi:10.1177/0962280216666564](https://doi.org/10.1177/0962280216666564)>
- Audigier, V., White, I. , Jolani ,S. Debray, T., Quartagno, M., Carpenter, J., van Buuren, S. and Resche-Rigon, M. Multiple imputation for multilevel data with continuous and binary variables (2018). *Statistical Science*. <[doi:10.1214/18-STS646](https://doi.org/10.1214/18-STS646)>.

See Also

[mice.impute.2l.2stage.norm](#)

mice.impute.2l.2stage.pois

Imputation by a two-level Poisson model based on a two-stage estimator

Description

Imputes univariate two-level count variable from a Poisson model. The imputation method is based on a two-stage estimator: at step 1, a Poisson regression model is fitted to each observed cluster; at step 2, estimates obtained from each cluster are combined according to a linear random effect model.

Usage

```
mice.impute.2l.2stage.pois(y, ry, x, type, method_est = "mm", ...)
```

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 variables are identified by a '2'. The class variable (only one is allowed) is coded as '-2'. Random variables also include the fixed effect.
method_est	Vector of string given the version of the estimator to used. Choose method_est="reml" for restricted maximum likelihood estimator or method_est="mm" for the method of moments. By default method_est="mm".
...	Other named arguments.

Details

Imputes univariate two-level count variable from a Poisson model. The imputation method is based on a two-stage estimator: at step 1, a Poisson regression model is fitted to each observed cluster; at step 2, estimates obtained from each cluster are combined according to a linear random effect model. Two possibilities are available to combine estimates at stage 2: by default, parameters of the linear random effect model are estimated according to the method of moments (MM), otherwise, parameters of the linear random effect model can be estimated according to the restricted maximum likelihood estimator (REML). The variability on the parameters of the imputation is propagated according to an asymptotic strategy requiring large samples and a large number of clusters. Compared to the REML version, the MM version is quicker to perform, but it provides less theoretical guarantees. Nevertheless, simulation studies show that both versions lead to similar inferences (Audigier et al, 2018; Resche-Rigon and White, 2016).

Value

A vector of length nmi s with imputations.

Author(s)

Vincent Audigier <vincent.audigier@cnam.fr>

References

Resche-Rigon, M. and White, I. R. (2016). Multiple imputation by chained equations for systematically and sporadically missing multilevel data. *Statistical Methods in Medical Research*. To appear. <doi:10.1177/0962280216666564>

Audigier, V., White, I. , Jolani ,S. Debray, T., Quartagno, M., Carpenter, J., van Buuren, S. and Resche-Rigon, M. Multiple imputation for multilevel data with continuous and binary variables (2018). *Statistical Science*. <doi:10.1214/18-STS646>.

See Also

[mice](#), [mice.impute.2l.glm.pois](#)

mice.impute.2l.glm.bin

Imputation of univariate missing data using a Bayesian logistic mixed model based on non-informative prior distributions

Description

Imputes univariate missing data using a Bayesian logistic mixed model based on non-informative prior distributions. The method is dedicated to a binary outcome stratified in several clusters. Should be used with few clusters and few individuals per cluster. Can be very slow to perform otherwise.

Usage

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

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 variables are identified by a '2'. The class variable (only one is allowed) is coded as '-2'. Random variables also include the fixed effect.
...	Other named arguments.

Details

Imputes univariate missing data using a Bayesian logistic mixed model based on non-informative prior distributions. The variability on the parameters of the imputation is propagated according to an explicit Bayesian modelling. More precisely, improper prior distributions are used for regression coefficients and covariance matrix of random effects. The method is recommended for datasets with a small number of clusters and a small number of individuals per cluster. Otherwise, the method can be very slow to perform.

Value

A vector of length `nmi`s with imputations.

Author(s)

Vincent Audigier <vincent.audigier@cnam.fr> from the R code of Shahab Jolani.

References

Jolani, S., Debray, T. P. A., Koffijberg, H., van Buuren, S., and Moons, K. G. M. (2015). Imputation of systematically missing predictors in an individual participant data meta-analysis: a generalized approach using MICE. *Statistics in Medicine*, 34(11):18411863. <doi:10.1002/sim.6451>

Audigier, V., White, I., Jolani, S., Debray, T., Quartagno, M., Carpenter, J., van Buuren, S. and Resche-Rigon, M. Multiple imputation for multilevel data with continuous and binary variables (2018). *Statistical Science*. <doi:10.1214/18-STS646>.

See Also

[mice](#), [mice.impute.2l.2stage.bin](#), [mice.impute.2l.jomo](#)

mice.impute.2l.glm.norm

Imputation of univariate missing data using a Bayesian linear mixed model based on non-informative prior distributions

Description

Imputes univariate missing data using a Bayesian linear mixed model based on non-informative prior distributions. The method is dedicated to a continuous outcome stratified in several clusters. Should be used with few clusters and few individuals per cluster. Can be very slow to perform otherwise.

Usage

```
mice.impute.2l.glm.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 × 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 allowed) is coded as '-2'. Random variables also include the fixed effect.
<code>...</code>	Other named arguments.

Details

Imputes univariate two-level continuous variable from a homoscedastic normal model. The variability on the parameters of the imputation is propagated according to an explicit Bayesian modelling. More precisely, improper prior distributions are used for regression coefficients and variances components. The method is recommended for datasets with a small number of clusters and a small number of individuals per cluster. Otherwise, confidence intervals after applying analysis method on the multiply imputed dataset tend to be anti-conservative. In addition, the imputation can be highly time consuming.

Value

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

Author(s)

Vincent Audigier <vincent.audigier@cnam.fr> from the R code of Shahab Jolani.

References

- Jolani, S. (2017) Hierarchical imputation of systematically and sporadically missing data: An approximate Bayesian approach using chained equations. *Biometrical Journal* <doi:10.1002/bimj.201600220>
- Jolani, S., Debray, T. P. A., Koffijberg, H., van Buuren, S., and Moons, K. G. M. (2015). Imputation of systematically missing predictors in an individual participant data meta-analysis: a generalized approach using MICE. *Statistics in Medicine*, 34(11):18411863. <doi:10.1002/sim.6451>
- Audigier, V., White, I., Jolani, S., Debray, T., Quartagno, M., Carpenter, J., van Buuren, S. and Resche-Rigon, M. Multiple imputation for multilevel data with continuous and binary variables (2018). *Statistical Science*. <doi:10.1214/18-STS646>.

See Also

[mice](#), [mice.impute.2l.2stage.norm](#), [mice.impute.2l.jomo](#)

`mice.impute.2l.glm.pois`*Imputation of count variable using a Bayesian mixed model based on non-informative prior distributions*

Description

Imputes univariate missing data using a Bayesian mixed model (Poisson regression) based on non-informative prior distributions. The method is dedicated to a count outcome stratified in several clusters. Should be used with few clusters and few individuals per cluster. Can be very slow to perform otherwise.

Usage

```
mice.impute.2l.glm.pois(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 x 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 allowed) is coded as '-2'. Random variables also include the fixed effect.
<code>...</code>	Other named arguments.

Details

Imputes univariate missing data using a Bayesian mixed model (Poisson regression) based on non-informative prior distributions. The variability on the parameters of the imputation is propagated according to an explicit Bayesian modelling. More precisely, improper prior distributions are used for regression coefficients and variances components. The method is recommended for datasets with a small number of clusters and a small number of individuals per cluster. Otherwise, the method can be very slow to perform.

Value

A vector of length `nmis` with imputations.

Author(s)

Vincent Audigier <vincent.audigier@cnam.fr> from the R code of Shahab Jolani.

References

Jolani, S., Debray, T. P. A., Koffijberg, H., van Buuren, S., and Moons, K. G. M. (2015). Imputation of systematically missing predictors in an individual participant data meta-analysis: a generalized approach using MICE. *Statistics in Medicine*, 34(11):1841-1863. <doi:10.1002/sim.6451>

See Also

[mice](#), [mice.impute.2l.2stage.pois](#)

mice.impute.2l.jomo *Imputation of univariate missing data by a Bayesian multivariate generalized model based on conjugate priors*

Description

Univariate imputation by a Bayesian multivariate generalized model based on conjugate priors. Can be used for a continuous or binary incomplete variable. For continuous variables, the modelling assumes heteroscedasticity for errors. For a binary variable, a probit link and a latent variables framework are used. The method should be used for a variable with large number of clusters and a large number of individuals per cluster.

Usage

```
mice.impute.2l.jomo(y, ry, x, type, nburn = 200, ...)
```

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 variables are identified by a '2'. The class variable (only one is allowed) is coded as '-2'. Random variables also include the fixed effect.
nburn	A scalar indicating the number of iterations for the Gibbs sampler. Default is nburn=200
...	Other named arguments.

Details

Contrary to the approach developed in the R jomo package, the imputation is here sequentially performed through a FCS approach, instead of imputing all variables simulatenously. The motivation for such a method is that jomo presents some advantages over other imputation methods, but not always for any type of variables (binary or continuous). By proposing a FCS version of jomo, we allow imputation of mixed variables (continuous and binary), while taking the best of jomo and of other imputation methods. To impute one variable according to this method, other variables are assumed to be full, like in any FCS approach. The imputation function is a direct use of the R function jomoIran from the jomo package. The argument meth is tuned to "random" to allow covariance matrices drawn from an inverse Wishart distribution. Only intercept are considered in covariates (X=NULL and Z=NULL), while the multivariate outcome corresponds to all variables of the datasets.

Value

A vector of length `nmi`s with imputations.

Author(s)

Vincent Audigier <vincent.audigier@cnam.fr> from the R code of Matteo Quartagno.

References

Carpenter J.R., Kenward M.G., (2013), Multiple Imputation and its Application. Chapters 3-5-9, Wiley, ISBN: 978-0-470-74052-1.

Yucel R.M., (2011), Random-covariances and mixed-effects models for imputing multivariate multilevel continuous data, *Statistical Modelling*, 11 (4), 351-370, <doi:10.1177/1471082X100110040>.

See Also

[mice](#), [jomo1ran](#)

mice.par

Parallel calculations for Multivariate Imputation by Chained Equations

Description

Parallel calculations for Multivariate Imputation by Chained Equations using the R package `parallel`.

Usage

```
mice.par(don.na, m = 5, method = NULL, predictorMatrix, where = NULL,
visitSequence = NULL, blots = NULL, post = NULL, blocks, formulas,
defaultMethod = c("pmm", "logreg", "polyreg", "polr"), maxit = 5,
seed = NA, data.init = NULL, nnodes = 5, path.outfile = NULL, ...)
```

Arguments

<code>don.na</code>	A data frame or a matrix containing the incomplete data. Missing values are coded as NA.
<code>m</code>	Number of multiple imputations. The default is <code>m=5</code> .
<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.

predictorMatrix	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.
where	A data frame or matrix with logicals of the same dimensions as <code>data</code> indicating where in the data the imputations should be created. The default, <code>where = is.na(data)</code> , specifies that the missing data should be imputed. The <code>where</code> argument may be used to overimpute observed data, or to skip imputations for selected missing values.
visitSequence	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.
blots	A named list of <code>alist</code> 's that can be used to pass down arguments to lower level imputation function. The entries of element <code>blots[[blockname]]</code> are passed down to the function called for block <code>blockname</code> .
post	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 ''.
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 <code>method</code> 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 <code>blocks</code> are imputed. The relevant columns in the <code>where</code> matrix are set to <code>FALSE</code> 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.
formulas	A named list of formula's, or expressions that can be converted into formula's by <code>as.formula</code> . 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 <code>formulas</code> argument is an alternative to the <code>predictorMatrix</code> argument that allows for more flexibility in specifying imputation models, e.g., for specifying interaction terms.
defaultMethod	A vector of three strings containing the default imputation methods for numerical columns, factor columns with 2 levels, and columns with (unordered or ordered) factors 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 for unordered categorical data (factor ≥ 2 levels) <code>po1r</code> , proportional odds model for (ordered, ≥ 2 levels)
<code>maxit</code>	A scalar giving the number of iterations. The default is 5.
<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.
<code>data.init</code>	A data frame of the same size and type as <code>data</code> , without missing data, used to initialize imputations before the start of the iterative process. The default NULL implies that starting imputation are created by a simple random draw from the data. Note that specification of <code>data.init</code> will start the <code>m</code> Gibbs sampling streams from the same imputations.
<code>nnodes</code>	A scalar indicating the number of nodes for parallel calculation. Default value is 5.
<code>path.outfile</code>	A vector of strings indicating the path for redirection of print messages. Default value is NULL, meaning that silent imputation is performed. Otherwise, print messages are saved in the files <code>path.outfile/output.txt</code> . One file per node is generated.
<code>...</code>	Named arguments that are passed down to the elementary imputation functions.

Details

Performs multiple imputation of `m` tables in parallel by generating `m` seeds, and then by performing multiple imputation by chained equations in parallel from each one. The output is the same as the `mice` function of the `mice` package.

Value

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

Author(s)

Vincent Audigier <vincent.audigier@cnam.fr>

References

Van Buuren, S., Groothuis-Oudshoorn, K. (2011). `mice`: Multivariate Imputation by Chained Equations in R. *Journal of Statistical Software*, **45**(3), 1-67. <https://www.jstatsoft.org/article/view/v045i03> <doi:10.18637/jss.v045.i03>

van Buuren, S. (2012). *Flexible Imputation of Missing Data*. Boca Raton, FL: Chapman & Hall/CRC Press.

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. <doi:10.1080/10629360600810434>

Van Buuren, S. (2007) Multiple imputation of discrete and continuous data by fully conditional specification. *Statistical Methods in Medical Research*, **16**, 3, 219–242. <doi:10.1177/0962280206074463>

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. <doi:10.1002/(SICI)1097-0258(19990330)18:6<681::AID-SIM71>3.0.CO;2-R>

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

[mice, parallel](#)

Examples

```
#####
# nhanes (one level data)
#####
data(nhanes, package = "mice")
#imp <- mice.par(nhanes)
#fit <- with(data = imp, exp = lm(bmi ~ hyp + chl))
#summary(pool(fit))

#####
#CHEM97Na (Two levels data with 1681 observations and 5 variables)
#####

data(CHEM97Na)

ind.clust<-1#index for the cluster variable

#initialisation of the argument predictorMatrix
predictor.matrix<-mice(CHEM97Na,m=1,maxit=0)$pred
predictor.matrix[ind.clust,ind.clust]<-0
predictor.matrix[-ind.clust,ind.clust]<- -2
predictor.matrix[predictor.matrix==1]<-2

#initialisation of the argument method
method<-find.defaultMethod(CHEM97Na,ind.clust)

#multiple imputation by chained equations (parallel calculation) [1 minute]
#(the imputation process can be followed by opening output.txt files in the working directory)
#res.mice<-mice.par(CHEM97Na,
#                   predictorMatrix = predictor.matrix,
#                   method=method,
#                   path.outfile=getwd())

#multiple imputation by chained equations (without parallel calculation) [4.8 minutes]
#res.mice<-mice(CHEM97Na,
#               predictorMatrix = predictor.matrix,
#               method=method)
```

```
#####
#IPDNa (Two levels data with 11685 observations and 10 variables)
#####

data(IPDNa)

ind.clust<-1#index for the cluster variable

#initialisation of the argument predictorMatrix
predictor.matrix<-mice(IPDNa,m=1,maxit=0)$pred
predictor.matrix[ind.clust,ind.clust]<-0
predictor.matrix[-ind.clust,ind.clust]<- -2
predictor.matrix[predictor.matrix==1]<-2

#initialisation of the argument method
method<-find.defaultMethod(IPDNa,ind.clust)

#multiple imputation by chained equations (parallel calculation)

#res.mice<-mice.par(IPDNa,
#                   predictorMatrix = predictor.matrix,
#                   method=method,
#                   path.outfile=getwd())
```

overimpute

Overimputation diagnostic plot

Description

Assess the fit of the predictive distribution after performing multiple imputation with mice

Usage

```
overimpute(res.mice, plotvars = NULL, plotinds = NULL,
           nnodes = 5, path.outfile = NULL, alpha = 0.1)
```

Arguments

res.mice	An object of class <code>mids</code>
plotvars	column index of the variables overimputed
plotinds	row index of the individuals overimputed
nnodes	A scalar indicating the number of nodes for parallel calculation. Default value is 5.
path.outfile	A vector of strings indicating the path for redirection of print messages. Default value is <code>NULL</code> , meaning that silent imputation is performed. Otherwise, print messages are saved in the files <code>path.outfile/output.txt</code> . One file per node is generated.
alpha	alpha level for prediction intervals

Details

This function imputes each observed values from each of the parameters of the imputation model obtained from the mice procedure. The comparison between the "overimputed" values and the observed values is made by building a confidence interval for each observed value using the quantiles of the overimputed values (Blackwell et al. (2015)). Note that confidence intervals builded with quantiles require a large number of imputations. If the model fits the data well, then the 90% confidence interval should contain the observed value in 90% of the cases (the proportion of intervals containing the observed value is reported in the title of each graph). The function `overimpute` takes as an input the output of the `mice` or `mice.par` function (`res.mice`), the indices of the incomplete continuous variables that are plotted (`plotvars`), the indices of individuals (can be useful for time consuming imputation methods), the number of nodes for parallel computation, and the path for exporting print message generated during the parallel process.

Value

A list of two matrices

<code>res.plot</code>	7-columns matrix that contains (1) the variable which is overimputed, (2) the observed value of the observation, (3) the mean of the overimputations, (4) the lower bound of the confidence interval of the overimputations, (5) the upper bound of the confidence interval of the overimputations, (6) the proportion of the other variables that were missing for that observation in the original data, and (7) the color for graphical representation.
<code>res.values</code>	A matrix with overimputed values for each cell. The number of columns corresponds to the number of values generated (i.e. the number of imputed tables)

Author(s)

Vincent Audigier <vincent.audigier@cnam.fr>

References

Blackwell, M., Honaker, J. and King. G. 2015. A Unified Approach to Measurement Error and Missing Data: Overview and Applications. *Sociological Methods and Research*, 1-39. <doi:10.1177/0049124115585360>

See Also

[mice,parallel](#), [mice.par](#)

Examples

```
require(parallel)
nnodes<-detectCores()-1#number of nodes
m<-1000#nb generated values per observation

#####
#one level data
#####
require(mice)
```

```

data(nhanes)
#res.mice<-mice.par(nhanes,m = m,nnodes = nnodes)
#res.over<-overimpute(res.mice, nnodes = nnodes)

#####
#two level data (time consuming)
#####
data(CHEM97Na)

ind.clust<-1#index for the cluster variable

#initialisation of the argument predictorMatrix
predictor.matrix<-mice(CHEM97Na,m=1,maxit=0)$pred
predictor.matrix[ind.clust,ind.clust]<-0
predictor.matrix[-ind.clust,ind.clust]<- -2
predictor.matrix[predictor.matrix==1]<-2

#initialisation of the argument method
method<-find.defaultMethod(CHEM97Na,ind.clust)

#multiple imputation by chained equations (time consuming)

#res.mice<-mice.par(CHEM97Na,
#                   predictorMatrix = predictor.matrix,
#                   method=method,m=m,nnodes = nnodes)

#overimputation on 30 individuals
#res.over<-overimpute(res.mice,
#                     nnodes=nnodes,
#                     plotinds=sample(x = seq(nrow(CHEM97Na)),size = 30))

```

plot.mira

Graphical investigation for the number of generated datasets

Description

The plot method for a mira object plots the confidence interval length against the number of multiply imputed datasets from 2 to m. This is a graphical tool to check if the variability due to the simulation of the multiple imputation process can be substantially reduced by increasing the number of generated datasets m.

Usage

```

## S3 method for class 'mira'
plot(x, ...)

```

Arguments

x An object of class `mira`.
 ... Extra arguments for `plot.mira`

Author(s)

Vincent Audigier <vincent.audigier@cnam.fr>

References

Schafer, J. L. (1997). Analysis of Incomplete Multivariate Data. Chapman & Hall/CRC, London

See Also

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

Examples

```
require(nlme)
data(CHEM97Na)

ind.clust<-1#index for the cluster variable

#initialisation of the argument predictorMatrix
predictor.matrix<-mice(CHEM97Na,m=1,maxit=0)$pred
predictor.matrix[ind.clust,ind.clust]<-0
predictor.matrix[-ind.clust,ind.clust]<- -2
predictor.matrix[predictor.matrix==1]<-2

#initialisation of the argument method
method<-c("", "2l.2stage.bin", "2l.2stage.pois", "2l.2stage.norm", "") #quickest methods

#multiple imputation by chained equations (parallel calculation)
#res.mice<-mice.par(CHEM97Na,m=15,predictorMatrix = predictor.matrix,method=method)

#analysis (apply a linear mixed effects model to each imputed dataset)
#ana<-with(res.mice,expr=lme(fixed=formula(Score~Sex+GSCE+Age),
#
#                          random=formula(~1|School),method="REML",
#                          control=list(maxIter=100,msMaxIter=100,niterEM=25)))

#graphical investigation for the number of generated datasets m
#plot(ana)
```

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