Package ‘CensMFM’

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Introduction

It implements finite mixture models for censored or/and missing data using several multivariate distributions. Point estimation and asymptotic inference (via empirical information matrix) are offered as well as censored data generation. Pairwise scatter and contour plots can be generated. Possible multivariate distributions are the well-known normal, Student-t and skew-normal distributions. This package is an complement of Lachos, V. H., Moreno, E. J. L., Chen, K. & Cabral, C. R. B. (2017) <doi:10.1016/j.jmva.2017.05.005> for the multivariate skew-normal case.

Details

The DESCRIPTION file:

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Version: 2.0
Date: 2020-01-11
Authors@R: c(person("Francisco H. C. ", "de Alencar", email = "hildemardealencar@gmail.com", role = c("aut", "cre")), ... = "larissa.amatos@gmail.com", role = "ctb"), person("Victor H.", "Lachos", email = "hlachos@gmail.com", role = "ctb"))
Imports: MomTrunc, mvtnorm, gridExtra, ggplot2, tlmvnmvt
Suggests: mixsmsn
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~ An overview of how to use the package, including the most important functions ~
**fit.FMMSNC**

**Author(s)**
NA
Maintainer: NA

**References**


**See Also**

`fit.FMMSNC`, `rMSN`, `rMMSN` and `rMMSN.contour`

---

**fit.FMMSNC**  
*Fitting Finite Mixture of Multivariate Distributions.*

**Description**

It adjusts a finite mixture of censored and/or missing multivariate distributions (FM-MC). These are the Skew-normal, normal and Student-t multivariate distributions. It uses a EM-type algorithm for iteratively computing maximum likelihood estimates of the parameters.

**Usage**

```r
fit.FMMSNC(cc, LI, LS, y, mu = NULL, Sigma = NULL, shape = NULL, pii = NULL, nu = NULL, g = NULL, get.init = TRUE, criteria = TRUE, family = "SN", error = 1e-05, iter.max = 350, uni.Gama = FALSE, kmeans.param = NULL, cal.im = FALSE)
```

**Arguments**

- `cc`  
  vector of censoring indicators. For each observation it takes 0 if non-censored, 1 if censored.

- `LI`  
  the matrix of lower limits of dimension nxp. See details section.

- `LS`  
  the matrix of upper limits of dimension nxp. See details section.

- `y`  
  the response matrix with dimension nxp.

- `mu`  
  a list with g entries, where each entry represents location parameter per group, being a vector of dimension p.
Sigma a list with $g$ entries, where each entry represents a scale parameter per group, a matrix with dimension $p \times p$.

shape a list with $g$ entries, where each entry represents a skewness parameter, being a vector of dimension $p$.

pii a vector of weights for the mixture (dimension of the number $g$ of clusters). Must sum to one!

nu the degrees of freedom for the Student-t distribution case, being a vector with dimension $g$.

g number of mixture components.

generate Logical, TRUE or FALSE. If (generate==TRUE) the function computes the initial values, otherwise (generate==FALSE) the user should enter the initial values manually.

criteria Logical, TRUE or FALSE. It indicates if likelihood-based criteria selection methods (AIC, BIC and EDC) are computed for comparison purposes.

family distribution family to be used. Available distributions are the Skew-normal ("SN"), normal ("Normal") or Student-t ("t") distribution.

error relative error for stopping criterion of the algorithm. See details.

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

uni.Gama Logical, TRUE or FALSE. If uni.Gama==TRUE, the scale matrices per group are considered to be equals.

kmeans.param a list with alternative parameters for the kmeans function when generating initial values. List by default is list(iter.max = 10, n.start = 1, algorithm = "Hartigan-Wong").

cal.im Logical, TRUE or FALSE. If cal.im==TRUE, the information matrix is calculated and the standard errors are reported.

Details

The information matrix is calculated with respect to the entries of the square root matrix of Sigma, this using the Empirical information matrix. Disclaimer: User must be careful since the inference is asymptotic, so it must be used for decent sample sizes. Stopping criterion is $\text{abs}((\loglik/\loglik-1))<\epsilon$.

Value

It returns a list that depending of the case, it returns one or more of the following objects:

mu a list with $g$ components, where each component is a vector with dimension $p$ containing the estimated values of the location parameter.

Sigma a list with $g$ components, where each component is a matrix with dimension $p \times p$ containing the estimated values of the scale matrix.

Gamma a list with $g$ components, where each component is a matrix with dimension $p \times p$ containing the estimated values of the Gamma scale matrix.

shape a list with $g$ components, where each component is a vector with dimension $p$ containing the estimated values of the skewness parameter.
nu a vector with one element containing the value of the degrees of freedom \( nu \) parameter.

\( \pii \) a vector with \( g \) elements containing the estimated values of the weights \( \pii \).

\( \text{Zij} \) a \( n \times p \) matrix containing the estimated weights values of the subjects for each group.

\( \text{yest} \) a \( n \times p \) matrix containing the estimated values of \( y \).

\( \text{MI} \) a list with the standard errors for all parameters.

logLik the log-likelihood value for the estimated parameters.

aic the AIC criterion value for the estimated parameters.

bic the BIC criterion value for the estimated parameters.

edc the EDC criterion value for the estimated parameters.

iter number of iterations until the EM algorithm converges.

group a \( n \times p \) matrix containing the classification for the subjects to each group.

time time in minutes until the EM algorithm converges.

Note

The \( \text{uni.Gama} \) parameter refers to the \( \Gamma \) matrix for the Skew-normal distribution, while for the normal and student-t distribution, this parameter refers to the \( \Sigma \) matrix.

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References


See Also

rMSN, rMMSN and rMMSN.contour
Examples

```r
mu <- Sigma <- shape <- list()
mu[[1]] <- c(-3,-4)
mu[[2]] <- c(2,2)
Sigma[[1]] <- matrix(c(3,1,1,4.5), 2,2)
Sigma[[2]] <- matrix(c(2,1,1,3.5), 2,2)
shape[[1]] <- c(-2,2)
shape[[2]] <- c(-3,4)
u <- c(0,0)
pici <- c(0.6,0.4)
percen <- c(0.1,0.2)
n <- 200
g <- 2
seed <- 654678

set.seed(seed)
test = rMMSN(n = n, pii = pii,mu = mu,Sigma = Sigma,shape = shape,
percen = percen, each = TRUE, family = "SN")
Zij <- test$G
c <- test$c
y <- test$y

## left censoring ##
LI <- cc
LS <- cc
LI[cc==1] <- -Inf
LS[cc==1] <- y[cc==1]

#full analysis may take a few seconds more...
test_fit.cc0 = fit.FMMSNC(cc, LI, LS, y, mu=mu,
Sigma = Sigma, shape=shape, pii = pii, g = 2, get.init = FALSE,
criteria = TRUE, family = "Normal", error = 0.0001,
iter.max = 200, uni.Gama = FALSE, cal.im = FALSE)

test_fit.cc = fit.FMMSNC(cc, LI, LS, y, mu=mu,
Sigma = Sigma, shape=shape, pii = pii, g = 2, get.init = FALSE,
criteria = TRUE, family = "SN", error = 0.00001,
iter.max = 350, uni.Gama = FALSE, cal.im = TRUE)

## missing data ##
pctmiss <- 0.2 # 20% of missing data in the whole data
missing <- matrix(runif(n*g), nrow = n) < pctmiss
y[missing] <- NA
c <- matrix(nrow = n, ncol = g)
c[!missing] <- 1
c[missing] <- 0
```
LI <- cc
LS <- cc
LI[cc==1]<- -Inf
LS[cc==1]<- +Inf

test_fit.mis = fit.FMMSNC(cc, LI, LS, y, mu=mu,
Sigma = Sigma, shape=shape, pii = pii, g = 2, get.init = FALSE,
criteria = TRUE, family = "SN", error = 0.00001,
iter.max = 350, uni.Gama = FALSE, cal.im = TRUE)

rMMSN

Random Generator of Finite Mixture of Multivariate Distributions.

Description

It generates random realizations following a multivariate finite mixture of Skew-normal (family == "SN") and normal (family == "Normal") distributions under censoring. Censoring level can be set as a percentage and it can be adjusted per group if desired.

Usage

rMMSN(n = NULL, mu = NULL, Sigma = NULL, shape = NULL, percent = NULL,
each = FALSE, pii = NULL, family = "SN")

Arguments

n number of observations
mu a list with g entries, where each entry represents location parameter per group, being a vector of dimension p.
Sigma a list with g entries, where each entry represents a scale parameter per group, a matrix with dimension pxp.
shape a list with g entries, where each entry represents a skewness parameter, being a vector of dimension p.
percent Percentage of censored data in each group or data as a whole (see next item).
each If each == TRUE, the data will be censored in each group, where percent must be a vector of dimension p. Besides, if each == FALSE (by default), the data will be censored in the whole set, then percent must be a vector of dimension 1.
pii a vector of weights for the mixture of dimension g, the number of clusters. It must sum to one!
family distribution family to be used for fitting. Options are "SN" for the Skew-normal and "Normal" for the Normal distribution respectively.
Value

It returns a list that depending of the case, it returns one or more of the following objects:

- **y**: a $n \times p$ matrix containing the generated random realizations.
- **G**: a vector of length $n$ containing the group classification per subject.
- **cutoff**: a vector containing the censoring cutoffs per group.

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References


See Also

fit.FMMSNC, rMSN and rMMSN.contour

Examples

```r
mu <- Sigma <- shape <- list()
mu[[1]] <- c(-3,-4)
mu[[2]] <- c(2,2)
shape[[1]] <- c(-2,2)
shape[[2]] <- c(-3,4)
Sigma[[1]] <- matrix(c(3,1,1,4.5), 2,2)
Sigma[[2]] <- matrix(c(2,1,1,3.5), 2,2)
pii <- c(0.6,0.4)
percent <- c(0.1,0.1)
family <- "SN"
n <- 100

set.seed(20)
rMMSN(n = n, pii = pii, mu = mu, Sigma = Sigma, shape = shape, percent = percent, each = TRUE, family = family)
```

Pairwise Scatter Plots and Histograms for Finite Mixture of Multivariate Distributions.

**Description**

It plots the scatter plots with density contours for different multivariate distributions. Possible options are the Skew-normal (family == "SN"), Normal (family == "Normal") and Student-t (family == "t") distribution. Different colors are used by groups. Histograms are shown in the diagonal.

**Usage**

```r
rMMSN.contour(model = NULL, y = NULL, mu = NULL, Sigma = NULL, shape = NULL, nu = NULL, pii = NULL, Zij = NULL, contour = FALSE, hist.Bin = 30, contour.Bin = 10, slice = 100, col.names = NULL, length.x = c(0.5, 0.5), length.y = c(0.5, 0.5), family = "SN")
```

**Arguments**

- `model` is an object resultant from the `codefit.FMMSNC` function.
- `y` the response matrix with dimension \( n \times p \).
- `mu` a list with \( g \) entries, where each entry represents location parameter per group, being a vector of dimension \( p \).
- `Sigma` a list with \( g \) entries, where each entry represents a scale parameter per group, a matrix with dimension \( p \times p \).
- `shape` a list with \( g \) entries, where each entry represents a skewness parameter, being a vector of dimension \( p \).
- `nu` the degrees of freedom for the Student-t distribution case, being a vector with dimension \( g \).
- `pii` a vector of weights for the mixture of dimension \( g \), the number of clusters. It must sum to one!
- `Zij` a matrix of dimension \( n \times p \) indicating the group for each observation.
- `contour` If `contour == TRUE` the density contour will be shown, if `contour == FALSE` the density contour must be not returned.
- `hist.Bin` number of bins in the histograms. Default is 30.
- `contour.Bin` creates evenly spaced contours in the range of the data. Default is 10.
- `slice` desired length of the sequence for the variables grid. This grid is build for the contours.
- `col.names` names passed to the data matrix \( y \) of dimension \( p \).
- `length.x` a vector of dimension 2 with the value to be subtracted and added from the minimum and maximum observation in the x-axis respectively. Default is \( c(0.5, 0.5) \).
length.y  a vector of dimension 2 with the value to be subtracted and added from the minimum and maximum observation in the y-axis respectively. Default is c(0.5, 0.5).

family  distribution family to be used. Available distributions are the Skew-normal ("SN"), normal ("Normal") or Student-t ("t") distribution.

Details
If the model object is used, the user still has the option to choose the family. If the model object is not used, the user must input all other parameters. User may use the rMMSN function to generate data.

Note
This functions works well for any length of \(g\) and \(p\), but contour densities are only shown for \(p = 2\).

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References

See Also
fit.FMMSNC, rMMSN and fit.FMMSNC

Examples
```r
mu <- Sigma <- shape <- list()
mu[[1]] <- c(-3,-4)
mu[[2]] <- c(2,2)
Sigma[[1]] <- matrix(c(3,1,1,4.5), 2,2)
Sigma[[2]] <- matrix(c(2,1,1,3.5), 2,2)
shape[[1]] <- c(-2,2)
shape[[2]] <- c(-3,4)
u <- 0
pii <- c(0.6,0.4)
```
percent <- c(0.1, 0.2)
n <- 100
seed <- 654678

set.seed(seed)
test = rMMSN(n = n, pii = pii, mu = mu, Sigma = Sigma, shape = shape, percent = percent, each = TRUE, family = "SN")

## SN ##
SN.contour = rMMSN.contour(model = NULL, y = test$y, Zij = test$G, mu = mu, Sigma = Sigma, shape = shape, pii = pii, family = "SN")

# Plotting contours may take some time...

## SN ##
SN.contour = rMMSN.contour(model = NULL, y = test$y, Zij = test$G, mu = mu, Sigma = Sigma, shape = shape, pii = pii, contour = TRUE, family = "SN")

## Normal ##
N.contour = rMMSN.contour(model = NULL, y = test$y, Zij = test$G, mu = mu, Sigma = Sigma, shape = shape, pii = pii, contour = TRUE, family = "Normal")

## t ##
t.contour = rMMSN.contour(model = NULL, y = test$y, Zij = test$G, mu = mu, Sigma = Sigma, shape = shape, pii = pii, nu = c(4, 3), contour = TRUE, family = "t")

---

rMSN  Generating from Multivariate Skew-normal and Normal Random Distributions.

Description

It generates random realizations from a multivariate Skew-normal and Normal distribution.

Usage

rMSN(n, mu, Sigma, shape)

Arguments

n  number of observations.

mu  a numeric vector of length \( p \) representing the location parameter.

Sigma  a numeric positive definite matrix with dimension \( pxp \) representing the scale parameter.
rMSN

shape a numeric vector of length \( p \) representing the skewness parameter for Skew-normal(SN) case. If \( \text{shape} == 0 \), the SN case reduces to a normal (symmetric) distribution.

Value

It returns a \( n \times p \) matrix containing the generated random realizations.

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References


See Also

fit.FMMSNC, rMMSN and rMMSN.contour

Examples

\[
\text{mu} <- c(-3,-4) \\
\text{Sigma} <- \text{matrix}(c(3,1,1,4.5), 2,2) \\
\text{shape} <- c(-3,2) \\
r\text{MSN}(10, \text{mu} = \text{mu}, \text{Sigma} = \text{Sigma}, \text{shape} = \text{shape})
\]
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