Package ‘miceMNAR’

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Title Missing not at Random Imputation Models for Multiple Imputation by Chained Equation

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Description Provides imputation models and functions for binary or continuous Missing Not At Random (MNAR) outcomes through the use of the 'mice' package. The mice.impute.hecknorm() function provides imputation model for continuous outcome based on Heckman’s model also named sample selection model as described in Galimard et al (2018) and Galimard et al (2016) <doi:10.1002/sim.6902>. The mice.impute.heckprob() function provides imputation model for binary outcome based on bivariate probit model as described in Galimard et al (2018).

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Description

Provides imputation models and functions for binary or continuous Missing Not At Random (MNAR) outcomes through the use of the 'mice' package. The `mice.impute.hecknorm()` function provides imputation model for continuous outcome based on Heckman’s model also named sample selection model as described in Galimard et al. (2018) and Galimard et al. (2016) <doi:10.1002/sim.6902>. The `mice.impute.heckprob()` function provides imputation model for binary outcome based on bivariate probit model as described in Galimard et al. (2018).

As these two previous imputation models require to specify a selection and an outcome equation, `mice()` function has to be adapted using `MNARargument()`.

Details

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- **MNARargument**
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- **generate_JointModelEq**
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- **miceMNAR-package**
  - Missing not at Random Imputation Models for Multiple Imputation by Chained Equation

Warning

This package is only validated for the imputation of MNAR outcome. However, it is implemented to impute several MNAR variables in the same process. Such implementation must be realised carefully.

Author(s)

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References


See Also

mice copulasampleSel SemiParBIV
selection

generate_JointModelEq  Generation of an empty matrix for sample selection model

Description

This function generates a matrix of 0 with rows corresponding to the names of variables included in the dataset and column corresponding to selection and outcome equations for each MNAR outcome. The user has to fill this matrix with 1 for variable included in selection and/or outcome equations of MNAR outcome imputation models.

Usage

generate_JointModelEq(varMNAR, data)

Arguments

varMNAR  The name of MNAR outcome to be imputed.
data  The dataset used for classical multiple imputation by chained equation and additional variables necessary for MNAR imputation models.

Details

Be careful to not define the same selection and outcome equations for MNAR imputation models. A constraint of the sample selection model implies the inclusion of different sets of covariates, which may or not be nested in the selection equation and the outcome equation, to avoid collinearity issues. It has been recommended to include at least a supplementary variable in the selection equation. This variable should be known to be unlinked directly to the outcome.
Value

A matrix such as:

- Rows correspond to names of variables included in the data argument
- Columns correspond to selection and outcome equations for each MNAR outcome imputation models

Each column is named as "MNAR outcome" names adding "._var_sel" or "._var_out" corresponding to variables included in selection and outcome equation respectively.

Author(s)

Jacques-Emmanuel Galimard

See Also

miceMNAR hiv

Examples

# Import dataset with a suspected MNAR mechanism
require(GJRM)
data("hiv")

# We select only one region (lusuka) and 5 variables
lusuka <- hiv[hiv$region==5,c("hiv", "age", "marital", "condom", "smoke")]

# Categorical variables have to be recoded as factor
lusuka$hiv <- as.factor(lusuka$hiv)

# Specify a selection (missing data mechanism) and an outcome equation (analyse model)

# Generate an empty matrix
JointModelEq <- generate_JointModelEq(data=lusuka,varMNAR = "hiv")

# Fill in with 1 for variable included in equations
JointModelEq[,]$"hiv_var_sel" <- c(0,1,1,1)

# This indicates that age, marital, condom and smoke are included in the selection equation of hiv
JointModelEq[,]$"hiv_var_out" <- c(0,1,1,0)

# This indicates that age, marital and condom are included in the outcome equation of hiv

mice.impute.hecknorm  Imputation by Heckman’s model for continuous outcome with Missing Not At Random mechanism using one-step estimator

Description

Imputes univariate missing continuous outcome using Heckman’s model with a one-step maximum likelihood estimator.
Usage

mice.impute.hecknorm(y, ry, x, JointModelEq, control, ...)

Arguments

y  
Incomplete data vector of length n.

ry  
Vector of missing data pattern of length n (FALSE=missing, TRUE=observed).

x  
Matrix (n x p) of complete covariates.

JointModelEq  
Output JointModelEq provided by MNARargument() function.

control  
Output control provided by MNARargument() function.

...  
Other named arguments.

Details

Imputation of continuous MNAR outcome using Heckman’s model. This imputation model requires to define a selection and an outcome equation for the imputation model. The imputation algorithm consists of the following steps:

1. Fit the one-step Heckman’s model and compute the posterior distribution of parameters
2. Draw imputation parameters from their posterior distribution
3. Draw imputed values from their predictive distribution

Value

A vector of length nmis with imputations.

Author(s)

Jacques-Emmanuel Galimard and Matthieu Resche-Rigon

References


See Also

miceMNAR

Examples

require("GJRM")
require(mvtnorm)

# Generation of a simulated dataset with MNAR mechanism on a continuous outcome
mice.impute.hecknorm2step

mice.impute.hecknorm2step

Imputation by Heckman's model for continuous Missing Not At Random outcome using a two-step estimator

Description

Imputes univariate continuous Missing Not At Random (MNAR) outcome using Heckman's model with a two-step estimator.

Usage

mice.impute.hecknorm2step(y, ry, x, JointModelEq, control, ...)

Arguments

y Incomplete data vector of length n.
**mice.impute.hecknorm2step**

- **ry**  Vector of missing data pattern of length \( n \) (FALSE=missing, TRUE=observed).
- **x**  Matrix \((n \times p)\) of complete covariates.
- **JointModelEq**  Output JointModelEq provided by `MNARargument()` function.
- **control**  Output control provided by `MNARargument()` function.
- **...**  Other named arguments.

**Details**

Imputation of continuous MNAR outcome using two-step Heckman’s model (Galimard, 2016). This imputation model requires to define a selection and an outcome equation. The imputation algorithm consists of the following steps:

1. Compute Inverse Mill’s Ratio (IMR) from the selection equation probit model
2. Include IMR as predictor in the imputation model
3. Draw imputation parameters using approximate proper imputation for the linear model and adding the Heckman variance correction as detailed in Galimard et al (2016)
4. Draw imputed values from their predictive distribution

**Value**

A vector of length \( n_{\text{mis}} \) with imputations.

**Note**

`mice.impute.hecknorm()` should be preferred as `mice.impute.hecknorm2step()`. Accordingly, for continuous outcome, `mice.impute.hecknorm()` is a default. However, it is possible to modify the method argument by hand.

**Author(s)**

Jacques-Emmanuel Galimard and Matthieu Resche-Rigon

**References**


**See Also**

`miceMNAR`
Examples

```r
require("GJRM")
require(mvtnorm)
require(sampleSelection)

# Generation of a simulated dataset with MNAR mechanism on a continuous outcome

X1 <- rnorm(500, 0, 1)
X2 <- rbinom(500, 1, 0.5)
X3 <- rnorm(500, 1, 0.5)

errors <- rmvnorm(500, mean=c(0,0), sigma=matrix(c(1,0.3,0.3,1),nrow=2,byrow=TRUE))

Y <- X1+X2+errors[,1]
Ry <- ifelse(0.66+1*X1-0.5*X2+X3+errors[,2]>0,1,0)

Y[Ry==0] <- NA

simul_data <- data.frame(Y,X1,X2,X3)

JointModelEq <- generate_JointModelEq(data=simul_data, varMNAR = "Y")

JointModelEq[,"Y_var_sel"] <- c(0,1,1)
JointModelEq[,"Y_var_out"] <- c(0,1,0)

arg <- MNARArgument(data=simul_data, varMNAR="Y", JointModelEq=JointModelEq)
arg$method["Y"] <- "hecknorm2step"

## Not run: imputation3 <- mice(data = arg$data_mod,
method = arg$method,
predictorMatrix = arg$predictorMatrix,
JointModelEq=arg$JointModelEq,
control=arg$control,
maxit=1,m=5)

analysis3 <- with(imputation3,lm(Y~X1+X2+X3))
result3 <- pool(analysis3)
summary(result3)
## End(Not run)
```

mice.impute.heckprob  
Imputation by bivariate probit sample selection model for binary Missing Not At Random outcome

Description

Imputes univariate binary Missing Not At Random (MNAR) outcome using the bivariate probit sample selection model.
Usage

mice.impute.heckprob(y, ry, x, JointModelEq, control, ...)

Arguments

y  Incomplete data vector of length n.
ry  Vector of missing data pattern of length n (FALSE=missing, TRUE=observed).
x  Matrix (n x p) of complete covariates.
JointModelEq  Output JointModelEq provided by MNRargument() function.
control  Output control provided by MNRargument() function.
...  Other named arguments.

Details

Imputation of binary MNAR outcome using the bivariate probit sample selection model. This imputation model requires defining a selection and an outcome equation for the bivariate probit model.
The imputation algorithm consists of the following steps:

1. Fit the bivariate probit model and compute the posterior distribution of parameters
2. Draw imputation parameters from their posterior distributions
3. Draw imputed values from their predictive distribution

Value

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

Author(s)

Jacques-Emmanuel Galimard and Matthieu Resche-Rigon

References


See Also

miceMNAR

Examples

# Import dataset with a suspected MNAR mechanism
require("GJRM")
require(mvtnorm)
require(pbivnorm)
data("hiv")
# We select only one region (lusuka) and 5 variables
lusuka <- hiv[hiv$region==5,c("hiv", "age", "marital", "condom", "smoke")]

# Categorical variables have to be recoded as factor
lusuka$hiv <- as.factor(lusuka$hiv)

# Specify a selection (missing data mechanism) and an outcome equation (analyse model)
# Generate an empty matrix
JointModelEq <- generate_JointModelEq(data=lusuka, varMNAR = "hiv")

# Fill in with 1 for variable included in equations
JointModelEq[,"hiv_var_sel"] <- c(0,1,1,1,1)
JointModelEq[,"hiv_var_out"] <- c(0,1,1,1,0)

# Generation of argument for MNAR imputation model in "mice()" function
arg <- MNARargument(data=lusuka, varMNAR="hiv", JointModelEq=JointModelEq)

# Imputation using mice() function
# Values returned have to be included in the "mice()" function as argument:
## Not run: imputation <- mice(data = arg$data_mod,
  method = arg$method,
  predictorMatrix = arg$predictorMatrix,
  JointModelEq=arg$JointModelEq,
  control=arg$control,
  maxit=1,m=5)

# Because of missing data only on one variable, fix maxit=1

# Estimation on each imputed dataset and pooling
analysis <- with(imputation, glm(hiv~age+condom+marital,family=binomial(link="probit")))
result <- pool(analysis)
summary(result)
## End(Not run)

---

**MNARargument**

Function providing modified arguments for imputation of Missing Not At Random (MNAR) outcomes using `mice()` function of the 'mice' package

**Description**

Imputation models for Missing Not At Random (MNAR) binary or continuous outcomes developed in this package use sample selection models. It is necessary, inside the imputation model, to specify a selection (i.e. missing data mechanism) and an outcome equation. The previous could be the model of interest (i.e. the post-imputation analysis model).

**MNARargument** adaptes `mice()` arguments:
1. data: Indicator of MNAR outcome missingness is included
2. method: For the MNAR outcome (varMNAR), MNAR imputation model is specified
3. predictorMatrix is modified to include MNAR indicator of missingness in other variable imputation model

Finally two new arguments are provided: JointModelEq, defining selection and outcome equation of the sample selection model; and control only for internal use.

The procedure is the following:
1. Use generate_JointModelEq() to construct an empty matrix of variable names allowing to specify selection and outcome equation
2. Fulfill the previous empty matrix adequately to selection and outcome equation specification of the sample selection model
3. Generate an object using MNARargument() function
4. Include in the mice() function the five arguments of the previous object generated by MNARargument()

Usage
MNARargument(data, method = NULL, predictorMatrix = NULL, varMNAR, JointModelEq = NULL)

Arguments
- **data**: The dataset used for classical mice() and additional variables necessary for MNAR imputation models.
- **method**: The mice() method argument.
- **predictorMatrix**: The mice() predictorMatrix argument.
- **varMNAR**: The name of MNAR outcome to be imputed.
- **JointModelEq**: Matrix indicating variables included in selection and outcome equations of MNAR outcome imputation models.

Details
Be careful to not define the same selection and outcome equations for MNAR imputation models. A constraint of the sample selection model implies the inclusion of different sets of covariates, which may or not be nested in the selection equation and the outcome equation, to avoid collinearity issues. It has been recommended to include at least a supplementary variable in the selection equation. This variable should be known to be unlinked directly to the outcome.

Value
- **data_mod**: Modified dataset including indicator of missingness for MNAR outcomes. Indicators of missingness are coded as "ind_" adding the name of MNAR outcomes.
- **method**: Modified mice() method argument using mice.impute.hecknorm() and mice.impute.heckprob() as imputation methods respectively for continuous and binary outcomes.
predictorMatrix

Modified mice() predictorMatrix argument including indicator of MNAR outcomes missingness as predictors for MAR covariates.

JointModelEq

For internal use: Modified JointModelEq entry argument.

control

For internal use: MNAR outcomes.

Warning

This package is only validated for the imputation of MNAR outcome. However, it is implemented to impute several MNAR variables in the same process. Such implementation must be realised carefully.

Note

For MNAR continuous outcome, the Heckman’s one step estimator is selected by default. However, the two-step estimator is available using mice.impute.hecknorm2step(). To use it, the method argument should be modified before inclusion in the mice() function.

Author(s)

Jacques-Emmanuel Galimard

References


See Also

mice copulaSampleSel SemiParBIV hiv selection generate_JointModelEq

Examples

require(GJRM)
require(mvtnorm)
require(pbivnorm)
require(sampleSelection)

# Import dataset with a suspected MNAR mechanism
data("hiv")

# We select only one region (lusuka) and 5 variables
lusuka <- hiv[hiv$region==5,c("hiv", "age", "marital", "condom", "smoke")]

# Categorical variables have to be recoded as factor
lusuka$hiv <- as.factor(lusuka$hiv)

# Specify a selection (missing data mechanism) and an outcome equation (analyse model)

# Generate an empty matrix
JointModelEq <- generate_JointModelEq(data=lusuka, varMNAR = "hiv")

# Fill in with 1 for variable included in equations
JointModelEq[, "hiv_var_sel"] <- c(0,1,1,1)
JointModelEq[, "hiv_var_out"] <- c(0,1,1,1,0)

# Generation of argument for MNAR imputation model in "mice()" function
arg <- MNARargument(data=lusuka, varMNAR="hiv", JointModelEq=JointModelEq)

# Imputation using mice() function
# Values returned have to be included in the "mice()" function as argument:
imputation <- mice(data = arg$data_mod,
                   method = arg$method,
                   predictorMatrix = arg$predictorMatrix,
                   JointModelEq=arg$JointModelEq,
                   control=arg$control,
                   maxit=1, m=5)

# Because of missing data only on one variable, fix maxit=1

# Estimation on each imputed dataset and pooling
analysis <- with(imputation, glm(hiv~age+condom+marital+family, family=binomial(link="probit")))
result <- pool(analysis)
summary(result)

# Generate missing values on the variable "condom"
# According to a MAR mechanism using a probit model
prob <- pnorm((35.5-lusuka$age)/10.74) # Depending on "age"
lusuka$condom[rbinom(nrow(lusuka), size=1, prob=prob)==0] <- NA

JointModelEq <- generate_JointModelEq(data=lusuka, varMNAR = c("hiv"))
JointModelEq[, "hiv_var_sel"] <- c(0,1,1,1,1)
JointModelEq[, "hiv_var_out"] <- c(0,1,1,1,0)

arg <- MNARargument(data=lusuka, varMNAR=c("hiv"), JointModelEq=JointModelEq)

# Not run: # Imputation using mice function
imputation <- mice(data = arg$data_mod,
method = arg$method,
predictorMatrix = arg$predictorMatrix,
JointModelEq = arg$JointModelEq,
control = arg$control,
maxit = 5, m = 5)

# As classically, estimation on each imputed datasets and pooling
analysis <- with(imputation, glm(hiv ~ age + condom + marital, family = binomial(link = "probit")))
result <- pool(analysis)
summary(result)
## End(Not run)

########################################################################
#### Missing data only on a continuous outcome ####
########################################################################

# Generation of a simulated dataset with MNAR mechanism on a continuous outcome
X1 <- rnorm(500, 0, 1)
X2 <- rbinom(500, 1, 0.5)
X3 <- rnorm(500, 1, 0.5)

errors <- rmvnorm(500, mean = c(0, 0), sigma = matrix(c(1, 0.3, 0.3, 1), nrow = 2, byrow = TRUE))
Y <- X1 + X2 + errors[, 1]
Ry <- ifelse(0.66 + 1 * X1 - 0.5 * X2 + X3 + errors[, 2] > 0, 1, 0)
Y[Ry == 0] <- NA
simul_data <- data.frame(Y, X1, X2, X3)

JointModelEq <- generate_JointModelEq(data = simul_data, varMNAR = "Y")
JointModelEq[,"Y_var_sel"] <- c(0, 1, 1, 1)
JointModelEq[,"Y_var_out"] <- c(0, 1, 1, 0)
arg <- MNARArgument(data = simul_data, varMNAR = "Y", JointModelEq = JointModelEq)
imputation2 <- mice(data = arg$data_mod,
method = arg$method,
predictorMatrix = arg$predictorMatrix,
JointModelEq = arg$JointModelEq,
control = arg$control,
maxit = 1, m = 5)

analysis2 <- with(imputation, lm(Y ~ X1 + X2 + X3))
result2 <- pool(analysis2)
summary(result2)

########################################################################
## Using 2-step estimation ##
########################################################################
arg <- MNARargument(data=simul_data, varMNAR="Y", JointModelEq=JointModelEq)
arg$method["Y"] <- "hecknorm2step"

## Not run: imputation3 <- mice(data = arg$data_mod,
   method = arg$method,
   predictorMatrix = arg$predictorMatrix,
   JointModelEq=arg$JointModelEq,
   control=arg$control,
   maxit=1,m=5)

analysis3 <- with(imputation3, lm(Y~X1+X2+X3))
result3 <- pool(analysis3)
summary(result3)
## End(Not run)
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