Package ‘CensMixReg’

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Type Package

Title Censored Linear Mixture Regression Models

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Author Luis Benites Sanchez[cre, aut], Victor Hugo Lachos[cre, aut], Edgar J. Lopez Moreno[ctb]

Maintainer Luis Benites Sanchez <lbenitesanchez@gmail.com>

Imports mixsmsn, mnormt, mvtnorm, ClusterR, trimcluster

Description Fit censored linear regression models where the random errors follow a finite mixture of Scale Mixture Normal distributions.
Fit censored linear models of finite mixture multivariate Student-t and Normal distributions.
Fit censored mixture regression models based on scale mixture of normal distributions.

License GPL (>= 2)

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Description
This package contains a principal function that performs to estimate the parameters of a regression model considering an error that follows a finite mixture of Scale mixture of normal distributions, using an analytically simple and efficient EM-type algorithm for iteratively computing maximum likelihood estimates of the parameters. Also contains a function for estimate the parameters of a censored linear models of finite mixture multivariate Student-t and Normal distributions.

Details

Package: CensMixReg
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Author(s)
Luis Benites Sanchez <lbenitesanchez@gmail.com>, Victor Hugo Lachos <hlachos@ime.unicamp.br> and Edgar J. Lopez Moreno <edgar.javier.lopez.moreno@gmail.com>
Maintainer: Luis Benites Sanchez <lbenitesanchez@gmail.com>

References
**CensMmix**

**See Also**

*fm.smn.cr*

**Examples**

#See examples for the CensMixReg function linked above.

<table>
<thead>
<tr>
<th>CensMmix</th>
<th>Censored multivariate finite mixture model</th>
</tr>
</thead>
</table>

**Description**

Performs a Finite Mixture Censored multivariate (FM-MC) Student-t and Normal distribution using an EM-type algorithm for iteratively computing maximum likelihood estimates of the parameters.

**Usage**

CensMmix(cc, y, nu=3, mu=NULL, Sigma = NULL, pii = NULL, g = NULL, get.init = TRUE, criteria = TRUE, group = FALSE, family = "normal", error = 0.0001, iter.max = 300, uni.Sigma = FALSE, obs.prob= FALSE, kmeans.param = NULL)

**Arguments**

- **cc** Vector of censoring indicators. For each observation: 0 if non-censored, 1 if censored.
- **y** Vector of responses in case of right censoring.
- **nu** Initial value for the EM algorithm, nu it’s degrees of freedom. Value of one size 1 (If Student’s t)
- **mu** Initial value for the EM algorithm. Each of them must be a vector of length g.(the algorithm considers the number of components to be fitted based on the size of these vectors)
- **Sigma** a list of g arguments of matrices of initial values (dimension pxp) for the scale parameters
- **pii** Initial value for the EM algorithm. The vector of initial values (dimension g) for the weights for each cluster. Must sum one!
- **g** Numbers of components
- **get.init** TRUE or FALSE. It indicates if the program (TRUE) is get the initial values or if the user (FALSE) entered manually the initial values.
- **criteria** It indicates if are calculated the criterion selection methods (AIC, BIC, EDC and ICL)
- **group** TRUE or FALSE.
family  "t": fits a t-student regression mixture for censored data or "Normal": fits a Normal regression mixture censored data

error  define the stopping criterion of the algorithm

iter.max  the maximum number of iterations of the EM algorithm

uni.Sigma  TRUE: if the covariance matrix are equals or FALSE if are not equal

obs.prob  TRUE or FALSE.

kmeans.param  Parameters for the k-means clustering algorithm

Author(s)

Luis Benites Sanchez <lbentesanchez@gmail.com>, Victor Hugo Lachos <hlachos@ime.unicamp.br>, Edgar J. Lopez Moreno <edgar.javier.lopez.moreno@gmail.com>

References


See Also

CensMmix,concentration

Examples

#See examples for the CensMmix function linked above.
The dataset corresponds to concentration levels of certain dissolved trace metals in freshwater streams across the Commonwealth of Virginia. This dataset consist of the concentration levels of the dissolved trace metals copper (Cu), lead (Pb), zinc (Zn), calcium (Ca) and magnesium (Mg) from 184 independent randomly selected sites in freshwater streams across Virginia. The Cu, Pb, and Zn concentrations are reported in ug/L of water, whereas Ca and Mg concentration are suitably reported in mg/L of water. Since the measurements are taken at different times, the presence of multiple limit of detection values are possible for each trace metal (VDEQ (2003)). The limit of detection but Cu and Pb is the 0.1ug/L, 1.0mg/L for Zn while Ca and Mg has limit of 0.5mg/L and 1.0mg/L. The percentage of left-censored values of 2.7% for (Ca), 4.9% for (Cu), 9.8% for (Mg) are small in comparison to 78.3% for (Pb) and 38.6% for (Zn), also note that 17.9% of the streams had 0 nondetected trace metals, 39.1% had 1, 37.0% had 2, 3.8% had 3, 1.1% had 4 and 1.1% had 5.

Usage

data(concentration)

Format

concentration is a data frame with 184 cases (rows) with 5 variables (columns).

Details

For a complete description of data concentration levels see VDEQ (2003).

Source


Examples

## Not run:
data(concentration)
p <- 5
y <- as.matrix(concentration[,1:p])
c <- as.matrix(concentration[(p+1):(2*p)])

fitN <- CensMmix(c, y, nu=3, mu=NULL, Sigma = NULL, pii = NULL, g = 2,
Description

Performs a Finite Mixture Censored (FM-CR) using using EM-type algorithm for iteratively computing maximum likelihood estimates of the parameters.

Usage

```
fm.smn.cr(cc, y, x1, Abetas = NULL, medj = NULL, sigma2 = NULL, pii = NULL, nu=NULL, g = NULL, family = "Normal", error = 0.00001, iter.max = 100, aitken = TRUE)
```

Arguments

- `cc`: Vector of censoring indicators. For each observation: 0 if non-censored, 1 if censored.
- `y`: Vector of responses in case of right censoring.
- `x1`: Matrix or vector of covariates.
- `Abetas`: Parameters of vector regression dimension \((p + 1)\) include intercept
- `medj`: Initial value for the EM algorithm. Each of them must be a vector of length \(g\). (the algorithm considers the number of components to be fitted based on the size of these vectors)
- `sigma2`: Initial value for the EM algorithm. Each of them must be a vector of length \(g\). (the algorithm considers the number of components to be adjusted based on the size of these vectors)
- `pii`: Initial value for the EM algorithm. Each of them must be a vector of length \(g\). (the algorithm considers the number of components to be adjusted based on the size of these vectors)
- `nu`: Initial value for the EM algorithm, nu it’s degrees of freedom. Value of one size 1 (If Student’s t)
- `g`: Numbers of components
- `family`: "T": fits a t-student regression mixture for censored data or "Normal": fits a Normal regression mixture censored data or "Slash": fits a Slash regression mixture censored data
- `error`: define the stopping criterion of the algorithm
- `iter.max`: the maximum number of iterations of the EM algorithm
- `aitken`: Aitken acceleration: TRUE or FALSE.
Author(s)
Luis Benites Sanchez <lbenitesanchez@gmail.com>, Victor Hugo Lachos <hlachos@ime.unicamp.br>, Edgar J. Lopez Moreno <edgar.javier.lopez.moreno@gmail.com>

References


See Also

fm.smn.cr,wage.rates

Examples

#See examples for the CensMixReg function linked above.
Censored mixture regression models based in the Scale Mixture of Normal (SMN) distribution

Description

Performs a Finite Mixture Regression (FMR) with censored based in the SMN using EM-type algorithm for iteratively computing maximum likelihood estimates of the parameters.

Usage

```r
fmr.smn.cr(cc, y, x, abetas = NULL, sigma2 = NULL, pii = NULL, nu=NULL, g = NULL, family = "Normal", error = 0.00001, iter.max = 100)
```

Arguments

- `cc`: Vector of censoring indicators. For each observation: 0 if non-censored, 1 if censored.
- `y`: Vector of responses in case of right censoring.
- `x`: Matrix or vector of covariates for each component
- `abetas`: Parameters of vector regression dimension \((p_j + 1)\) include or not intercept, \(j=1,...,G\)
- `sigma2`: Initial value for the EM algorithm. Each of them must be a vector of length \(g\). (the algorithm considers the number of components to be adjusted based on the size of these vectors)
- `pii`: Initial value for the EM algorithm. Each of them must be a vector of length \(g\). (the algorithm considers the number of components to be adjusted based on the size of these vectors)
- `nu`: Initial value for the EM algorithm, nu it’s degrees of freedom. Value of one size 1 (If Student’s t or Slash) or size 2 (if Contaminated Normal)
- `g`: Numbers of components
- `family`: “T”: fits a t-student regression mixture for censored data or "Normal": fits a Normal regression mixture censored data or "Slash": fits a Slash regression mixture censored data or "NormalC": fits a Contaminated Normal regression mixture censored data
- `error`: define the stopping criterion of the algorithm
- `iter.max`: the maximum number of iterations of the EM algorithm

Author(s)

Luis Benites Sanchez <lbenitesanchez@gmail.com>, Victor Hugo Lachos <hlachos@ime.unicamp.br>
References


See Also

fmr.smn.cr, wage.rates

Examples

# See examples for the fmr.smn.cr function linked above.

<table>
<thead>
<tr>
<th>imm.fm.smn.cr</th>
<th>Information matrix</th>
</tr>
</thead>
</table>

Description

Calculate the information matrix of returned analysis based on the model family choice (univariate case, p=1).

Usage

imm.fm.smn.cr(cc, y, x1, model)

Arguments

- `y`: Vector of responses in case of right censoring.
- `x1`: Matrix or vector of covariates.
- `cc`: Vector of censoring indicators. For each observation: 0 if non-censored, 1 if censored.
- `model`: a variable returned by fm.smn.cr

Value

Estimate the Information Matrix of the parameters.

Author(s)

Luis Benites Sanchez <lbenitesanchez@gmail.com>, Victor Hugo Lachos <hlachos@ime.unicamp.br>, Edgar J. Lopez Moreno <edgar.javier.lopez.moreno@gmail.com>

See Also

fm.smn.cr

Examples

## see \code{\link{wage.rates}}
initial.values.fm.smn.cr

*Initial values for the FMR-SMN-CR*

**Description**

Obtained the initial values for the parameter beta_j, sigma_j, p_j and nu the SMN distribution.

**Usage**

```r
initial.values.fm.smn.cr(cc, y, x, g=2, algorithm="k-medoids", family="T", lower=1, upper=20, space=0.1, plotLog = TRUE, searchNU=TRUE, printNU=TRUE, saveFigure = FALSE)
```

**Arguments**

- `cc` Vector of censoring indicators. For each observation: 0 if non-censored, 1 if censored.
- `y` Vector of responses in case of right censoring.
- `x` Matrix or vector of covariates for each component
- `g` Numbers of components
- `algorithm` It indicates the algorithm: "trim-kmeans", "MinMax_kmeans", "k-means" and "k-medoids"
- `family` "T", "Normal", "Slash" or "NormalC"
- `lower` lower value of the search of the nu or gamma parameter
- `upper` upper value of the search of the nu or gamma parameter
- `space` number: increment of the sequence
- `plotLog` TRUE or FALSE the figure of profile
- `searchNU` TRUE or FALSE the search the nu or gamma parameter
- `printNU` TRUE or FALSE the print the nu or gamma parameter
- `saveFigure` TRUE or FALSE save the figure of profile

**Examples**

#See examples for the wage.rates function linked above.
**Description**

Obtained the initial values for the parameter $\beta_j, \sigma_j, p_j$ and $\nu$ the SMN distribution.

**Usage**

```r
initial.values.fmr.smn.cr(cc, y, x, g=2, algorithm="k-medoids", family="T", lower=1, upper=20, space=0.1, plotLog = TRUE, searchNU=TRUE, printNU=TRUE, saveFigure = FALSE)
```

**Arguments**

- `cc`: Vector of censoring indicators. For each observation: 0 if non-censored, 1 if censored.
- `y`: Vector of responses in case of right censoring.
- `x`: Matrix or vector of covariates for each component
- `g`: Numbers of components
- `algorithm`: It indicates the algorithm: "trim-kmeans" , "MinMax_kmeans", "k-means" and "k-medoids"
- `family`: "T", "Normal", "Slash" or "NormalC"
- `lower`: lower value of the search of the $\nu$ or gamma parameter
- `upper`: upper value of the search of the $\nu$ or gamma parameter
- `space`: number: increment of the sequence
- `plotLog`: TRUE or FALSE the figure of profile
- `searchNU`: TRUE or FALSE the search the $\nu$ or gamma parameter
- `printNU`: TRUE or FALSE the print $\nu$ or gamma parameter
- `saveFigure`: TRUE or FALSE save the figure of profile

**Examples**

```
#See examples for the wage.rates function linked above.
```
Random multivariate Finite Mixture Censored generator

Description

Random generator of multivariate FM-SMSN distributions.

Usage

rmmixcr(n, pii, mu, Sigma, shape, nu, perccensu, family)

Arguments

n number of observations
pii a vector of weights for the mixture (dimension of the number g of clusters). Must sum to one!
mu a list of g lists with each list containing the necessary parameters of the selected family
Sigma a list of g arguments of matrices of initial values (dimension pxp) for the scale parameters.
shape a list of g arguments of vectors of initial values (dimension p) for the skewness parameters.
nu nu it's degrees of freedom.
perccensu Matrix of censoring indicators. For each observation: 0 if non-censored, 1 if censored.
family distribution family to be used in fitting ("t", "Skew.t", "Skew.slash", "Skew.normal", "Normal")

Author(s)

Luis Benites Sanchez <lbenitesanchez@gmail.com>, Victor Hugo Lachos <hlachos@ime.unicamp.br>, Edgar J. Lopez Moreno <edgar.javier.lopez.moreno@gmail.com>

See Also

smsn.mmix

Examples

mu <- Sigma <- shape <- family <- list()
mu[[1]] <- c(-3,-1)
mu[[2]] <- c(2,3)
Sigma[[1]] <- matrix(c(8,1,1,5.5), 2,2)
Sigma[[2]] <- matrix(c(2,1,1,2.5), 2,2)
family[[1]] <- "Skew.t"
family[[2]] <- "Skew.normal"
wage.rates

\begin{verbatim}
shape[[1]] <- c(4,5)
shape[[2]] <- c(1,1)
nu <- c(3.3)
pii <- c(0.65,0.35)
percCensu <- c(0.15,0.15)
data <- rmixcr(100, pii , mu , Sigma, shape, nu, percCensu, family)
\end{verbatim}

---

**wage.rates**

**Wage Rates of 753 Women**

---

**Description**

Wage rates of 753 married white women with left censoring.

**Usage**

```r
data(wage.rates)
```

**Format**

A data frame with 753 observed wage rates of married white women in 1975. Some wage rates are set equal to zero, this means that those wives did not work in 1975, therefore, these observations are considered left censored at zero.

- **inlf** = 1 if in labor force, 1975
- **hours** hours worked, 1975
- **kidslt6** # kids < 6 years
- **kidsge6** # kids 6-18
- **age** woman’s age in yrs
- **educ** years of schooling
- **wage** estimated wage from earns., hours
- **huseduc** husband’s years of schooling
- **faminc** family income, 1975
- **motheduc** mother’s years of schooling
- **fatheduc** father’s years of schooling
- **unem** unem. rate in county of resid.
- **city** = 1 if live in SMSA
- **exper** actual labor mkt exper
- **nwifeinc** (faminc - wage*hours)/1000
- **expersq** exper^2
Source


Examples

```r
# Load the data
data(wage.rates)

# Set the response y and covariate x
y <- wage.rates$wage
x1 <- cbind(1, wage.rates$age, wage.rates$educ, wage.rates$hours/1000)
c <- c(rep(0, 428), rep(1, 325))

# Fits a left mixture censored Student-t model to the data
initial <- initial.values.fm.smn.cr(cc, y, x1, g = 2, algorithm = "k-means", family = "T", lower = 1, upper = 20, space = 1, plotLog = TRUE, searchNu = TRUE, printNu = FALSE, saveFigure = FALSE)
fitT <- fm.smn.cr(cc, y, x1, Abetas = initial$Abetas, medj = initial$medj, sigma2 = initial$sigma2, pii = initial$pii, nu = initial$nu, g = 2, family = "T", error = 0.00001, iter.max = 500)

# Fits a left mixture censored Normal model to the data
fitN <- fm.smn.cr(cc, y, x1, Abetas = initial$Abetas, medj = initial$medj, sigma2 = initial$sigma2, pii = initial$pii, nu = initial$nu, g = 2, family = "Normal", error = 0.00001, iter.max = 500)
```
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