Package ‘mi’

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CHAIN

Subset of variables from the CHAIN project, a longitudinal cohort study of people living with HIV in New York City.

Description

The CHAIN cohort was recruited in 1994 from a large number of medical care and social service agencies serving HIV in New York City. Cohort members were interviewed up to 8 times through 2002. A total of 532 CHAIN participants completed at least one interview at either the 6th, 7th or 8th, and 508, 444, 388 interviews were completed respectively at rounds 6, 7 and 8th.

Usage

data(CHAIN)

Format

A data frame with 532 observations on the following 8 variables.

- hSYbNw1 log of self reported viral load level at round 6th (0 represents undetectable level).
- ageNw1 age at time of interview at round 6th.
- cRXNw1 family annual income. Values range from under $5,000 to $70,000 or over at round 6th.
- pcsNw1 a continuous scale of physical health with a theoretical range between 0 and 100 (better health is associated with higher scale values) at round 6th.
- mcsSWNw1 a binary measure of poor mental health (1=Yes, 0=No) at round 6th.
- bPUNw1 ordered interval for the CD4 count (indicator of how much damage HIV has caused to the immune system) at round 6th.
- haartadhereNw1 a three-level ordered variable: 0=Not currently taking HAART (highly Active antiretroviral therapy), 1=taking HAART nonadherent, 2=taking HAART adherent at round 6th.
Details

A missing value in the virus load level (h39b) was assigned to individuals who either could not recall their viral load level, did not have a viral load test in the six month preceding the interview, or reported their viral loads as "good" or "bad".

Source

http://cchps.columbia.edu/research.cfm

References


See Also

mi

convergence.plot  Convergence Plot of mi Object

Description

Function to plot trace of mi iterative samples.

Usage

convergence.plot ( mi.object, ... )
conv.plot ( mi.object, ... )

Arguments

mi.object  mi object generated from mi function
...  Other options for traceplot function.

Details

Convergence plot plots the convergence of the means and the standard deviations of each variable for the different imputations.

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mi

**Multiple Iterative Regression Imputation**

**Description**

Generate a multiply imputed matrix applying the elementary functions iteratively to the variables with missingness in the data randomly imputing each variable and looping through until approximate convergence.

**Usage**

```r
## S4 method for signature 'data.frame'
mi(object, info, n.imp = 3, n.iter = 30,
    R.hat = 1.1, max.minutes = 20, rand.imp.method = "bootstrap",
    run.past.convergence = FALSE,
    seed = NA, check.coef.convergence = FALSE,
    add.noise = noise.control())

## S4 method for signature 'mi.preprocessed'
mi(object, n.imp = 3, n.iter = 30,
    R.hat = 1.1, max.minutes = 20, rand.imp.method = "bootstrap",
    run.past.convergence = FALSE,
    seed = NA, check.coef.convergence = FALSE,
    add.noise = noise.control())

## S4 method for signature 'mi'
mi(object, n.iter = 30,
    R.hat = 1.1, max.minutes = 20, rand.imp.method = "bootstrap",
    run.past.convergence = FALSE, seed = NA)
```

**Examples**

```r
# NOT RUN
#==============================================
# data(CHAIN)
# CHAIN <- mi.preprocess(CHAIN)
# imp.CHAIN <- mi(CHAIN, n.iter=6, add.noise=noise.control(post.run.iter=0))
# convergence.plot(imp.CHAIN,mfrow=c(2,4))
#==============================================
```

**References**

**Arguments**

- **object**: A data frame or an mi object that contains an incomplete data. mi identifies NAs as the missing data.
- **info**: The mi.info object.
- **n.imp**: The number of multiple imputations. Default is 3 chains.
- **n.iter**: The maximum number of imputation iterations. Default is 30 iterations.
- **R.hat**: The value of the R.hat statistic used as a convergence criterion. Default is 1.1.
- **max.minutes**: The maximum minutes to operate the whole imputation process. Default is 20 minutes.
- **rand.imp.method**: The methods for random imputation. Currently, mi implements only the bootstrap method.
- **run.past.convergence**: Default is FALSE. If the value is set to be TRUE, mi will run until the values of either n.iter or max.minutes are reached even if the imputation is converged.
- **seed**: The random number seed.
- **check.coef.convergence**: Default is FALSE. If the value is set to be TRUE, mi will check the convergence of the coefficients of imputation models.
- **add.noise**: A list of parameters for controlling the process of adding noise to mi via noise.control.

**Details**

Generate multiple imputations for incomplete data using iterative regression imputation. If the variables with missingness are a matrix Y with columns Y(1), . . . , Y(K) and the fully observed predictors are X, this entails first imputing all the missing Y values using some crude approach (for example, choosing imputed values for each variable by randomly selecting from the observed outcomes of that variable); and then imputing Y(1) given Y(2), . . . , Y(K) and X; imputing Y(2) given Y(1), Y(3), . . . , Y(K) and X (using the newly imputed values for Y(1)), and so forth, randomly imputing each variable and looping through until approximate convergence.

**Value**

A list of object of class mi, which stands for “multiple imputation”.

Each object is itself a list of 10 elements.

- **call**: The imputation model.
- **data**: The original data frame.
- **m**: The number of imputations.
- **mi.info**: Information matrix of the mi.
- **imp**: A list of length(m) of imputations.
- **mcmc**: A mcmc list that stores lists of means and sds of the imputed data.
- **converged**: Binary variable to indicate if the mi has converged.
coef.mcmc  A mcmc list that stores lists of means of regression coefficients of the conditional models.

coef.converged  Binary variable to indicate if the coeffs of mi model have converged, return NULL if check.coef.convergence = FALSE

preprocess  Binary variable to indicate if preprocess=TRUE in the mi process

mi.info.preprocessed  Information matrix that actually used in the mi if preprocess=TRUE.

Each imp[[m]] is itself a list containing k variable lists of 3 objects:

imp[[m]][[k]]@model  the specified models used for imputing missing values

imp[[m]][[k]]@expected  a list of vectors of length n-n.mis (number of complete observed data), specifying the estimated values of the models

imp[[m]][[k]]@random  a list of vectors of length n.mis (number of NAs), specifying the random predicted values for imputing missing data

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References


See Also

`mi.completed, mi.data.frame, mi.continuous, mi.binary, mi.count, mi.categorical, mi.polr, typecast, mi.info, mi.preprocess`

Examples

```r
# simulate fake data
set.seed(100)
n <- 100
u1 <- rbinom(n, 1, .5)
v1 <- log(rnorm(n, 5, 1))
x1 <- u1*exp(v1)
u2 <- rbinom(n, 1, .5)
v2 <- log(rnorm(n, 5, 1))
x2 <- u2*exp(v2)
```
x3 <- rbinom(n, 1, prob=0.45)
x4 <- ordered(rep(seq(1, 5),100)[sample(1:n, n)])
x5 <- rep(letters[1:10],10)[sample(1:n, n)]
x6 <- trunc(runif(n, 1, 10))
x7 <- rnorm(n)
x8 <- factor(rep(seq(1,10),10)[sample(1:n, n)])
x9 <- runif(n, 0.1, .99)
x10 <- rpois(n, 4)
y <- x1 + x2 + x7 + x9 + rnorm(n)
fakedata <- cbind.data.frame(y, x1, x2, x3, x4, x5, x6, x7, x8, x9, x10)

# randomly create missing values
dat <- mi:::create_missing(fakedata, pct.mis=30)

# get information matrix of the data
inf <- mi.info(dat)

# update the variable type of a specific variable to mi.info
inf <- update(inf, "type", list(x10="count"))

# run the imputation without data transformation
#IMP <- mi(dat, info=inf, check.coef.convergence=TRUE,
# add.noise=noise.control(post.run.iter=10))

# run the imputation with data transformation
dat.transformed <- mi.preprocess(dat, inf)
#IMP <- mi(dat.transformed, n.iter=6, check.coef.convergence=TRUE,
# add.noise=noise.control(post.run.iter=6))

IMP <- mi(dat.transformed, n.iter=6, add.noise=FALSE)

# no noise
# IMP <- mi(dat, info=inf, n.iter=6, add.noise=FALSE) ## NOT RUN

# pick up where you left off
# IMP <- mi(IMP, n.iter = 6)

## this is the suggested (default) way of running mi
# IMP <- mi(dat, info=inf) ## NOT RUN

# convergence checking
converged(IMP, check = "data") ## You should get FALSE here because only n.iter is small
converged(IMP, check = "coeffs")
IMP.bugs1 <- bugs.mi(IMP, check = "data") ## BUGS object to look at the R hat statistics
IMP.bugs2 <- bugs.mi(IMP, check = "coeffs") ## BUGS object to look at the R hat statistics
plot(IMP.bugs1) ## visually check R.hat

# visually check the imputation
plot(IMP)
### mi.binary

**Elementary function:** Bayesian logistic regression to impute a binary variable.

### Description

Imputes univariate missing data using bayesglm, an R function for generalized linear modeling with independent normal, t, or Cauchy prior distribution for the coefficients.

### Usage

```r
mi.binary(formula, data = NULL, start = NULL, n.iter = 100,
   draw.from.beta = TRUE, missing.index = NULL, ...)
```

```
## S4 method for signature 'mi.binary'
resid(object, y)
## S4 method for signature 'mi.binary'
residuals(object, y)
## S4 method for signature 'mi.binary,ANY'
plot( x, y, main=deparse( substitute( y ) ), gray.scale = FALSE, ...)
```

### Arguments

- **formula**: an object of class "formula" (or one that can be coerced to that class): a symbolic description of the model to be fitted. See bayesglm 'formula' for details.
- **data**: A data frame containing the incomplete data and the matrix of the complete predictors.
- **start**: Starting value for bayesglm.
- **n.iter**: Maximum number of iteration for bayesglm. The default is 100.
- **draw.from.beta**: Draws from posterior distribution of the betas to add randomness.
- **missing.index**: The index of missing units of the outcome variable.
- **...**: Currently not used.
- **object**: mi.binary object.
- **x**: mi.binary object.
- **y**: Observed values.
- **main**: main title of the plot.
- **gray.scale**: When set to TRUE, makes the plot into gray scale with predefined color and line type.

### Details

In bayesglm default the prior distribution is Cauchy with center 0 and scale 2.5 for all coefficients (except for the intercept, which has a prior scale of 10). See also glm for other details.
Value

- **model**: A summary of the bayesian fitted model.
- **expected**: The expected values estimated by the model.
- **random**: Vector of length n.mis of random predicted values predicted by using the binomial distribution.

Note

see also [http://www.stat.columbia.edu/~gelman/standardize/](http://www.stat.columbia.edu/~gelman/standardize/)

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References


See Also

- `mi.info`, `mi.method`, `mi`

Examples

```r
# true data
x <- rnorm(100, 0, 1) # N(0,1)
y <- rbinom(100, 1, invlogit(1+2*x)) # y ~ Bin(1, invlogit(1 + 2*x))
# create artificial missingness on y
y[seq(1, 100, 10)] <- NA
dat.xy <- data.frame(x, y)
# imputation
mi.binary(y~x, data = dat.xy)
```

---

`mi.categorical`  
**Elementary function: multinomial log-linear models to impute a categorical variable.**

Description

Imputes missing data in a categorical variable using multinomial Log-linear Models.
Usage

mi.categorical( formula, data = NULL, n.iter = 100, 
MaxNWts = 1500, missing.index = NULL, ...)

## S4 method for signature 'mi.categorical'
residuals(object, y)

## S4 method for signature 'mi.categorical,ANY'
plot( x, y, main=deparse( substitute( y ) ), gray.scale = FALSE, ...)

Arguments

- **formula**: a formula expression as for regression models, of the form `response ~ predictors`. The response should be a factor or a matrix with K columns, which will be interpreted as counts for each of K classes. A log-linear model is fitted, with coefficients zero for the first class. An offset can be included: it should be a numeric matrix with K columns if the response is either a matrix with K columns or a factor with K > 2 classes, or a numeric vector for a response factor with 2 levels. See the documentation of `formula()` for other details.

- **data**: A data frame containing the incomplete data and the matrix of the complete predictors.

- **n.iter**: Maximum number of iteration.

- **MaxNWts**: The maximum allowable number of weights. See nnet for detail.

- **missing.index**: The index of missing units of the outcome variable

- **object**: mi.categorical object.

- **x**: mi.categorical object.

- **y**: Observed values.

- **main**: main title of the plot.

- **gray.scale**: When set to TRUE, makes the plot into gray scale with predefined color and line type.

- **...**: Currently not used.

Details

`multinom` calls the library `nnet`. See `multinom` for other details.

Value

- **model**: A summary of the multinomial fitted model.

- **expected**: The expected values estimated by the model.

- **random**: Vector of length `n.mis` of random predicted values predicted by using the multinomial distribution.

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mi.completed

References


See Also

`mi.info`, `mi.method`, `mi`

Examples

```r
x <- rnorm(100, 0, 1)
y <- x + 4
y <- round(y)
y[y < 0] <- 0
# create artificial missingness on y
y[seq(1, 100, 10)] <- NA
dat.xy <- data.frame(x, y)
mi.categorical(formula = y ~ x, data = dat.xy)
```

mi.completed

Multiply Imputed Dataframes

Description

Function to return completed data set from result of mi program.

Usage

```r
## S4 method for signature 'mi'
mi.completed(object)
## S4 method for signature 'mi'
mi.data.frame(object, m = 1)
```

Arguments

- `object` mi object containing a multiply imputed data set. The mi object is generated by the mi function.
- `m` Index of the imputed data set. The default is 1.

Value

A data set or a list of datasets with the missing data imputed.
mi.continuous

Description

Imputes univariate missing data using linear regression.

Usage

```r
mi.continuous(formula, data = NULL, start = NULL, n.iter = 100,
               draw.from.beta = TRUE, missing.index = NULL, ...)
```

Arguments

- `formula` an object of class "formula" (or one that can be coerced to that class): a symbolic description of the model to be fitted. See `bayesglm`'s `formula` for details.
- `data` A data frame containing the incomplete data and the matrix of the complete predictors.
- `start` Starting value for `bayesglm`.
- `n.iter` Maximum number of iteration for `bayesglm`. The default is 100.
- `draw.from.beta` Draws from posterior distribution of the betas to add randomness.
- `missing.index` The index of missing units of the outcome variable
- `...` Currently not used.

Examples

```r
# data(CHAIN)
# IMP <- mi(CHAIN, n.iter=6, add.noise=FALSE)
## get all imputed dataset
# imputed.matrix <- mi.completed(IMP)
## get the 3rd chain of the imputed dataset
# imputed.data.frame <- mi.data.frame(IMP, m=3)
```
mi.count

Details

see bayesglm

Value

- model: A summary of the fitted model.
- expected: The expected values estimated by the model.
- random: Vector of length n.mis of random predicted values predicted by using the normal distribution.

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References


See Also

mi.info, mi.method, mi

Examples

```r
# true data
x <- rnorm(100, 0, 1)  # N(0,1)
y <- rnorm(100, (1+2*x), 1.2)  # y ~ 1 + 2*x + N(0, 1.2)
# create artificial missingness on y
y[seq(1, 100, 10)] <- NA
dat.xy <- data.frame(x, y)
# imputation
mi.continuous(y=y, data = dat.xy)
```

mi.count

Elementary function: Bayesian overdispersed poisson regression to impute a count variable.

Description

Imputes univariate missing data using bayesglm, an R function for generalized linear modeling with independent normal, t, or Cauchy prior distribution for the coefficients.
Usage

mi.count(formula, data = NULL, start = NULL, n.iter = 100,
  draw.from.beta = TRUE, missing.index = NULL, ...)
## S4 method for signature 'mi.count'
resid(object, y)
## S4 method for signature 'mi.count'
residuals(object, y)

Arguments

formula an object of class formula (or one that can be coerced to that class): a symbolic
description of the model to be fitted. See bayesglm formula for details.
data A data frame containing the incomplete data and the matrix of the complete
predictors.
start Starting value for bayesglm.
n.iter Maximum number of iteration for bayesglm. The default is 100.
draw.from.beta Draws from posterior distribution of the betas to add randomness.
missing.index The index of missing units of the outcome variable
... Currently not used.
object mi.count object.
y Observed values.

Details

In bayesglm default the prior distribution is Cauchy with center 0 and scale 2.5 for all coefficients
(except for the intercept, which has a prior scale of 10). See also glm for other details.

Value

model A summary of the bayesian fitted model.
expected The expected values estimated by the model.
random Vector of length n.mis of random predicted values predicted by using the binomial
distribution.

Note

see also http://www.stat.columbia.edu/~gelman/standardize/

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References


See Also

mi.info, mi.method, mi

Examples

# true data
x <- rnorm(100,0,1)
y <- rpois(100,40)
# create artificial missingness on y
y[seq(1,100,10)] <- NA
dat.xy <- data.frame(x,y)
# imputation
mi.count(y ~ x, data = dat.xy)

mi.fixed

Elementary function: imputation of constant variable.

Description

Imputes univariate constant missing data.

Usage

mi.fixed(formula, data = NULL, missing.index = NULL, ...)
mi.copy(Y, X, missing.index = NULL, ...)

Arguments

formula an object of class "formula" (or one that can be coerced to that class): a symbolic description of the model to be fitted. See bayesglm 'formula' for details.
data A data frame containing the incomplete data and the matrix of the complete predictors.
missing.index The index of missing units of the outcome variable
Y A variable that is collinear with X.
X A variable that is collinear with Y.
... Currently not used
Value

- **model**: A summary of the fitted model.
- **expected**: The expected values estimated by the model.
- **random**: Vector of length n.mis of random predicted values predicted by using the normal distribution.

Author(s)

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References


See Also

- `mi.info`, `mi.method`, `mi`

Examples

```r
# fake data
n <- 100
x1 <- rbinom(n, 1, .45)
xx2 <- 2*x1
x1[c(1, 3, 5, 20, 26)] <- NA

# impute data
mi.copy(x1, xx2)
```

---

### mi.hist

**Multiple Imputation Histogram**

Description

A function for plotting the histogram of each variable and of its observed and imputed values.

Usage

```r
mi.hist(object, Yobs, ...)
```

## S4 method for signature 'mi.method,ANY'

```r
mi.hist(object, Yobs, ...)
```

## S4 method for signature 'mi.categorical,ANY'

```r
mi.hist(object, Yobs, ...)
```

## S4 method for signature 'mi.binary,ANY'

```r
mi.hist(object, Yobs, ...)
```
mi.hist

mi.hist( object, Yobs,...)
## S4 method for signature 'mi.polr,ANY'
mi.hist( object, Yobs,...)
## S4 method for signature 'mi.pmm,ANY'
mi.hist( object, Yobs,...)

Arguments

Yobs observed values.
object imputed values or member object of mi.method object family.
... Other options for plot function.

Value

The histogram (in black) of the complete variable, the histogram (in blue) of the observed values and the histogram (in red) of the imputed values.

Note

The histogram of the completed values (observed plus imputed) is in black, the histogram of the imputed values in red, while the one of the observed values in blue.

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References


See Also

plot.mi.hist

Examples

# true data
x<-rnorm(100,0,1) # N(0,1)
y<-rnorm(100,(1+2*x),1.2) # y ~ 1 + 2*x + N(0,1.2)
# create artificial missingness on y
y[seq(2,100,10)]<-NA
dat.xy <- data.frame(x,y)
# imputation
mi.info

Function to create information matrix for missing data imputation

Description

Produces matrix of information needed to impute the missing data. After the information is extracted user has the option of changing the default.

Usage

mi.info(data, threshold = 0.99999)

## S4 method for signature 'mi.info'
print(x, ...)

## S4 method for signature 'mi.info'
show(object)

Arguments

data  dataframe or matrix of dataset with missing data coded as NAs.
threshold  Threshold value for correlation to be considered a problem.
x  An object of a class mi.info.
object  An object of a class mi.info.
...  Currently not used.

Value

info  information matrix

- name: Name of variable
- imp.order: Imputation Order
- nmis: Number of missing
- type: Type of variable
- var.class: Class of input variable
- level: Levels in the input variable
- include: Include in the imputation process or not
- is.ID: Is ID variable or not
- all.missing: All observation missing or not
- collinear: Collineared variables
- determ.pred: Deterministic predictor
- imp.formula: Imputation formula
mi.info.update

-params: Parameters for the imputation model
-other: Currently not used

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References

See Also
mi

Examples
data(CHAIN)
info.CHAIN <- mi.info(CHAIN)

info.CHAIN$imp.order # imputation order

info.CHAIN$imp.formula # imputation formula
info.CHAIN["age.WT"]$imp.formula # imputation formula for specific variable

mi.info.update function to update mi.info object to use for multiple imputation

Description
This function is internal function to update the mi.info object.

Usage
## S3 method for class 'mi.info'
update(object, target, list, ...)
mi.info.update.type(object, list)
mi.info.update.level(object, list)
mi.info.update.include(object, list)
mi.info.update.is.ID(object, list)
mi.info.update.collinear(object, list)

mi.info.update.imp.order(object, list)
mi.info.update.determ.pred(object, list)
mi.info.update.params(object, list)
mi.info.update.imp.formula(object, list)
mi.info.update.other(object, list)
mi.method

Arguments

object mi.info object that is result of mi.info function.
target which part of mi.info object to modify.
list list that has same length as the number of variables in the mi.info object. Element which are left NULL will not be updated.

Value

info updated mi.info object.

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References


See Also

mi.completed

Examples

data(CHAIN)
CHAIN.info <- mi.info(CHAIN)

# You can update the mi.info object in the below two ways
CHAIN.info <- update(CHAIN.info, "type",
  list(age.W1="continuous", b05.W1="unordered-categorical"))
CHAIN.info <- mi.info.update.type(CHAIN.info,
  list(age.W1="continuous", b05.W1="unordered-categorical"))

---

mi.method

Virtual class for all mi classes.

Description

Imputes univariate missing data using linear regression.
**Usage**

```r
## S4 method for signature 'mi.method'
imputed(object, y)
## S4 method for signature 'mi.categorical'
imputed(object, y)
## S4 method for signature 'mi.polr'
imputed(object, y)
## S4 method for signature 'mi.method'
coeff(object)
## S4 method for signature 'mi.method'
coefficients(object)
## S4 method for signature 'mi.method'
sigma.hat(object)
## S4 method for signature 'mi.method'
fitted(object)
## S4 method for signature 'mi.method'
resid(object, y)
## S4 method for signature 'mi.method'
residuals(object, y)
## S4 method for signature 'mi.method'
print(x, ...)
## S4 method for signature 'mi.method,ANY'
plot(x, y, main=deparse( substitute( y ) ), gray.scale = FALSE, ...)
```

**Arguments**

- **object**: mi.method object.
- **...**: Currently not used.
- **x**: mi.method object.
- **y**: Observed values.
- **main**: main title of the plot.
- **gray.scale**: When set to TRUE, makes the plot into gray scale with predefined color and line type.

**Details**

mi.method is a virtual class for all the mi classes. Basically all the necessary functions are defined under mi.method class, thus most of the mi classes that do not have specific method defined for them inherits their methods from this class. For some special class as mi.nonnegative these methods are extended to tailor to the needs.

**Author(s)**

Masanao Yajima <yajima@stat.columbia.edu>, M.Grazia Pittau <grazia@stat.columbia.edu>, Andrew Gelman <gelman@stat.columbia.edu>
References

See Also
mi

---

`mi.pmm`  
*Elementary function: Predictive Mean Matching for imputation.*

**Description**
Imputes univariate missing data using bayesglm and predictive mean matching.

**Usage**
`mi.pmm(formula, data = NULL, start = NULL, n.iter = 100, missing.index = NULL, ...)`

**Arguments**
- `formula`: an object of class "formula" (or one that can be coerced to that class): a symbolic description of the model to be fitted. See `bayesglm` 'formula' for details.
- `data`: A data frame containing the incomplete data and the matrix of the complete predictors.
- `start`: Starting value for `bayesglm`.
- `n.iter`: Maximum number of iteration for `bayesglm`. The default is 100.
- `missing.index`: The index of missing units of the outcome variable
- `...`: Currently not used.

**Details**
In `bayesglm` default the prior distribution is Cauchy with center 0 and scale 2.5 for all coefficients (except for the intercept, which has a prior scale of 10). See also `glm` for other details.

**Value**
- `model`: A summary of the bayesian fitted model.
- `expected`: The expected values estimated by the model.
- `random`: Vector of length n.mis of random predicted values predicted by using the binomial distribution.

**Note**
see also [http://www.stat.columbia.edu/~gelman/standardize/](http://www.stat.columbia.edu/~gelman/standardize/)
**mi.polr**

**Author(s)**
Masanao Yajima <yajima@stat.columbia.edu>, M.Grazia Pittau <grazia@stat.columbia.edu>, Andrew Gelman <gelman@stat.columbia.edu>

**References**

**See Also**
mi.info, mi.method, mi

---

**mi.polr**

Elementary function: multinomial log-linear models to impute an ordered categorical variable.

**Description**
Imputes missing data in a categorical variable using multinomial Log-linear Models.

**Usage**
```r
mi.polr(formula, data = NULL, drop.unused.levels = TRUE, start = NULL, n.iter = 100, missing.index = NULL, ...)
## S4 method for signature 'mi.polr'
residuals(object, y)
## S4 method for signature 'mi.polr,ANY'
plot( x, y, main=deparse( substitute( y ) ), gray.scale = FALSE, ... )
```

**Arguments**
- `formula`: a formula expression as for regression models, of the form `response ~ predictors`. The response should be a factor (preferably an ordered factor), which will be interpreted as an ordinal response, with levels ordered as in the factor. The model must have an intercept: attempts to remove one will lead to a warning and be ignored. An offset may be used. See the documentation of `formula` for other details.
- `data`: A data frame containing the incomplete data and the matrix of the complete predictors.
- `drop.unused.levels`: Drops unused levels.
- `start`: Starting value for bayespolr.
n.iter Maximum number of iteration for bayespolr. The default is 100.
missing.index The index of missing units of the outcome variable.
... Currently not used.
object mi.polr object.
x mi.polr object.
y Observed values.
main main title of the plot.
gray.scale When set to TRUE, makes the plot into gray scale with predefined color and line type.

Details

multinom calls the library \texttt{nnet}. See multinom for other details.

Value

model A summary of the multinomial fitted model
expected The expected values estimated by the model
random Vector of length n.mis of random predicted values predicted by using the multinomial distribution
residual The residual vector of length same as y

Author(s)

Masanao Yajima <yajima@stat.columbia.edu>, Yu-Sung Su <ys463@stat.columbia.edu>, M.Grazia Pittau <grazia@stat.columbia.edu>, Andrew Gelman <gelman@stat.columbia.edu>

References


See Also

\texttt{mi.info}, \texttt{mi.method}, \texttt{mi}

Examples

```r
# true data
x<-rnorm(100,0,1) # N(0,1)
y<(1+2*x)+rnorm(100,0,1)
y<-round(y)
y[y<0]<-0
# create artificial missingness on y
y[seq(1,100,10)]<-NA
```
mi.pooled

Modeling Functions for Multiply Imputed Dataset

Description

Modeling Function that pulls together the estimates from multiply imputed dataset.

Usage

```
mi.pooled(coef, se)
```

```
lm.mi(formula, mi.object, ...)
```

```
glm.mi(formula, mi.object, family = gaussian, ...)
bayesglm.mi(formula, mi.object, family = gaussian, ...)
polr.mi(formula, mi.object, ...)
bayespolr.mi(formula, mi.object, ...)
lmer.mi(formula, mi.object, rescale=FALSE, ...)
glmer.mi(formula, mi.object, family = gaussian, rescale=FALSE, ...)
```

```r
## S3 method for class 'mi.pooled'
print(x, ...)
## S4 method for signature 'mi.pooled'
coef(object)
## S4 method for signature 'mi.pooled'
se(coef)
## S4 method for signature 'mi.pooled'
display(object, digits=2)
```

Arguments

- `coef`: list of coefficients
- `se`: list of standard errors
- `formula`: See `lm, glm, polr, lmer` for detail.
- `mi.object`: mi object
- `family`: See `glm, polr, lmer` for detail.
- `rescale`: default is FALSE, see `rescale` for detail.
- `x`: mi.pooled object.
- `object`: mi.pooled object.
- `digits`: number of significant digits to display, default=2.

... Any option to pass on to `lm, glm, bayesglm, bayespolr, polr, and lmer` functions
Value

call  the matched call.
mi.pooled  pulled estimates from the multiple dataset.
mi.fit  estimates from each dataset.

Author(s)

Yu-Sung Su <suyusung@tsinghua.edu.cn>,

References


See Also

lm, glm, bayesglm, bayespolr, polr, and lmer

Examples

# true data
n <- 100
x <- rbinom(n, 1, .45)
z <- ordered(rep(seq(1, 5), n)[sample(1:n, n)])
y <- rnorm(n)
group <- rep(1:10, 10)

# create artificial missingness
dat.xy <- data.frame(x, y, z)
dat.xy <- mi:::create.missing(dat.xy, pct.mis=10)

# imputation
IMP <- mi(dat.xy, n.iter=6, add.noise=FALSE)

# fit models
M1 <- lm.mi(y ~ x + z, IMP)
display(M1)
coef(M1)
se.coef(M1)

M2 <- glm.mi(x ~ y, IMP, family = binomial(link="logit"))
display(M2)
coef(M2)
se.coef(M2)

M3 <- bayesglm.mi(x ~ y, IMP, family = binomial(link="logit"))
display(M3)
coef(M3)
se.coef(M3)

M4 <- polr.mi(ordered(z) ~ y, IMP)
mi.preprocess

Preprocessing and Postprocessing mi data object

Description
Function for preprocessing and postprocessing nonnegative, and positive-continuous variable types in mi data object

Usage
mi.preprocess(data, info)
mi.postprocess(mi.data, info)

Arguments
data the data.frame to be imputed.
info the information matrix, see mi.info.
mi.data the imputed data list, obtained from mi.completed

Details
mi.proprocess will transform the nonnegative and positive-continuous variable types. If the variable is of nonnegative type, the function transforms the variable into two variables: an indicator indicates whether the value is positive or not and a transformed variable that takes on all positive value and is transformed either by taking a log; 0 and NA will be treated as missing for such a variable. If the variable is of positive-continuous type, it will be transformed by taking a log.

mi.postprocess will transform the imputed dataset back to its original form. The imputed dataset is obtained from mi.completed function.
Value

data  a data.frame or a list of dataframe
mi.info  a mi.info matrix

Author(s)

Yu-Sung Su <suyusung@tsinghua.edu.cn>, Andrew Gelman <gelman@stat.columbia.edu>

References


See Also

*mi.completed*

**mi.scatterplot**  
Multiple Imputation Scatterplot

Description

A function for plotting observed and imputed values for a variable.

Usage

```r
mi.scatterplot(Yobs, Yimp, X = NULL, xlab = NULL, ylab = NULL,
    main = "Imputed Variable Scatter Plot",
    display.zero = TRUE, gray.scale = FALSE,
    obs.col = rgb(0, 0, 1),
    imp.col = rgb(1, 0, 0),
    obs.pch = 20, imp.pch = 20,
    obs.cex = 0.3, imp.cex = 0.3,
    obs.lty = 1, imp.lty = 1,
    obs.lwd = 2.5, imp.lwd = 2.5, ...
)
```

marginal.scatterplot ( data, object, use.imputed.X = FALSE, ...
)

Arguments

Yobs  observed values.
Yimp  imputed values.
X  variable to plot on the x axis.
xlab  label on the x axis.
ylab  label on the y axis.
display.zero  if set to FALSE zeros will not be displayed. Default is TRUE.
mi.scatterplot

main

main title of the plot.

gray.scale

When set to TRUE, makes the plot into gray scale with predefined color and line type.

obs.col

color for the observed variable. Default is "blue".

imp.col

color for the imputed variable. Default is "red".

obs.pch

data symbol for observed variable. Default is 20.

imp.pch

data symbol for imputed variable. Default is 20.

obs.cex

text size for observed variable. Default is 0.3.

imp.cex

text size for imputed variable. Default is 0.3.

obs.lty

line type for observed variable. Default is 1.

imp.lty

line type for imputed variable. Default is 1.

obs.lwd

line width for observed variable. Default is 2.5.

imp.lwd

line width for imputed variable. Default is 2.5.

...  

Other options for 'plot' function.

data

missing data.

object

mi object.

use.imputed.X

If you want to use the imputed X. Default is FALSE.

Details

Since several data points can have the same data values, especially in discrete variables, small random number is added to each value so that points do not fall on top of each other. See help on jitter for more details. Lowess line is fitted to both imputed and observed data.

Value

A scatterplot with the observed and the imputed values plotted against a chosen variable.

Note

By default imputed values are in red, while the observed values are in blue.

Author(s)

Masanao Yajima <yajima@stat.columbia.edu>, M.Grazia Pittau <grazia@stat.columbia.edu>, Andrew Gelman <gelman@stat.columbia.edu>

References


See Also

mi.plot

Examples

```r
# true data
x <- rnorm(100, 0, 1) # N(0,1)
y <- rnorm(100, (1+2*x), 1.2) # y = 1 + 2*x + N(0,1.2)
# create artificial missingness on y
y[seq(1, 100, 10)] <- NA
dat.xy <- data.frame(x, y)
# imputation
imp.cont <- mi.continuous(y ~ x, data = dat.xy)
mi.scatterplot(y, imputed(imp.cont))
```

Description

Function to plot a missing pattern plot.

Usage

```r
missing.pattern.plot(data, y.order = FALSE, x.order = FALSE, clustered = TRUE,
xlab = "Index", ylab = "Variable",
main = NULL, gray.scale = FALSE,
obs.col = "blue", mis.col = "red", ... )
```

Arguments

data
data.frame or matrix of data with missing data coded as "NA".
y.order
if TRUE, orders the variable by number of missing value. Default is FALSE.
x.order
if TRUE, orders the data by number of missing value. Default is FALSE.
clustered
if TRUE, data are grouped together with similair missingness patterns.
xlab
a title for the x axis: see 'title'.
ylab
a title for the y axis: see 'title'.
main
an overall title for the plot: see 'title'.
gray.scale
if TRUE, makes the plot into black and white. This option overwrites the color specification.
ob.col
color used for observed values. Default is "blue".
mis.col
color used for missing values. Default is "red".
...
additional parameters passed to 'image' function.
Details

Color image with different color for missing and observed value in the dataset is plotted. By default the observed is in "blue" and missing is in "red".

Value

Plot to visualize pattern of missingness in the data.

Author(s)

Masanao Yajima <yajima@stat.columbia.edu>, M.Grazia Pittau <grazia@stat.columbia.edu>, Andrew Gelman <gelman@stat.columbia.edu>

References


See Also

mi.plot

Examples

data(CHAIN)
missing.pattern.plot(CHAIN)

Description

Auxiliary function as user interface for adding noise for mi procedure. Typically only used when calling mi.

Usage

noise.control(method=c("reshuffling", "fading"), pct.aug=10, K=1, post.run.iter=20)
Arguments

method two methods are implemented: reshuffling and fading.
pct.aug percent of N being add into the existing data, where N is the number of observations of the completed data set, default is 10.
K the cooling parameter, default is 1.
post.run.iter number of iterations after a imputation, default is 20. This is to mitigate the influence of a imputation with the noise.

Details

If reshuffling method is used, the imputation will randomly switch between randomly imputing data from marginal (imputing data from the observed values) and drawing from the modeled based values. And with each iteration (s), the probability of cooling (q) decreases by number of iterations, such that $q = K/s$.

If fading method is used, the imputation will augment

Author(s)

Yu-Sung Su <yusung@stat.columbia.edu>

References


See Also

mi

Examples

```r
### NOT RUN
# add fadding empirical noise by augmenting 10% of the data
data(CHAIN)
IMP <- mi(CHAIN, add.noise=noise.control(method="fading", pct.aug=10, post.run.iter=20))
# add noise by randomly drawing from the marginal
# This is the default setting
IMP <- mi(CHAIN, add.noise=noise.control(method="reshuffling", K=1, post.run.iter=20))
# add no noise
IMP <- mi(CHAIN, add.noise=FALSE)
# add noise but no post.run
IMP <- mi(CHAIN, add.noise=noise.control(post.run.iter=0))
```
plot.mi

Diagnostic Plots for multiple imputation object

Description

Diagnostic plots for testing the fit of the imputation method to the observed data.

Usage

```r
## S4 method for signature 'mi,ANY'
plot(x, y, ...)

plot.mi(x, y, m = 1, vr = NULL, vr.name = "Variable Score",
        gray.scale = FALSE, mfrow=c(1, 3), ...)
```

Arguments

- `x` mi object generated by the mi function.
- `y` currently not used.
- `...` Arguments for other methods, not used.
- `m` The m-th imputation. By default is 1.
- `vr` A chosen variable for the scatter plot.
- `vr.name` A name of the vr variable.
- `gray.scale` When set to TRUE, makes the plot into gray scale with predefined color and line type.
- `mfrow` See “par” for details.

Details

For each variable, observed values are in blue, the imputed values are in red. In the scatterplot the observed and the imputed are plotted versus a variable the users can choose. By default the values are plotted against an index number but it strongly recommended to use a variable containing more information. Fitted lowess lines are also plotted for both observed and imputed data. A small amount of random noise (jittering) is added to the points so that they do not fall on top of each other.

Value

Histograms, scatterplots, and residual plots of the fit of the imputation models. Binned residual plots are for each binary variable.

Author(s)

Masanao Yajima <yajima@stat.columbia.edu>, Yu-Sung Su <suyusung@tsinghua.edu.cn>, M.Grazia Pittau <grazia@stat.columbia.edu>, Andrew Gelman <gelman@stat.columbia.edu>
random.imp

References


See Also

`mi, mi.scatterplot, mi.hist`

Examples

```r
### NOT RUN
#--------------------------------------------------------------
# data(CHAIN)
# imp.CHAIN <- mi(CHAIN, n.iter=6, add.noise=FALSE)
# plot(imp.CHAIN)
#--------------------------------------------------------------
```

---

random.imp | Random Imputation of Missing Data

Description

Simple random imputation of missing values in given data set.

Usage

```r
random.imp(data, imp.method = c( "bootstrap", "pca" ), ...)
```

Arguments

- **data**: A vector, matrix, or data frame with missing data.
- **imp.method**: Character to specify which method of random imputation to use. Default is "bootstrap". Note: pca is not implemented in the current version.
- **...**: Unused

Details

Impute missing values based on the observed data for the variable.

Value

Data with its missing values imputed using the specified method.
type.models

Author(s)
Masanao Yajima <yajima@stat.columbia.edu>, M.Grazia Pittau <grazia@stat.columbia.edu>, Andrew Gelman <gelman@stat.columbia.edu>

References

See Also
mi

Examples

data(CHAIN)
data.imp <- random.imp(CHAIN)

type.models               Functions to identify types of the models of the mi object

Description
The function to select the model based on the variable type

Usage

type.models(type)
mi.types()

Arguments
type                  Nine types: continuous, log-continuous, count, ordered-categorical, unordered-categorical, binary, positive-continuous, proportion, predictive-mean-matching, nonnegative, fixed

Author(s)
Yu-Sung Su <suyusung@tsinghua.edu.cn>, Masanao Yajima <yajima@stat.columbia.edu>, Andrew Gelman <gelman@stat.columbia.edu>

References
typecast

See Also
mi.info

Description
Function for determining the variable type.

Usage

```r
  typecast(object)
```

Arguments

- `object` Vector, matrix, or data frame of data to determine the type of.

Details
The variable type of a vector, or vector of variable types for each variable in the dataset.

Value

- `fixed` variables that contain only one value.
- `binary` variables that contain two values.
- `ordered-categorical` variables that contain 3 to 5 positive values.
- `unordered-categorical` variables that contain characters or more than 5 positive levels.
- `positive-continuous` variables that contain more than 5 positive values, NOT including 0s.
- `nonnegative` variables that contain more than 5 positive values, including 0s.
- `continuous` variables that are not belong to any of the above types.
- `log-continuous` log-scaled continuous variable
write.mi

Author(s)

Yu-Sung Su <suyusung@tsinghua.edu.cn>, Masanao Yajima <yajima@stat.columbia.edu>, M.Grazia Pittau <grazia@stat.columbia.edu>

References


See Also

mi

Examples

data(CHAIN)
class(CHAIN)

typecast(CHAIN[,1]) # for vector

typecast(as.matrix(CHAIN))# for matrix

typecast(CHAIN) # for data.frame

write.mi

Writes mi impuations to file

Description

Writes the imputed datasets to file for the mi object into the csv, dta, and table format.

Usage

write.mi(object, format = c("csv", "dta", "table"), ...)

Arguments

object mi object
format output format, only "csv", "dta" and "table" format are supported.
... further arguments for write functions
Details

`write.mi` write each imputed dataset to a file in one of the three formats: `csv`, `dta` and `table`, using `write.csv`, `write.dta` and `write.table` respectively.

The output files should be

```
midata1.csv
midata2.csv
omidata3.csv
...
```

Author(s)

Yu-Sung Su <suyusung@tsinghua.edu.cn>,

References


See Also

`write.csv`, `write.table`, `write.dta`

Examples

```
# data(CHAIN)
# IMP <- mi(CHAIN)
# write.mi(IMP)
```
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