Package 'micemd'

July 22, 2025

Type Package

Title Multiple Imputation by Chained Equations with Multilevel Data

Version 1.10.0

Date 2023-11-17

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>, 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 (>= 0.2-6.4), mgcv, mixmeta, pbivnorm

Suggests VIM, ggplot2, data.table, broom.mixed

RoxygenNote 6.1.0

NeedsCompilation no

Author Vincent Audigier [aut, cre] (CNAM MSDMA team),
Matthieu Resche-Rigon [aut] (INSERM ECSTRA team),
Johanna Munoz Avila [ctb] (Julius Center Methods Group UMC, 2022)

Maintainer Vincent Audigier <vincent.audigier@cnam.fr>

Repository CRAN

Date/Publication 2023-11-17 10:40:02 UTC

Contents

`micemd-package` *Multiple Imputation by Chained Equations with Multilevel Data*

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)

Vincent Audigier, Matthieu Resche-Rigon

Maintainer: 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:10.1214/18STS646.

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, 27(6):1634-1649. 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):4890-4905. 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 consumming]
#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+GSCE+(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/mmsoftware/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):4890-4905. 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)
```

`find.defaultMethod` *Suggestion of conditional imputation models to use accordingly to the incomplete dataset*

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:10.1214/18STS646.

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. (2018). Multiple imputation by chained equations for systematically and sporadically missing multilevel data. Statistical Methods in Medical Research, 27(6):1634-1649. 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:10.1214/18STS646.

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):4890-4905. 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

`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 garanties. 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 `nmis` with imputations.

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>.

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 both outcome or predictor incomplete variables that follow an indirectly non-ignorable Missing Not at Random (MNAR) mechanism, i.e., the likelihood of a missing value in the incomplete variable depends on other unobserved variable(s) that are also correlated with the incomplete variable. This imputation is based on Heckman's selection model and is suitable for multilevel databases, such as individual participant data, with both systematic or sporadic missing data.

Usage

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

Arguments

`y`	Vector to be imputed
`ry`	A 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`	A numeric design matrix with `length(y)` rows with predictors for `y`. Matrix `x` may have no missing values.
`wy`	A 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, which can be one of the following: No predictor (0), Cluster variable (-2), Predictor in both the outcome and selection equation (2), Predictor only in the selection equation (-3), Predictor only in the outcome equation (-4). In this method all predictors are considered random variables that also included the fixed effect.
`pmm`	A logical value that specifies whether the predictive mean matching method is applied.(default = "FALSE"). This method is only applicable to missing continuous variables.
`ypmm`	A continuous vector of donor values for y used in the predictive mean matching method. if ypmm is not provided, the observable values of y are used as donors.
`meta_method`	A character value that indicates the method for estimating meta_analysis random effects: "ml" (maximum likelihood), "reml" (restricted maximum likelihood) or "mm" (method of moments).
`pred_std`	A logical value that indicates whether internally standardize the set of predictor variables (default = FALSE).
`...`	Other named arguments. Not used.

Details

This function imputes systematically and sporadically missing binary and continuous univariate variables that follow an MNAR mechanism according to the Heckman selection model. It is specifically designed for clustered datasets. The imputation method employs 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 type

Note

Missing binary variables should be included as two-level factor type variables in the incomplete dataset.The cluster variable should be included as a numeric variable in the dataset. When the cluster variable is not specified, the imputation method defaults to a simple Heckman model, which does not take in account the hierarchical structure. In cases where the Heckman model cannot be estimated at the hierarchical level, the imputation method reverts to the simple Heckman model.

Author(s)

Julius Center Methods Group UMC, 2022 <`J.MunozAvila@umcutrecht.nl`>

References

Munoz J,Hufstedler 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, doi:10.48550/arXiv.2301.05043.

See Also

mice

Examples

```
require(mice)
require(nlme)
require(broom.mixed)
require(parallel)

# Load dataset
data(Obesity)

# Define imputation methods for each incomplete variables
meth <- find.defaultMethod(Obesity, ind.clust = 1)

# Modify some of the proposed imputation methods
# Deterministic imputation
meth["BMI"] <- "~ I(Weight / (Height)^2)"
meth["Age"] <- "2l.2stage.pmm"

# Set method, here Weight variable is assumed an MNAR variable
# Weight imputed with the Heckman method
meth["Weight"] <- "2l.2stage.heckman"

# Set type of predictor variable,
# All covariates are included in both outcome and selection equation
ini <- mice(Obesity, maxit = 0)
pred <- ini$pred
pred[,"Time"] <- 0
pred[,"Cluster"] <- -2
pred[pred == 1] <- 2

# Time was used as exclusion restriction variable
pred["Weight","Time"]  <- -3
# Deterministic imputation, to avoid circular predictions
pred[c("Height", "Weight"), "BMI"] <- 0

# Imputation of continuous variables (time consumming)

# nnodes <- detectCores()
# imp <- mice.par(Obesity, meth = meth, pred = pred, m=10, seed = 123,
#                  nnodes = nnodes)
# summary(complete(imp,"long")$Weight)

# Imputation of continuous variables using the predictor mean matching method.
# Imputed values fall within the range of observable variables.

# imp_pmm <- mice.par(Obesity, meth = meth, pred = pred, m = 10,
#                      seed = 123, pmm=TRUE, nnodes = nnodes)
# summary(complete(imp_pmm,"long")$Weight)
# Fit the model

# model_MNAR <- with(imp,lme( BMI ~ Age + FamOb + Gender,random=~1+Age|Cluster))
# model_MNAR_pmm <- with(imp_pmm,lme( BMI ~ Age + FamOb + Gender,random=~1+Age|Cluster))

# summary(pool(model_MNAR))
# 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 garanties. Nevertheless, simulation studies show that both versions lead to similar inferences (Resche-Rigon, M. and White, I. R. (2016)).

Value

A vector of length `nmis` 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

`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"`.

`incluster` 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 `incluster=FALSE`.

`kpmm` The size of the donor pool among which a draw is made. The default is `k = 5`.

`...` 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>

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.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 garanties. 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 `nmis` 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 severals 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 `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

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:10.1214/18STS646.

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 severals 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

`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 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 consumming.

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. (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):1841-1863. 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:10.1214/18STS646.

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 severals 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

`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 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 developped 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 jomo1ran 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 `nmis` 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

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

`m` Number of multiple imputations. The default is `m=5`.

`method` Can be either a single string, or a vector of strings with length `ncol(data)`, 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 `defaultMethod` argument. Columns that need not be imputed have the empty method `''`. See details for more information.

`predictorMatrix` A square matrix of size `ncol(data)` 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 `predictorMatrix` must be zero. The default for `predictorMatrix` 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 `data` indicating where in the data the imputations should be created. The default, `where = is.na(data)`, specifies that the missing data should be imputed. The `where` argument may be used to overimpute observed data, or to skip imputations for selected missing values.

`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 `1:ncol(data)` 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 `alist`'s that can be used to pass down arguments to lower level imputation function. The entries of element `blots[[blockname]]` are passed down to the function called for block `blockname`.

`post` A vector of strings with length `ncol(data)`, specifying expressions. Each string is parsed and executed within the `sampler()` 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 `method` argument). By default each variable is placed into its own block, which is effectively fully conditional specification (FCS) by univariate models (variable-by-variable imputation). Only variables whose names appear in `blocks` are imputed. The relevant columns in the `where` matrix are set to `FALSE` of variables that are not block members. A variable may appear in multiple blocks. In that case, it is effectively re-imputed each time that it is visited.

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

`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: `pmm`, predictive mean matching (numeric data) `logreg`, logistic regression imputation (binary data, factor with 2 levels) `polyreg`, polytomous regression imputation for unordered categorical data (factor >= 2 levels) `polr`, proportional odds model for (ordered, >= 2 levels)

`maxit` A scalar giving the number of iterations. The default is 5.

`seed` An integer that is used as argument by the `set.seed()` for offsetting the random number generator. Default is to leave the random number generator alone.

`data.init` A data frame of the same size and type as `data`, 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 `data.init` will start the `m` Gibbs sampling streams from the same imputations.

`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 NULL, meaning that silent imputation is performed. Otherwise, print messages are saved in the files path.outfile/output.txt. One file per node is generated.

`...` 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())
```

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

Description

This synthetic dataset was generated from an online survey on obesity, which collected information on the dietary behavior of 2111 participants. We made the assumption that the data was gathered from five distinct locations or clusters. To account for potential selection bias in the responses related to weight, we simulated the values and observability of this variable using the Heckman selection model within a hierarchical structure.

Additionally, we assumed that in one of the locations, the weight variable was systematically missing. We also introduced missing values for some other variables in the dataset using a Missing at Random (MAR) mechanism.

Format

A dataframe with 2111 observations with the following variables:

Gender a factor variable with two levels: 1 ("Female"), 0 ("Male").
Age a numeric variable indicating the subject's age in years.
Height a numeric value with Height in meters.
FamOb a factor variable describing the subject's family history of obesity with two levels: 1("Yes"), 0("No").
Weight a numeric variable indicating the subject's weight in kilograms.
Time a numeric variable indicating the time taken by the subject to respond to the surveys questions in minutes.
BMI a numeric variable with the subject's body mass index.
Cluster a numeric variable indexing the cluster.

Details

Data generation code availble on https://github.com/johamunoz/Statsmed_Heckman/blob/main/4.Codes/gendata_Obesity.R

Source

Synthetic data based on the data retrieved from "https://www.kaggle.com/datasets/fabinmndez/obesitydata/"

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

```
library(mice)
library(ggplot2)
library(data.table)
```

```
data(Obesity)
summary(Obesity)
md.pattern(Obesity)

# Missingness per region (Weight)
dataNA <- setDT(Obesity)[, .(nNA = sum(is.na(Weight)),n=.N), by = Cluster]
dataNA[, propNA:=nNA/n]
dataNA

# Density per region (Weight)
Obesity$Cluster <- as.factor(Obesity$Cluster)
ggplot(Obesity, aes(x = Weight, group=Cluster)) +
  geom_histogram(aes(color = Cluster,fill= Cluster),
                 position = "identity", bins = 30) +
                 facet_grid(Cluster~.)
```

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 mids
`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 NULL, meaning that silent imputation is performed. Otherwise, print messages are saved in the files path.outfile/output.txt. 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 consumming 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

`res.plot` 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.

`res.values` 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 consumming)
################
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 consumming)

#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)
```

Index