

Package ‘HeckmanEM’

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Type Package

Title Fit Normal or Student-t Heckman Selection Models

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Description Maximum likelihood estimation by an EM algorithm of Heckman-type sample selection Normal or Student-t models. The reference is Lachos, Prates and Dey (2020) <doi:10.1016/j.jmva.2021.104737>.

Imports mvtnorm (>= 1.1-0), sampleSelection (>= 1.2-6), MomTrunc (>= 5.79), PerformanceAnalytics (>= 2.0.4)

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 HeckmanEM

Fit the Normal or Student-t Heckman Selectio model.

Description

'HeckmanEM()' fit the Heckman selection model.

Usage

```
HeckmanEM(
  y,
  x,
  w,
  cc,
  nu = 4,
  family = "T",
  error = 1e-05,
  iter.max = 500,
  im = TRUE,
  criteria = TRUE
)
```

Arguments

y	A response vector.
x	A covariate matrix for the response y.
w	A covariate matrix for the missing indicator cc.
cc	A missing incidator vector (1=observed, 0=missing) .
nu	The initial value for the degrees of freedom.
family	The family to be used (Normal or T).
error	The absolute convergence error for the EM stopping rule.
iter.max	The maximum number of iterations for the EM algorithm.
im	TRUE/FALSE, boolean to decide if the standard errors of the parameters should be computed.
criteria	TRUE/FALSE, boolean to decide if the model selection criteria should be computed.

Value

An object of the class HeckmanEM with all the outputs provided from the function.

Examples

```
n <- 100
family <- "T"
nu <- 4
rho <- .6
cens <- .25

set.seed(20200527)
w <- cbind(1,runif(n,-1,1),rnorm(n))
x <- cbind(w[,1:2])
c <- qt(cens, df=nu)

sigma2 <- 1

beta <- c(1,0.5)
gamma <- c(1,0.3,-.5)
gamma[1] <- -c*sqrt(sigma2)

set.seed(1)
datas <- rHeckman(x,w,beta,gamma,sigma2,rho,nu,family=family)
y <- datas$y
cc <- datas$cc

# Normal EM
res.N <- HeckmanEM(y, x, w, cc, nu = 4, family="Normal", error = 1e-05, iter.max = 50,
  im=TRUE, criteria = TRUE)

# Student-t: EM
res.T <- HeckmanEM(y, x, w, cc, nu = 4, family="T", error = 1e-05, iter.max = 50,
  im=TRUE, criteria = TRUE)
```

HeckmanEM.criteria *Model selection criteria for the Heckman Selectio model*

Description

'HeckmanEM.criteria()' calculate the AIC, AICc, BIC selection criteria for the fitted Heckman selection model.

Usage

```
HeckmanEM.criteria(obj)
```

Arguments

obj An object of the class HeckmanEM.

Value

The calculated AIC, AICc, and BIC for the parameters of the fitted model.

Examples

```
## Not run:
res <- HeckmanEM(y, x, w, cc, nu = 4, family = "Normal", error = 1e-05, iter.max = 500,
                im = TRUE, criteria = FALSE)
cr <- HeckmanEM.criteria(res)

## End(Not run)
```

HeckmanEM.envelope *Envelope for the Heckman Selectio model.*

Description

'HeckmanEM.envelope()' plot the envelope for the fitted Heckman selection model.

Usage

```
HeckmanEM.envelope(obj, envelope = 0.95, ...)
```

Arguments

obj	An object of the class HeckmanEM.
envelope	The envelope corverage percertange.
...	Other option for chart.QQPlot from PerformanceAnalytics package.

Value

A residual plot of the fitted data and its envelope.

Examples

```
## Not run:
res <- HeckmanEM(y, x, w, cc, nu = 4, family = "Normal", error = 1e-05, iter.max = 500,
                im = TRUE, criteria = TRUE)
HeckmanEM.envelope(res, ylab="Normalized Quantile Residuals", xlab="Standard normal quantile",
                  line="quartile", col=c(20,1), pch=19, ylim = c(-5,4))

## End(Not run)
```

HeckmanEM.infomat	<i>Standard error estimation for the Heckman Selectio model by the Information Matrix.</i>
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Description

'HeckmanEM.infomat()' estimate the standard errors for the parameters for the fitted Heckman selection model.

Usage

```
HeckmanEM.infomat(obj)
```

Arguments

obj An object of the class HeckmanEM.

Value

The estimated standard errors for the parameters of the fitted model.

Examples

```
## Not run:
res <- HeckmanEM(y, x, w, cc, nu = 4, family = "Normal", error = 1e-05, iter.max = 500,
                im = FALSE, criteria = TRUE)
im <- HeckmanEM.infomat(res)

## End(Not run)
```

rHeckman	<i>Generate data from the Heckman Selectio model (Normal or Student-t).</i>
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Description

'rHeckman()' generate a random sample from the Heckman selection model (Normal or Student-t).

Usage

```
rHeckman(x, w, beta, gamma, sigma2, rho, nu = 4, family = "T")
```

Arguments

x	A covariate matrix for the response y.
w	A covariate matrix for the missing indicator cc.
beta	Values for the beta vector.
gamma	Values for the gamma vector.
sigma2	Value for the variance.
rho	Value for the dependence between the response and missing value.
nu	Value for the degrees of freedom.
family	The family to be used (Normal or T).

Value

Return an object with the response (y) and missing values (cc).

Examples

```
## Not run:
cens <- 0.25
nu <- 4
set.seed(20200527)
w <- cbind(1,runif(n,-1,1),rnorm(n))
x <- cbind(w[,1:2])

family <- "T"
c <- qt(cens, df=nu)

sigma2 <- 1
beta <- c(1,0.5)
gamma <- c(1,0.3,-.5)
gamma[1] <- -c*sqrt(sigma2)
set.seed(iter)
data <- rHeckman(x,w,beta,gamma,sigma2,rho,nu,family=family)

## End(Not run)
```

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