Package ‘mvnimpute’

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mvnimpute: Multiple imputation for multivariate data with missing and censored values

Description

The mvnimpute package implements multiple imputation for simultaneously imputing missing and censored values based on the joint normal model assumption.

Author(s)

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acf.calc

Autocorrelation function

Description

Calculates the autocorrelation function and draws the plots.

Usage

acf.calc(data.mat, lag = 50, plot = TRUE, title = NULL, details = FALSE)

Arguments

data.mat matrix including the variables of which autocorrelations are calculated.
lag lag at which the autocorrelation is calculated, default is set as 50.
plot logical variable to specify whether the plot is generated, default is set to TRUE.
title title of each generated autocorrelation plot.
details boolean variable to specify whether the autocorrelation values are returned, default is set to FALSE.
Details
This function calculates the autocorrelations of all the variables on a column by column base. The default value of lag is set as 50, the maximum number of lag should not exceed the number of rows of the dataset, which reflects the corresponding number of iteration of running the multiple imputation.

Value
If details = TRUE, a matrix containing the calculated autocorrelations of all the variables in the dataset will be returned. If plot = TRUE, the autocorrelation plots of all the variables will be drawn.

Examples
### generate some data
dat <- MASS::mvrnorm(n = 1000, mu = c(1, 2, 3, 4), Sigma = diag(4))

### ACF plots
acf.calc(data.mat = dat, title = paste0("Var ", 1:nrow(dat)))

### Generate some data

dat <- MASS::mvrnorm(n = 1000, mu = c(1, 2, 3, 4), Sigma = diag(4))

### ACF plots
acf.calc(data.mat = dat, title = paste0("Var ", 1:nrow(dat)))

---

avg.plot  

Averaged simulated values plot function

Description
Calculates the average simulated values of all parameters and generates plots.

Usage
avg.plot(
  data.mat,  
  start,  
  end,  
  x.lab = "Iteration number",  
  y.lab = "Average of simulated values",  
  title = NULL,  
  details = FALSE
)

Arguments
- data.mat: data matrix including the simulated values for plot.
- start: the number of cycle to start.
- end: the number of cycle to end.
- x.lab: label of the x axis in the generated plot, default is set to "Iteration number".
conv.plot

| y.lab | label of the y axis in the generated plot, default is set to "Average of simulated values". |
| title | title of each generated plot. |
| details | logical variable to specify whether the average simulated values are returned, default is set to FALSE. |

**Details**

This function calculates the average simulated values across simulations. `iter` can be any number of iterations you want to draw, the corresponding number of rows of the data should be `iter + 1`.

**Value**

The plot of averaged values across iterations. If `details = TRUE`, a matrix containing the averaged values of all the variables across iterations will be returned.

**Examples**

```r
### generate some normal data
dat <- MASS::mvrnorm(n = 1000, mu = c(1, 2, 3, 4), Sigma = diag(4))

### set column names
colnames(dat) <- paste0("Var ", 1:ncol(dat))

### average values plot: take sample from 500 to 1000 rows
avg.plot(data.mat = dat[500:1000, ], start = 500, end = 1000, title = "Random Variables")
```

**conv.plot**

_Convergence plot function_

**Description**

Draws convergence plot for the simulated parameter values of all variables.

**Usage**

```r
conv.plot(
  data.mat,
  start,
  end,
  x.lab = "Iteration number",
  y.lab = "Simulated values",
  title = NULL
)
```
data.generation

Description

Simulates multivariate normal data with missing and censored values. In this function, missing values will be generated first in the multivariate data, then censored values will be generated for the non-missing data.

Usage

data.generation(
  num_ind = 2000,
  mean_vec = rnorm(5),
  cov_mat = diag(5),
  miss_var = c(2, 3),
)
miss_mech = "MCAR",
miss_prob = c(0.2, 0.4),
censor_var = 4,
censor_type = "interval",
censor_param = 0.1
)

Arguments

num_ind number of subjects.
mean_vec mean vectors.
cov_mat covariance matrix.
miss_var variables that have missing values.
miss_mech missing mechanism. "MCAR" or "MAR". Default "MCAR".
miss_prob missing data probability when missing data is MCAR.
censor_var variables that have censored values.
censor_type type of censoring. "interval", "right" or "left. Default "interval".
censor_param rate parameter of the exponential distribution that the censoring times come from.

Value

A list containing the fully observed data, the observed data, the bounds information of the observed data and the data type indicator matrix.

Examples

### generate a multivariate normal dataset of 2000 sample size
### using the default arguments
data.generation()

marg.plot(data.mat, title = NULL)

marg.plot Marginal density plots function

Description

Draws marginal density plots for all variables

Usage

marg.plot(data.mat, title = NULL)

Arguments

data.mat data matrix including all the variables.
title title of each generated plot.
Value

Marginal density plot for each variable in the dataset.

Examples

```r
### generate some data
dat <- MASS::mvrnorm(n = 1000, mu = c(1, 2, 3, 4), Sigma = diag(4))

### set column names
colnames(dat) <- paste0("Var ", 1:ncol(dat))

### marginal plots
marg.plot(data.mat = dat, title = paste0("Var", 1:nrow(dat)))
```

multiple.imputation  *Multiple imputation function*

Description

Multiply imputes the missing and censored values in multivariate data.

Usage

```r
multiple.imputation(data, prior.params, initial.values, iter, verbose = TRUE)
```

Arguments

data  a list of data containing the lower and upper bounds information for the missing and censored values.
prior.params  list of prior parameter specifications.
initial.values  list of initial values.
iter  number of rounds for doing multiple imputation.
verbose  boolean variable indicating whether the running status is printed in the console. Default is set to TRUE.

Details

A multivariate normal model is assumed on the data, the sweep operator is adopted to calculate the parameters of the conditional models. The implemented multiple imputation algorithm is based on the data augmentation algorithm proposed by Tanner and Wong (1987). The Gibbs sampling algorithm is adopted to update the model parameters and draw imputations of the coarse data. Output is a list including the parameters of the normal models and the imputed data across different iterations of multiple imputation.
Value

A list including the simulated mean and variance values of the assumed normal model, the covariance matrix, the imputed data, and the conditional model parameters across different iterations of multiple imputation.

References


Examples

```r
## Not run:
### data and indicator
miss.dat <- simulated.dat[[1]]
data.ind <- simulated.dat[[2]]

### number of observations and variables
n <- nrow(miss.dat); p <- ncol(miss.dat)

### bound matrices
b1 <- b2 <- matrix(nrow = nrow(data.ind), ncol = ncol(data.ind))
for (i in 1:nrow(b1)) {
  for (j in 1:ncol(b1)) {
    b1[i, j] <- ifelse(data.ind[i, j] != 1, NA, miss.dat[i, j])
    b2[i, j] <- ifelse(data.ind[i, j] == 0, NA, miss.dat[i, j])
  }
}
colnames(b1) <- colnames(b2) <- colnames(miss.dat)

### prior specifications
prior.param <- list(
  mu.0 = rep(0, p),
  Lambda.0 = diag(100, p),
  kappa.0 = 2,
  nu.0 = p * (p + 1) / 2
)

### starting values
start.vals <- list(
  mu = rep(0, p),
  sigma = diag(100, p)
)
```
\begin{verbatim}
### imputation
sim.res <- multiple.imputation(
    data = bounds,
    prior.params = prior.param,
    initial.values = start.vals,
    iter = 500,
    verbose = FALSE
)

## End(Not run)
\end{verbatim}

---

**NHANES.dat**

*Combined NHANES dataset from 1999-2004 NHANES study*

**Description**

A dataset including the age, gender and diastolic blood pressure, body mass index and 24 PCB measurements.

**Usage**

NHANES.dat

**Format**

A list including data frame with 5874 rows and 24 variables and associated indicator matrix:

- **BPXDAR**: Diastolic blood pressure
- **RIAGENDR**: Gender, 1 = male, 2 = female
- **RIDAGEYR**: Age in years
- **BMXBMI**: Body mass index

**Details**

The dataset is combined from the NHANES release cycles 1999-2000, 2001-2002, and 2003-2004. Almost all PCB have both the missing and censored values as falling below the limits of detection (LODs). The dataset include two components, the first component is the observed NHANES data where the censored PCB measurements are replaced by the LODs dividing the square root of 2. The second component is a data frame including the censoring indicators of the data, in that data frame, 0 indicates an observed PCB measurement, 1 indicates a censored PCB measurement, and ‘NA’ indicates a missing PCB measurement.

**Note**

The subset provided here was selected to demonstrate the functionality of the mvnimpute package, no clinical conclusions should be derived from it.
**Source**

https://www.cdc.gov/nchs/nhanes/index.htm

---

**simulated.dat**  
*Simulated continuous data with missing and censored values*

---

**Description**

A dataset including simulated data with missing and censored values

**Usage**

simulated.dat

**Format**

A list including data matrix with 200 rows and 4 variables and associated indicator matrix:

- **y**  
  Outcome variable to be used in the regression model after imputation

- **x1**  
  First covariate variable subject to MAR missing and non-informative censored values

- **x2**  
  Second covariate variable subject to MAR missing and non-informative censored values

- **x3**  
  Third covariate variable that is fully observed

**Details**

A simulated dataset and its associated indicator matrix are included into a list. In the indicator matrix, 0 stands for the missing values, 1 stands for the observed values, and 3 stands for the left censored values.

---

**visual.plot**  
*Draws percentage plot for different type of values*

---

**Description**

Draws plot that graphically shows the percentages of the missing, censored and observed data. It supports generating plots for all major types of censoring including left, right and interval censoring.

**Usage**

visual.plot(data.indicator, title = "Percentages of different data type")

**Arguments**

- **data.indicator**  
  matrix including the data type indicators of the original data.

- **title**  
  title of the generated plot, default is set to "Percentages of different data type".
visual.plot

Details

The function draws the plot that graphically shows the percentages of the missing, censored and observed data in the dataset. data.indicator should be a matrix containing the data type indicators as generated in the data preparation step. 0 for missing values, 1 for observed values, and 2 for right censored values, 3 for left censored values, and 4 for interval censored values. title is the title of the generated plot.

Value

The plot that shows the details of the different type of data in the dataset.

Examples

data.ind <- simulated.dat[[2]]
visual.plot(data.ind)
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