Package ‘LMest’

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**LMest-package**

**Overview of the Package LMest**

**Description**

The package LMest is a framework for specifying and fitting Latent (or Hidden) Markov (LM) models, which are tailored for the analysis of longitudinal continuous and categorical data. Covariates are also included in the model specification through suitable parameterizations.

**Details**

Different LM models are estimated through specific functions requiring a data frame in long format. The functions are the following:

- **lmest** Function to estimate LM models for categorical responses generating the following classes:
  - **LMbasic-class** for the basic LM model without covariates.
  - **LMmanifest-class** for the LM model with covariates in the measurement model.
  - **LMlatent-class** for the LM model with covariates in the latent model.

- **lmestCont** Function to estimate LM models for continuous outcomes generating the following classes:
  - **LMbasiccont-class** for the basic LM model for continuous responses without covariates.
  - **LMlatentcont-class** for the LM model for continuous responses with covariates in the latent model.

- **lmestMixed** Function to estimate Mixed LM models for categorical responses with discrete random effects in the latent model generating the following class:
  - **LMmixed-class** for the mixed LM model.

- **lmestMc** Function to estimate Markov Chain models for categorical responses generating the following classes:
  - **MCbasic-class** for the MC model without covariates.
  - **MCcov-class** for the MC model with covariates.

Maximum likelihood estimation of model parameters is performed through the Expectation-Maximization algorithm, which is implemented by relying on Fortran routines.

Model selection is provided by **lmest** and **lmestCont** functions. In addition, function **lmestSearch** allows us to deal with both model selection and multimodality of the likelihood function. Two main criteria are provided to select the number of latent states: the Akaike Information Criterion and the Bayesian Information Criterion.

Prediction of the latent states is performed by the function **lmestDecoding**: for local and global decoding (Viterbi algorithm) from the output of functions **lmest**, **lmestCont** and **lmestMixed**.

The package allows us to deal with missing responses, including drop-out and non-monotonic missingness, under the missing-at-random assumption.

Standard errors for the parameter estimates are obtained by exact computation of the information matrix or through reliable numerical approximations of this matrix.
The print method shows some convergence information, and the summary method shows the estimation results.

The package also provides some real and simulated data sets that are listed using the function `data(package = "LMest")`.

**Author(s)**

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**References**


**See Also**

`lmest`, `lmestCont`, `lmestMc`, `lmestMixed`, `LMMixed-class`, `LMbasic-class`, `LMbasiccont-class`, `LMlatent-class`, `LMlatentcont-class`, `LMmanifest-class`

---

**bootstrap**

**Parametric bootstrap**

**Description**

Function that performs bootstrap parametric resampling to compute standard errors for the parameter estimates.

**Usage**

```r
bootstrap(est, ...)  
## S3 method for class 'LMbasic'
bootstrap(est, n = 1000, B = 100, seed = NULL, ...)
## S3 method for class 'LMbasiccont'
bootstrap(est, n = 1000, B=100, seed = NULL, ...)
## S3 method for class 'LMlatent'
bootstrap(est, B = 100, seed = NULL, ...)
## S3 method for class 'LMlatentcont'
bootstrap(est, B = 100, seed = NULL, ...)
```
Arguments

- `est`: an object obtained from a call to `lmest` and `lmestCont`
- `n`: sample size
- `B`: number of bootstrap samples
- `seed`: an integer value with the random number generator state
- `...`: further arguments

Value

Average of bootstrap estimates and standard errors for the model parameters in `est` object.

Author(s)

Francesco Bartolucci, Silvia Pandolfi, Fulvia Pennoni, Alessio Farcomeni, Alessio Serafini

Examples

```r
## Not run:
data("data_SRHS_long")
SRHS <- data_SRHS_long[1:2400,]
SRHS$srh <- 5 - SRHS$srh

out1 <- lmest(responsesFormula = srhs ~ NULL,
              index = c("id", "t"),
              data = SRHS,
              k = 3,
              tol = 1e-8,
              start = 1,
              modBasic = 1,
              out_se = TRUE,
              seed = 123)

boot1 <- bootstrap(out1)

out2 <- lmest(responsesFormula = srhs ~ NULL,
              latentFormula = ~
                            I(gender - 1) +
                            I(0 + (race == 2) + (race == 3)) +
                            I(0 + (education == 4)) +
                            I(0 + (education == 5)) +
                            I(age - 50) + I((age-50)^2/100),
              index = c("id", "t"),
              data = SRHS,
              k = 2,
              paramLatent = "multilogit",
              start = 0)

boot2 <- bootstrap(out2)

require(mmm)
```
data(multiLongGaussian)

t <- rep(1:4, times = max(multiLongGaussian$ID))
multiLongGaussian <- data.frame(t = t, multiLongGaussian)

out3 <- lmestCont(responsesFormula = resp1 + resp2 ~ NULL,
                   index = c("ID", "t"),
                   data = multiLongGaussian,
                   k = 3,
                   modBasic=1,
                   tol=10^-5)

boot3 <- bootstrap(out3)

out4 <- lmestCont(responsesFormula = resp1 + resp2 ~ NULL,
                   latentFormula = ~ X + time,
                   index = c("ID", "t"),
                   data = multiLongGaussian,
                   k = 3,
                   output=TRUE)

boot4 <- bootstrap(out4)

## End(Not run)

---

**bootstrap_lm_basic**

*Parametric bootstrap for the basic LM model*

**Description**

Function that performs bootstrap parametric resampling to compute standard errors for the parameter estimates.

*The function is no longer maintained. Please look at bootstrap function.*

**Usage**

```r
bootstrap_lm_basic(piv, Pi, Psi, n, B = 100, start = 0, mod = 0, tol = 10^-6)
```

**Arguments**

- `piv`: initial probability vector
- `Pi`: probability transition matrices (k x k x TT)
- `Psi`: matrix of conditional response probabilities (mb x k x r)
- `n`: sample size
- `B`: number of bootstrap samples
- `start`: type of starting values (0 = deterministic, 1 = random)
- `mod`: model on the transition probabilities (0 for time-heter., 1 for time-homog., from 2 to (TT-1) partial homog. of that order)
- `tol`: tolerance level for convergence
Value

- mPsi: average of bootstrap estimates of the conditional response probabilities
- mpiv: average of bootstrap estimates of the initial probability vector
- mPi: average of bootstrap estimates of the transition probability matrices
- sePsi: standard errors for the conditional response probabilities
- sepiv: standard errors for the initial probability vector
- sePi: standard errors for the transition probability matrices

Author(s)

Francesco Bartolucci, Silvia Pandolfi, University of Perugia (IT), http://www.stat.unipg.it/bartolucci

Examples

```r
## Not run:
# Example of drug consumption data
# load data
data(data_drug)
data_drug <- as.matrix(data_drug)
S <- data_drug[,1:5]-1
yv <- data_drug[,6]
n <- sum(yv)
# fit of the Basic LM model
k <- 3
out1 <- est_lm_basic(S, yv, k, mod = 1, out_se = TRUE)
out2 <- bootstrap_lm_basic(out1$piv, out1$Pi, out1$Psi, n, mod = 1, B = 1000)
## End(Not run)
```

bootstrap_lm_basic_cont

---

**Parametric bootstrap for the basic LM model for continuous outcomes**

Description

Function that performs bootstrap parametric resampling to compute standard errors for the parameter estimates.

The function is no longer maintained. Please look at bootstrap function.

Usage

```r
bootstrap_lm_basic_cont(piv, Pi, Mu, Si, n, B = 100, start = 0, mod = 0, tol = 10^-6)
```
Arguments

- **piv**: initial probability vector
- **Pi**: probability transition matrices (k x k x TT)
- **Mu**: matrix of conditional means for the response variables (r x k)
- **Si**: var-cov matrix common to all states (r x r)
- **n**: sample size
- **B**: number of bootstrap samples
- **start**: type of starting values (0 = deterministic, 1 = random)
- **mod**: model on the transition probabilities (0 for time-heter., 1 for time-homog., from 2 to (TT-1) partial homog. of that order)
- **tol**: tolerance level for convergence

Value

- **mMu**: average of bootstrap estimates of the conditional means of the response variables
- **mSi**: average of bootstrap estimates of the var-cov matrix
- **mpiv**: average of bootstrap estimates of the initial probability vector
- **mPi**: average of bootstrap estimates of the transition probability matrices
- **seMu**: standard errors for the conditional means of the response variables
- **seSi**: standard errors for the var-cov matrix
- **sepiv**: standard errors for the initial probability vector
- **sePi**: standard errors for the transition probability matrices

Author(s)

Francesco Bartolucci, Silvia Pandolfi, University of Perugia (IT), http://www.stat.unipg.it/bartolucci

Examples

```r
## Not run:
# Example based on multivariate longitudinal continuous data

# load data
require(mmm)
data(multiLongGaussian)
res <- long2matrices(multiLongGaussian$ID, X = cbind(multiLongGaussian$X, multiLongGaussian$time),
                      Y = cbind(multiLongGaussian$resp1, multiLongGaussian$resp2))
Y <- res$YY
n <- dim(Y)[1]
# fit of the Basic LM model for continuous outcomes
k <- 3
out1 <- est_lm_basic_cont(Y, k, mod = 1)
out2 <- bootstrap_lm_basic_cont(out1$piv, out1$Pi, out1$Mu, out1$Si, n, mod = 1, B = 1000)

## End(Not run)
```
bootstrap_lm_cov_latent

Description

Function that performs bootstrap parametric resampling to compute standard errors for the parameter estimates.

The function is no longer maintained. Please look at bootstrap function.

Usage

`bootstrap_lm_cov_latent(X1, X2, param = "multilogit", Psi, Be, Ga, B = 100, fort = TRUE)`

Arguments

- `X1`: matrix of covariates affecting the initial probabilities (n x nc1)
- `X2`: array of covariates affecting the transition probabilities (n x TT-1 x nc2)
- `param`: type of parametrization for the transition probabilities ("multilogit" = standard multinomial logit for every row of the transition matrix, "difflogit" = multinomial logit based on the difference between two sets of parameters)
- `Psi`: array of conditional response probabilities (mb x k x r)
- `Be`: parameters affecting the logit for the initial probabilities
- `Ga`: parameters affecting the logit for the transition probabilities
- `B`: number of bootstrap samples
- `fort`: to use fortran routine when possible (FALSE for not use fortran)

Value

- `mPsi`: average of bootstrap estimates of the conditional response probabilities
- `mBe`: average of bootstrap estimates of the parameters affecting the logit for the initial probabilities
- `mGa`: average of bootstrap estimates of the parameters affecting the logit for the transition probabilities
- `sePsi`: standard errors for the conditional response probabilities
- `seBe`: standard errors for the parameters in Be
- `seGa`: standard errors for the parameters in Ga

Author(s)

Francesco Bartolucci, Silvia Pandolfi - University of Perugia (IT)
Examples

```r
## Not run:
# Example based on self-rated health status (SRHS) data
# load SRHS data
data(data_SRHS_long)
dataSRHS <- data_SRHS_long

TT <- 8
head(dataSRHS)
res <- long2matrices(dataSRHS$id, X = cbind(dataSRHS$gender-1,
dataSRHS$race == 2 | dataSRHS$race == 3, dataSRHS$education == 4,
dataSRHS$education == 5, dataSRHS$age-50, (dataSRHS$age-50)^2/100),
Y = dataSRHS$srhs)

# matrix of responses (with ordered categories from 0 to 4)
S <- 5-res$YY

# matrix of covariates (for the first and the following occasions)
# columns are: gender, race, educational level (2 columns), age, age^2
X1 <- res$XX[,1,]
X2 <- res$XX[,2:TT,]

# estimate the model
out1 <- est_lm_cov_latent(S, X1, X2, k = 2, output = TRUE, out_se = TRUE)

out2 <- bootstrap_lm_cov_latent(X1, X2, Psi = out1$Psi, Be = out1$Be, Ga = out1$Ga, B = 1000)
## End(Not run)
```

### bootstrap_lm_cov_latent_cont

**Parametric bootstrap for LM models for continuous outcomes with individual covariates in the latent model**

**Description**

Function that performs bootstrap parametric resampling to compute standard errors for the parameter estimates.

The function is no longer maintained. Please look at bootstrap function.

**Usage**

`bootstrap_lm_cov_latent_cont(X1, X2, param = "multilogit", Mu, Si, Be, Ga, B = 100)`

**Arguments**

- `X1` matrix of covariates affecting the initial probabilities (n x nc1)
- `X2` array of covariates affecting the transition probabilities (n x TT-1 x nc2)
param

param type of parametrization for the transition probabilities ("multilogit" = standard multinomial logit for every row of the transition matrix, "difflogit" = multinomial logit based on the difference between two sets of parameters)

Mu

Mu matrix of conditional means for the response variables (r x k)

Si

Si var-cov matrix common to all states (r x r)

Be

Be parameters affecting the logit for the initial probabilities

Ga

Ga parameters affecting the logit for the transition probabilities

B

B number of bootstrap samples

Value

mMu

mMu average of bootstrap estimates of the conditional means for the response variables

mSi

mSi average of bootstrap estimates of the var-cov matrix

mBe

mBe average of bootstrap estimates of the parameters affecting the logit for the initial probabilities

mGa

mGa average of bootstrap estimates of the parameters affecting the logit for the transition probabilities

seMu

seMu standard errors for the conditional means

seSi

seSi standard errors for the var-cov matrix

seBe

seBe standard errors for the parameters in Be

seGa

seGa standard errors for the parameters in Ga

Author(s)

Francesco Bartolucci, Silvia Pandolfi - University of Perugia (IT)

Examples

## Not run:
# Example based on multivariate longitudinal continuous data

# load data
require(mmm)
data(multLongGaussian)
TT <- 4
res <- long2matrices(multLongGaussian$ID, X = cbind(multLongGaussian$X, multLongGaussian$time),
                     Y = cbind(multLongGaussian$resp1, multLongGaussian$resp2))
Y <- res$YY
X1 <- res$XX[,1,]
X2 <- res$XX[,2:TT,]

# estimate the model
est <- est_lm_cov_latent_cont(Y, X1, X2, k = 3, output = TRUE)
out <- bootstrap_lm_cov_latent_cont(X1, X2, Mu = est$Mu, Si = est$Si,
                                Be = est$Be, Ga = est$Ga, B = 1000)
# Criminal dataset

Simulated dataset about crimes committed by a cohort of subjects.

## Usage

```r
data(data_criminal_sim)
```

## Format

A data frame with 60000 observations on the following 13 variables.

- `id`  subject id
- `sex` gender of the subject
- `time` occasion of observation
- `y1` crime of type 1 (violence against the person)
- `y2` crime of type 2 (sexual offences)
- `y3` crime of type 3 (burglary)
- `y4` crime of type 4 (robbery)
- `y5` crime of type 5 (theft and handling stolen goods)
- `y6` crime of type 6 (fraud and forgery)
- `y7` crime of type 7 (criminal damage)
- `y8` crime of type 8 (drug offences)
- `y9` crime of type 9 (motoring offences)
- `y10` crime of type 10 (other offences)

## References


## Examples

```r
data(data_criminal_sim)
```
**data_drug**

**Dataset about marijuana consumption**

**Description**

Longitudinal dataset about marijuana consumption measured by ordinal variables with 3 categories with increasing levels of consumption (1 "never in the past year", 2 "no more than once in a month in the past year", 3 "more than once a month in the past year").

**Usage**

data(data_drug)

**Format**

A data frame with 51 observations on the following 6 variables.

- V1  reported drug use at the 1st occasion
- V2  reported drug use at the 2nd occasion
- V3  reported drug use at the 3rd occasion
- V4  reported drug use at the 4th occasion
- V5  reported drug use at the 5th occasion
- V6  frequency of the response configuration

**Source**


**References**


**Examples**

data(data_drug)
data_SRHS_long  Self-reported health status dataset

Description
Dataset about self-reported health status derived from the Health and Retirement Study conducted by the University of Michigan.

Usage
data(data_SRHS_long)

Format
A data frame with 56592 observations on the following 6 variables.

- t  occasion of observation
- id  subject id
- gender  sex of the subject coded as 1 for "male", 2 for "female"
- race  race coded as 1 for "white", 2 for "black", 3 for "others"
- education  educational level coded as 1 for "high school", 2 for "general educational diploma", 3 for "high school graduate", 4 for "some college", 5 for "college and above"
- age  age at the different time occasions
- srhs  self-reported health status at the different time occasions coded as 1 for "excellent", 2 for "very good", 3 for "good", 4 for "fair", 5 for "poor"

References

Examples
data(data_SRHS_long)
decoding

Perform local and global decoding

Description

Function that performs local and global decoding (Viterbi) from the output of `est_lm_basic`, `est_lm_cov_latent`, `est_lm_cov_manifest`, and `est_lm_mixed`.

The function is no longer maintained. Please look at `lmestDecoding` function

Usage

`decoding(est, Y, X1 = NULL, X2 = NULL, fort = TRUE)`

Arguments

- `est` output from `est_lm_basic`, `est_lm_cov_latent`, `est_lm_cov_manifest`, or `est_lm_mixed`
- `Y` single vector or matrix of responses
- `X1` matrix of covariates on the initial probabilities (`est_lm_cov_latent`) or on the responses (`est_lm_cov_manifest`)
- `X2` array of covariates on the transition probabilities
- `fort` to use Fortran routines

Value

- `Ul` matrix of local decoded states corresponding to each row of `Y`
- `Ug` matrix of global decoded states corresponding to each row of `Y`

Author(s)

Francesco Bartolucci, Silvia Pandolfi, University of Perugia (IT), http://www.stat.unipg.it/bartolucci

References


Examples

```r
# Not run:
# example for the output from est_lm_basic
data(data_drug)
data_drug <- as.matrix(data_drug)
S <- data_drug[,1:5]-1
yv <- data_drug[,6]
n <- sum(yv)
# fit the Basic LM model
k <- 3
est <- est_lm_basic(S, yv, k, mod = 1)
# decoding for a single sequence
out1 <- decoding(est, S[1,])
# decoding for all sequences
out2 <- decoding(est, S)
```

```r
# example for the output from est_lm_cov_latent with difflogit parametrization
data(data_SRHS_long)
dataSRHS <- data_SRHS_long[1:1600,]
TT <- 8
head(dataSRHS)
res <- long2matrices(dataSRHS$id, X = cbind(dataSRHS$gender-1,
dataSRHS$race == 2 | dataSRHS$race == 3, dataSRHS$education == 4,
dataSRHS$education == 5, dataSRHS$age-50,(dataSRHS$age-50)^2/100),
Y= dataSRHS$srhs)
# matrix of responses (with ordered categories from 0 to 4)
S <- 5-res$YY
# matrix of covariates (for the first and the following occasions)
# columns are: gender,race,educational level (2 columns),age,age^2
X1 <- res$XX[,1,]
X2 <- res$XX[,2:TT,]
# estimate the model
est <- est_lm_cov_latent(S, X1, X2, k = 2, output = TRUE, param = "difflogit")
# decoding for a single sequence
out1 <- decoding(est, S[,1], X1[,1], X2[,1])
# decoding for all sequences
out2 <- decoding(est, S, X1, X2)
```

## End(Not run)

drawLMbasic

Draw samples from the basic LM model

Description

Function that draws samples from the basic LM model.
**drawLMbasic**

**Usage**

```r
drawLMbasic(piv, Pi, Psi, n, est = NULL, format = c("long", "matrices"), seed = NULL)
```

**Arguments**

- **piv**: vector of initial probabilities of the latent Markov chain
- **Pi**: set of transition probabilities matrices (k x k x TT)
- **Psi**: array of conditional response probabilities (mb x k x r)
- **n**: sample size
- **est**: object of class `LMbasic` (**LMbasic-class**)
- **format**: character string indicating the format of final responses matrix
- **seed**: an integer value with the random number generator state

**Value**

- **Y**: matrix of response configurations unit by unit
- **S**: matrix of distinct response configurations
- **yv**: corresponding vector of frequencies
- **piv**: vector of initial probabilities of the latent Markov chain
- **Pi**: set of transition probabilities matrices (k x k x TT)
- **Psi**: array of conditional response probabilities (mb x k x r)
- **n**: sample size
- **est**: object of class `LMbasic` (**LMbasic-class**)

**Author(s)**

Francesco Bartolucci, Silvia Pandolfi, Fulvia Pennoni, Alessio Farcomeni, Alessio Serafini

**Examples**

```r
## Not run:
# draw a sample for 1000 units and only one response variable
n <- 1000
TT <- 6
k <- 2
r <- 1 #number of response variables
mb <- 3 #maximum number of response categories
piv <- c(0.7,0.3)
Pi <- matrix(c(0.9,0.1,0.1,0.9), k, k)
Pi <- array(Pi, c(k, k, TT))
Pi[,1] <- 0
Psi <- matrix(c(0.7,0.2,0.1,0.5,0.4,0.1), mb, k)
Psi <- array(Psi, c(mb, k, r))
```
out <- drawLMbasic(piv, Pi, Psi, n = 1000)

data("data_SRHS_long")
SRHS <- data_SRHS_long[1:2400,]
SRHS$srhs <- 5 - SRHS$srhs

est <- lmest(responsesFormula = srhs ~ NULL, 
             index = c("id","t"), 
             data = SRHS, 
             k = 3)

out1 <- drawLMbasic(est = est, format = "matrices", seed = 4321, n = 100)

## End(Not run)

drawLMbasiccont  
Draw samples from the basic LM model for continuous outcomes

Description

Function that draws samples from the basic LM model for continuous outcomes with specific parameters.

Usage

drawLMbasiccont(piv, Pi, Mu, Si, n, est = NULL, 
               format = c("long","matrices"), seed = NULL)

Arguments

piv  vector of initial probabilities of the latent Markov chain
Pi   set of transition probabilities matrices (k x k x TT)
Mu   matrix of conditional means for the response variables (r x k)
Si   var-cov matrix common to all states (r x r)
n    sample size
est  object of class LMbasiccont (LMbasiccont-class)
format character string indicating the format of final responses matrix
seed  an integer value with the random number generator state
Value

- **Y**: array of continuous outcomes (n x TT x r)
- **piv**: vector of initial probabilities of the latent Markov chain
- **Pi**: set of transition probabilities matrices (k x k x TT)
- **Mu**: matrix of conditional means for the response variables (r x k)
- **Si**: var-cov matrix common to all states (r x r)
- **n**: sample size
- **est**: object of class `LMBasiccont` (**LMBasiccont-class**)

Author(s)

Francesco Bartolucci, Silvia Pandolfi, Fulvia Pennoni, Alessio Farcomeni, Alessio Serafini

Examples

```r
## Not run:
# draw a sample for 1000 units and 3 response variable
n <- 1000
TT <- 5
k <- 2
r <- 3 # number of response variables

piv <- c(0.7, 0.3)
Pi <- matrix(c(0.9, 0.1, 0.1, 0.9), k, k)
Pi[,1] <- 0
Mu <- matrix(c(-2, -2, 0, 0, 2, 2), r, k)
Si <- diag(r)
out <- drawLMbasiccont(piv, Pi, Mu, Si, n)

require(mmm)
data(multiLongGaussian)
t <- rep(1:4, times = max(multiLongGaussian$ID))
multiLongGaussian <- data.frame(t = t, multiLongGaussian)
est <- lmestCont(responsesFormula = resp1 + resp2 ~ NULL,
                 index = c("ID", "t"),
                 data = multiLongGaussian,
                 k = 3,
                 modBasic = 1,
                 tol = 10^-5)
out2 <- drawLMbasiccont(est = est, n = 100, format = "long", seed = 4321)

## End(Not run)
```
**drawLMlatent**

*Draw samples from LM model with covariates in the latent model*

**Description**

Function that draws samples from the LM model with individual covariates with specific parameters.

**Usage**

```r
drawLMlatent(Psi, Be, Ga, latentFormula, data, index,
            paramLatent = c("multilogit","difflogit"), est = NULL,
            format = c("long","matrices"), fort = TRUE, seed = NULL)
```

**Arguments**

- **Psi**: array of conditional response probabilities (mb x k x r)
- **Be**: parameters affecting the logit for the initial probabilities
- **Ga**: parameters affecting the logit for the transition probabilities
- **latentFormula**: a symbolic description of the model to be fitted. Detailed description is given in `lmest`
- **data**: a data frame in long format, with rows corresponding to observations and columns corresponding to variables, a column corresponding to time occasions and a column containing the unit identifier
- **index**: a character vector with two elements indicating the name of the "id" column as first element and the "time" column as second element
- **paramLatent**: type of parametrization for the transition probabilities ("multilogit" = standard multinomial logit for every row of the transition matrix, "difflogit" = multinomial logit based on the difference between two sets of parameters)
- **est**: object of class `LMlatent` (`LMlatent-class`)
- **format**: character string indicating the format of final responses matrix
- **fort**: to use fortran routine when possible (FALSE for not use fortran)
- **seed**: an integer value with the random number generator state

**Value**

- **Y**: matrix of response configurations
- **U**: matrix containing the sequence of latent states (n x TT)
- **Psi**: array of conditional response probabilities (mb x k x r)
- **Be**: parameters affecting the logit for the initial probabilities
- **Ga**: parameters affecting the logit for the transition probabilities
- **latentFormula**: a symbolic description of the model to be fitted. Detailed description is given in `lmest`
**drawLMlatentcont**

Draw samples from LM model for continuous outcomes with covariates in the latent model

**data**

a data frame in long format, with rows corresponding to observations and columns corresponding to variables, a column corresponding to time occasions and a column containing the unit identifier

**est**

object of class LMLatent (LMLatent-class)

**Author(s)**

Francesco Bartolucci, Silvia Pandolfi, Fulvia Pennoni, Alessio Farcomeni, Alessio Serafini

**Examples**

```r
## Not run:
data(data_SRHS_long)
data_SRHS <- data_SRHS_long
data_SRHS_long$srhs <- 5 - data_SRHS_long$srhs
est <- lmest(responsesFormula = srhs ~ NULL,
            latentFormula = ~
              I(gender - 1) +
              I(0 + (race == 2) + (race == 3)) +
              I(0 + (education == 4)) +
              I(0 + (education == 5)) +
              I(age - 50) + I((age-50)^2/100),
            index = c("id","t"),
            data = data_SRHS_long,
            k = 2,
            paramLatent = "multilogit",
            start = 0)
out <- drawLMlatent(est = est, format = "matrices", seed = 4321)
out1 <- drawLMlatent(Psi = est$Psi, Be = est$Be, Ga = est$Ga,
                      data = data_SRHS_long, index = c("id","t"),
                      latentFormula = ~
                        I(gender - 1) +
                        I(0 + (race == 2) + (race == 3)) +
                        I(0 + (education == 4)) +
                        I(0 + (education == 5)) +
                        I(age - 50) + I((age-50)^2/100),
                      paramLatent = "multilogit", format = "matrice",
                      seed = 4321)
## End(Not run)
```
drawLMlatentcont

Description
Function that draws samples from the LM model for continuous outcomes with individual covariates with specific parameters.

Usage
drawLMlatentcont(Mu, Si, Be, Ga, latentFormula, data, index,
    paramLatent = c("multilogit", "difflogit"), est = NULL,
    format = c("long", "matrices"), fort = TRUE, seed = NULL)

Arguments
Mu array of conditional means for the response variables (r x k)
Si var-cov matrix common to all states (r x r)
Be parameters affecting the logit for the initial probabilities
Ga parameters affecting the logit for the transition probabilities
latentFormula a symbolic description of the model to be fitted. A detailed description is given in \texttt{lmestCont}
data a data frame in long format, with rows corresponding to observations and columns corresponding to variables, a column corresponding to time occasions and a column containing the unit identifier
index a character vector with two elements indicating the name of the "id" column as first element and the "time" column as second element
paramLatent type of parametrization for the transition probabilities ("multilogit" = standard multinomial logit for every row of the transition matrix, "difflogit" = multinomial logit based on the difference between two sets of parameters)
est object of class \texttt{LMlatentcont} (\texttt{LMlatentcont-class})
format character string indicating the format of final responses matrix
fort to use fortran routine when possible (FALSE for not use fortran)
seed an integer value with the random number generator state

Value
Y array of continuous outcomes (n x TT x r)
U matrix containing the sequence of latent states (n x TT)
Mu array of conditional means for the response variables (r x k)
Si var-cov matrix common to all states (r x r)
Be parameters affecting the logit for the initial probabilities
Ga parameters affecting the logit for the transition probabilities
latentFormula a symbolic description of the model to be fitted. A detailed description is given in \texttt{lmestCont}
data a data frame in long format, with rows corresponding to observations and columns corresponding to variables, a column corresponding to time occasions and a column containing the unit identifier
est object of class \texttt{LMlatentcont} (\texttt{LMlatentcont-class})
drawLMmixed

Draws samples from the mixed LM model

Description

Function that draws samples from the mixed LM model with specific parameters.

Usage

drawLMmixed(la, Piv, Pi, Psi, n, TT, est = NULL,
format = c("long","matrices"), seed = NULL)

Arguments

la vector of mass probabilities for the first latent variable
Piv matrix of initial probabilities of the latent Markov chain (k2 x k1)
Pi set of transition matrices (k2 x k2 x k1)
Psi array of conditional response probabilities (mb x k2 x r)
n sample size
TT number of time occasions
est object of class LMmixed (LMmixed-class)
format character string indicating the format of final responses matrix
seed an integer value with the random number generator state

Value
Y matrix of response configurations unit by unit
S matrix of distinct response configurations
yv corresponding vector of frequencies
la vector of mass probabilities for the first latent variable
Piv matrix of initial probabilities of the latent Markov chain (k2 x k1)
Pi set of transition matrices (k2 x k2 x k1)
Psi array of conditional response probabilitles (mb x k2 x r)
n sample size
TT number of time occasions
est object of class LMmixed (LMmixed-class)

Author(s)
Francesco Bartolucci, Silvia Pandolfi, Fulvia Pennoni, Alessio Farcemeni, Alessio Serafini

Examples
# draw a sample for 1000 units and only one response variable and 5 time occasions
k1 <- 2
k2 <- 3
la <- rep(1/k1, k1)
Piv <- matrix(1/k2, k2, k2)
Pi <- array(0, c(k2, k2, k1))
Pi[,,1] <- diag(k2)
Pi[,,2] <- 1/k2
Psi <- cbind(c(0.6,0.3,0.1), c(0.1,0.3,0.6), c(0.3,0.6,0.1))
out <- drawLMmixed(la, Piv, Pi, Psi, n = 1000, TT = 5)

## Not run:
# Example based on criminal data
data(data_criminal_sim)
data_criminal_sim = data.frame(data_criminal_sim)
# Estimate mixed LM model for females
responsesFormula <- lmestFormula(data = data_criminal_sim, response = "y")$responsesFormula
est <- lmestMixed(responsesFormula = responsesFormula, index = c("id","time"),
The function is no longer maintained. Please look at `drawLMbasic` function.

**Usage**

draw_lm_basic(piv, Pi, Psi, n)

**Arguments**

- **piv**: vector of initial probabilities of the latent Markov chain
- **Pi**: set of transition probabilities matrices (k x k x TT)
- **Psi**: array of conditional response probabilities (mb x k x r)
- **n**: sample size

**Value**

- **Y**: matrix of response configurations unit by unit
- **S**: matrix of distinct response configurations
- **yv**: corresponding vector of frequencies

**Author(s)**

Francesco Bartolucci, Silvia Pandolfi, University of Perugia (IT), http://www.stat.unipg.it/bartolucci

**Examples**

```r
## Not run:
# draw a sample for 1000 units and only one response variable
n <- 1000
TT <- 6
k <- 2
r <- 1 #number of response variables
```
mb <- 3  # maximum number of response categories

piv <- c(0.7, 0.3)
Piv <- matrix(c(0.9, 0.1, 0.1, 0.9), k, k)
Piv[,1] <- 0
Psi <- matrix(c(0.7, 0.2, 0.1, 0.5, 0.4, 0.1), mb, k)
Psi <- array(Psi, c(mb, k, r))
out <- draw_lm_basic(piv, Piv, Psi, n = 1000)

## End(Not run)

draw_lm_basic_cont  
\underline{Draw samples from the basic LM model for continuous outcomes}

Description

Function that draws samples from the basic LM model for continuous outcomes with specific parameters.

The function is no longer maintained. Please look at drawLMbasiccont function.

Usage

draw_lm_basic_cont(piv, Piv, Mu, Si, n)

Arguments

- `piv`: vector of initial probabilities of the latent Markov chain
- `Piv`: set of transition probabilities matrices (k x k x TT)
- `Mu`: matrix of conditional means for the response variables (r x k)
- `Si`: var-cov matrix common to all states (r x r)
- `n`: sample size

Value

- `Y`: array of continuous outcomes (n x TT x r)

Author(s)

Francesco Bartolucci, Silvia Pandolfi, University of Perugia (IT), http://www.stat.unipg.it/bartolucci
Examples

```r
## Not run:

# draw a sample for 1000 units and 3 response variable
n <- 1000
TT <- 5
k <- 2
r <- 3 #number of response variables

piv <- c(0.7,0.3)
Pi <- matrix(c(0.9,0.1,0.1,0.9), k, k)
Pi <- array(Pi, c(k, k, TT))
Pi[,,1] <- 0
Mu <- matrix(c(-2,-2,0,0,2,2), r, k)
Si <- diag(r)
out <- draw_lm_basic_cont(piv, Pi, Mu, Si, n)
```

## End(Not run)

---

draw_lm_cov_latent

**Draw samples from LM model with covariates in the latent model**

**Description**

Function that draws samples from the LM model with individual covariates with specific parameters.

*The function is no longer maintained. Please look at drawLMlatent function.*

**Usage**

draw_lm_cov_latent(X1, X2, param = "multilogit", Psi, Be, Ga, fort = TRUE)

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>X1</td>
<td>desing matrix for the covariates on the initial probabilities (n x nc1)</td>
</tr>
<tr>
<td>X2</td>
<td>desing matrix for the covariates on the transition probabilities (n x TT-1 x nc2)</td>
</tr>
<tr>
<td>param</td>
<td>type of parametrization for the transition probabilities (&quot;multilogit&quot; = standard multinominal logit for every row of the transition matrix, &quot;difflogit&quot; = multinomial logit based on the difference between two sets of parameters)</td>
</tr>
<tr>
<td>Psi</td>
<td>array of conditional response probabilities (mb x k x r)</td>
</tr>
<tr>
<td>Be</td>
<td>parameters affecting the logit for the initial probabilities</td>
</tr>
<tr>
<td>Ga</td>
<td>parametes affecting the logit for the transition probabilities</td>
</tr>
<tr>
<td>fort</td>
<td>to use fortran routine when possible (FALSE for not use fortran)</td>
</tr>
</tbody>
</table>
**Value**

Y  
matrix of response configurations unit by unit (n x TT x r)  
U  
matrix containing the sequence of latent states (n x TT)

**Author(s)**

Francesco Bartolucci, Silvia Pandolfi, University of Perugia (IT), http://www.stat.unipg.it/bartolucci

**Examples**

```r
## Not run:

# draw a sample for 1000 units, 10 response variable and 2 covariates
n <- 1000
TT <- 5
k <- 2
c <- 2 #number of covariates
r <- 10 #number of response variables
mb <- 2 #maximum number of response categories
fort <- TRUE

Psi <- matrix(c(0.9,0.1,0.1,0.9), mb, k)
Psi <- array(Psi, c(mb, k, r))
Ga <- matrix(c(-log(0.9/0.1),0.5,1), (c+1)*(k-1), k)
Be <- array(c(0,0.5,1), (c+1)*(k-1))

#Simulate covariates
X1 <- matrix(0, n, c)
for(j in 1:c) X1[,j] <- rnorm(n)
X2 <- array(0,c(n, TT-1, c))
for (t in 1:(TT-1)) for(j in 1:c){
  if(t==1){
    X2[,t,j] <- 0.5*X1[,j] + rnorm(n)
  }else{
    X2[,t,j] <- 0.5*X2[,t-1,j] + rnorm(n)
  }
}

out <- draw_lm_cov_latent(X1, X2, Psi = Psi, Be = Be, Ga = Ga, fort = fort)

## End(Not run)
```

---

**draw_lm_cov_latent_cont**

*Draw samples from LM model for continuous outcomes with covariates in the latent model*
draw_lm_cov_latent_cont

Description

Function that draws samples from the LM model for continuous outcomes with individual covariates with specific parameters.

The function is no longer maintained. Please look at drawLMlatentcont function.

Usage

draw_lm_cov_latent_cont(X1, X2, param = "multilogit", Mu, Si, Be, Ga, fort = TRUE)

Arguments

X1  desing matrix for the covariates on the initial probabilities (n x nc1)
X2  desing matrix for the covariates on the transition probabilities (n x TT-1 x nc2)
param  type of parametrization for the transition probabilities ("multilogit" = standard multinomial logit for every row of the transition matrix, "difflogit" = multinomial logit based on the difference between two sets of parameters)
Mu  array of conditional means for the response variables (r x k)
Si  var-cov matrix common to all states (r x r)
Be  parameters affecting the logit for the initial probabilities
Ga  parameters affecting the logit for the transition probabilities
fort  to use fortran routine when possible (FALSE for not use fortran)

Value

Y  array of continuous outcomes (n x TT x r)
U  matrix containing the sequence of latent states (n x TT)

Author(s)

Francesco Bartolucci, Silvia Pandolfi, University of Perugia (IT), http://www.stat.unipg.it/bartolucci

Examples

## Not run:
# draw a sample for 1000 units, 10 response variable and 2 covariates
n <- 1000
TT <- 5
k <- 2
nc <- 2 #number of covariates
r <- 3 #number of response variables
fort <- TRUE
Mu <- matrix(c(-2,-2,0,0,2,2), r, k)
Si <- diag(r)
Ga <- matrix(c(-log(0.9/0.1),0.5,1), (nc+1)*(k-1), k)
Be <- array(c(0,0.5,1), (nc+1)*(k-1))
#Simulate covariates
X1 <- matrix(0, n, nc)
for(j in 1:nc) X1[,j] <- rnorm(n)
X2 <- array(0, c(n,TT-1,nc))
for (t in 1:(TT-1)) for(j in 1:nc){
  if(t==1){
    X2[,t,j] <- 0.5*X1[,j] + rnorm(n)
  }else{
    X2[,t,j] <- 0.5*X2[,t-1,j] + rnorm(n)
  }
}

out <- draw_lm_cov_latent_cont(X1, X2, param = "multilogit", Mu, Si, Be, Ga, fort = fort)

## End(Not run)

draw_lm_mixed

Draws samples from the mixed LM model

Description

Function that draws samples from the mixed LM model with specific parameters.

The function is no longer maintained. Please look at drawLMmixed function.

Usage

draw_lm_mixed(la, Piv, Pi, Psi, n, TT)

Arguments

la vector of mass probabilities for the first latent variable
Piv matrix of initial probabilities of the latent Markov chain (k2 x k1)
Pi set of transition matrices (k2 x k2 x k1)
Psi array of conditional response probabilities (mb x k2 x r)
n sample size
TT number of time occasions

Value

Y matrix of response configurations unit by unit
S matrix of distinct response configurations
yv corresponding vector of frequencies

Author(s)

Francesco Bartolucci, Silvia Pandolfi, University of Perugia (IT), http://www.stat.unipg.it/bartolucci
## Not run:
# draw a sample for 1000 units and only one response variable and 5 time occasions
k1 <- 2
k2 <- 3
la <- rep(1/k1,k1)
Piv <- matrix(1/k2,k2,k1)
Pi <- array(0,c(k2,k2,k1))
Pi[,1] <- diag(k2)
Pi[,2] <- 1/k2
Psi <- cbind(c(0.6,0.3,0.1),c(0.1,0.3,0.6),c(0.3,0.6,0.1))
out <- draw_lm_mixed(la,Piv,Pi,Psi,n=1000,TT=5)

## End(Not run)

---

**est_lm_basic**  
*Estimate basic LM model*

---

**Description**

Main function for estimating the basic LM model.

The function is no longer maintained. Please look at `lmest` function.

**Usage**

```r
est_lm_basic(S, yv, k, start = 0, mod = 0, tol = 10^-8, maxit = 1000,
              out_se = FALSE, piv = NULL, Pi = NULL, Psi = NULL)
```

**Arguments**

- **S**: array of available configurations (n x TT x r) with categories starting from 0 (use NA for missing responses)
- **yv**: vector of frequencies of the available configurations
- **k**: number of latent states
- **start**: type of starting values (0 = deterministic, 1 = random, 2 = initial values in input)
- **mod**: model on the transition probabilities (0 for time-heter., 1 for time-homog., from 2 to (TT-1) partial homog. of that order)
- **tol**: tolerance level for convergence
- **maxit**: maximum number of iterations of the algorithm
- **out_se**: to compute the information matrix and standard errors
- **piv**: initial value of the initial probability vector (if start=2)
- **Pi**: initial value of the transition probability matrices (k x k x TT) (if start=2)
- **Psi**: initial value of the conditional response probabilities (mb x k x r) (if start=2)
Value

lk      maximum log-likelihood
piv     estimate of initial probability vector
Pi      estimate of transition probability matrices
Psi     estimate of conditional response probabilities
np      number of free parameters
aic     value of AIC for model selection
bic     value of BIC for model selection
lkv     log-likelihood trace at every step
V       array containing the posterior distribution of the latent states for each response configuration and time occasion
sepiv   standard errors for the initial probabilities
sePi    standard errors for the transition probabilities
sePsi   standard errors for the conditional response probabilities
call    command used to call the function

Author(s)

Francesco Bartolucci, Silvia Pandolfi, University of Perugia (IT), http://www.stat.unipg.it/bartolucci

References


Examples

## Not run:
# Example of drug consumption data

# load data
data(data_drug)
data_drug <- as.matrix(data_drug)
S <- data_drug[,1:5]-1
yv <- data_drug[,6]

# fit of the Basic LM model
k <- 3
out <- est_lm_basic(S, yv, k, mod = 1)
summary(out)

# Example based on criminal data

# load criminal data
data(data_criminal_sim)
out <- long2wide(data_criminal_sim, "id", "time", "sex", "..."
Estimate basic LM model for continuous outcomes

**Description**

Main function for estimating the basic LM model for continuous outcomes.

The function is no longer maintained. Please look at `lmestCont` function.

**Usage**

```r
est_lm_basic_cont(Y, k, start = 0, mod = 0, tol = 10^-8, maxit = 1000,
                   out_se = FALSE, piv = NULL, Pi = NULL, Mu = NULL, Si = NULL)
```

**Arguments**

- **Y**: array of continuous outcomes (n x TT x r)
- **k**: number of latent states
- **start**: type of starting values (0 = deterministic, 1 = random, 2 = initial values in input)
- **mod**: model on the transition probabilities (0 for time-heter., 1 for time-homog., from 2 to (TT-1) partial homog. of that order)
- **tol**: tolerance level for convergence
- **maxit**: maximum number of iterations of the algorithm
- **out_se**: to compute the information matrix and standard errors
- **piv**: initial value of the initial probability vector (if start=2)
- **Pi**: initial value of the transition probability matrices (k x k x TT) (if start=2)
- **Mu**: initial value of the conditional means (r x k) (if start=2)
- **Si**: initial value of the var-cov matrix common to all states (r x r) (if start=2)
Value

- **lk**: maximum log-likelihood
- **piv**: estimate of initial probability vector
- **Pi**: estimate of transition probability matrices
- **Mu**: estimate of conditional means of the response variables
- **Si**: estimate of var-cov matrix common to all states
- **np**: number of free parameters
- **aic**: value of AIC for model selection
- **bic**: value of BIC for model selection
- **lkv**: log-likelihood trace at every step
- **V**: array containing the posterior distribution of the latent states for each units and time occasion
- **call**: command used to call the function

Author(s)

Francesco Bartolucci, Silvia Pandolfi, University of Perugia (IT), http://www.stat.unipg.it/bartolucci

References


Examples

```r
## Not run:
# Example based on multivariate longitudinal continuous data

# load data
require(mmm)
data(multiLongGaussian)
res <- long2matrices(multiLongGaussian$ID, X=cbind(multiLongGaussian$X, multiLongGaussian$time),
                     Y=cbind(multiLongGaussian$resp1, multiLongGaussian$resp2))
Y <- res$YY

# fit of the Basic LM model for continuous outcomes
k <- 3
out <- est_lm_basic_cont(Y, k, mod = 1, tol = 10^-5)
summary(out)
## End(Not run)
```
est_lm_cov_latent

Estimate LM model with covariates in the latent model

Description

Main function for estimating the LM model with covariates in the latent model.

The function is no longer maintained. Please look at lmest function.

Usage

```
est_lm_cov_latent(S, X1=NULL, X2=NULL, yv = rep(1,nrow(S)), k, start = 0, tol = 10^-8, maxit = 1000, param = "multilogit", Psi, Be, Ga, fort = TRUE, output = FALSE, out_se = FALSE, fixPsi = FALSE)
```

Arguments

- `S`: array of available configurations (n x TT x r) with categories starting from 0 (use NA for missing responses)
- `X1`: matrix of covariates affecting the initial probabilities (n x nc1)
- `X2`: array of covariates affecting the transition probabilities (n x TT-1 x nc2)
- `yv`: vector of frequencies of the available configurations
- `k`: number of latent states
- `start`: type of starting values (0 = deterministic, 1 = random, 2 = initial values in input)
- `tol`: tolerance level for checking convergence of the algorithm
- `maxit`: maximum number of iterations of the algorithm
- `param`: type of parametrization for the transition probabilities ("multilogit" = standard multinomial logit for every row of the transition matrix, "difflogit" = multinomial logit based on the difference between two sets of parameters)
- `Psi`: initial value of the array of the conditional response probabilities (mb x k x r)
- `Be`: initial value of the parameters affecting the logit for the initial probabilities (if start=2)
- `Ga`: initial value of the parameters affecting the logit for the transition probabilities (if start=2)
- `fort`: to use fortran routine when possible (FALSE for not use fortran)
- `output`: to return additional output (V,PI,Piv,Ul)
- `out_se`: to compute the information matrix and standard errors
- `fixPsi`: TRUE if Psi is given in input and is not updated anymore
Value

1k  maximum log-likelihood
Be  estimated array of the parameters affecting the logit for the initial probabilities
Ga  estimated array of the parameters affecting the logit for the transition probabilities
Piv estimate of initial probability matrix
PI  estimate of transition probability matrices
Psi estimate of conditional response probabilities
np  number of free parameters
aic value of AIC for model selection
bic value of BIC for model selection
lkv log-likelihood trace at every step
V  array containing the posterior distribution of the latent states for each response configuration and time occasion
Ul  matrix containing the predicted sequence of latent states by the local decoding method
sePsi standard errors for the conditional response matrix
seBe standard errors for Be
seGa standard errors for Ga
call command used to call the function

Author(s)

Francesco Bartolucci, Silvia Pandolfi, University of Perugia, http://www.stat.unipg.it/bartolucci

References


Examples

```r
## Not run:
# Example based on self-rated health status (SRHS) data
# load SRHS data
data(data_SRHS_long)
dataSRHS = data_SRHS_long

TT <- 8
head(dataSRHS)
res <- long2matrices(dataSRHS$id, X = cbind(dataSRHS$gender-1,
dataSRHS$race == 2 | dataSRHS$race == 3, dataSRHS$education == 4,
dataSRHS$education == 5, dataSRHS$age-50, (dataSRHS$age-50)^2/100),
Y = dataSRHS$srhs)
```
# matrix of responses (with ordered categories from 0 to 4)
S <- 5-res$YY
n <- dim(S)[1]

# matrix of covariates (for the first and the following occasions)
# columns are: gender, race, educational level (2 columns), age, age^2
X1 <- res$XX[,1,]
X2 <- res$XX[,2:TT,]

# estimate the model
est2f <- est_lm_cov_latent(S, X1, X2, k = 2, output = TRUE, out_se = TRUE)
summary(est2f)

# average transition probability matrix
PI <- round(apply(est2f$PI[,,,2:TT], c(1,2), mean), 4)

# Transition probability matrix for white females with high educational level
ind1 <- X1[,1] == 1 & X1[,2] == 0 & X1[,4] == 1
PI1 <- round(apply(est2f$PI[,ind1,2:TT], c(1,2), mean), 4)

# Transition probability matrix for non-white male, low educational level
ind2 <- (X1[,1] == 0 & X1[,2] == 1 & X1[,3] == 0 & X1[,4] == 0)
PI2 <- round(apply(est2f$PI[,ind2,2:TT], c(1,2), mean), 4)

## End(Not run)

---

**est_lm_cov_latent_cont**

*Estimate LM model for continuous outcomes with covariates in the latent model*

---

**Description**

Main function for estimating the LM model for continuous outcomes with covariates in the latent model.

The function is no longer maintained. Please look at `lmestCont` function.

**Usage**

`est_lm_cov_latent_cont(Y, X1 = NULL, X2 = NULL, yv = rep(1,nrow(Y)), k, start = 0, tol = 10^-8, maxit = 1000, param = "multilogit", Mu = NULL, Si = NULL, Be = NULL, Ga = NULL, output = FALSE, out_se = FALSE)`

**Arguments**

- `Y` array of continuous outcomes (n x TT x r)
X1 matrix of covariates affecting the initial probabilities (n x nc1)
X2 array of covariates affecting the transition probabilities (n x TT-1 x nc2)
yv vector of frequencies of the available configurations
k number of latent states
start type of starting values (0 = deterministic, 1 = random, 2 = initial values in input)
tol tolerance level for checking convergence of the algorithm
maxit maximum number of iterations of the algorithm
param type of parametrization for the transition probabilities ("multilogit" = standard multinomial logit for every row of the transition matrix, "difflogit" = multinomial logit based on the difference between two sets of parameters)
Mu initial value of the conditional means (r x k) (if start=2)
Si initial value of the var-cov matrix common to all states (r x r) (if start=2)
Be initial value of the parameters affecting the logit for the initial probabilities (if start=2)
Ga initial value of the parameters affecting the logit for the transition probabilities (if start=2)
output to return additional output (V,Pi,Piv,Ul)
out_se to compute the information matrix and standard errors

Value
1k maximum log-likelihood
Be estimated array of the parameters affecting the logit for the initial probabilities
Ga estimated array of the parameters affecting the logit for the transition probabilities
Mu estimate of conditional means of the response variables
Si estimate of var-cov matrix common to all states
np number of free parameters
aic value of AIC for model selection
bic value of BIC for model selection
1kv log-likelihood trace at every step
Piv estimate of initial probability matrix
PI estimate of transition probability matrices
Ul matrix containing the predicted sequence of latent states by the local decoding method
call command used to call the function

Author(s)
Francesco Bartolucci, Silvia Pandolfi, University of Perugia, http://www.stat.unipg.it/bartolucci
est_lm_cov_manifest

References


Examples

```r
## Not run:
# Example based on multivariate longitudinal continuous data

# load data
require(mmm)
data(multiLongGaussian)
TT <- 4
res <- long2matrices(multiLongGaussian$ID, X = cbind(multiLongGaussian$X, multiLongGaussian$time),
                     Y = cbind(multiLongGaussian$resp1, multiLongGaussian$resp2))
Y <- res$YY
X1 <- res$XX[,1,]
X2 <- res$XX[,2:TT,]

# estimate the model
est <- est_lm_cov_latent_cont(Y, X1, X2, k = 3, output = TRUE)
summary(est)

# average transition probability matrix
PI <- round(apply(est$PI[,1:TT,2:TT], c(1,2), mean), 4)
PI

## End(Not run)
```

est_lm_cov_manifest  

*Estimate LM model with covariates in the measurement model*

Description

Main function for estimating LM model with covariates in the measurement model based on a global logit parameterization.

The function is no longer maintained. Please look at `lmest` function.

Usage

```r
est_lm_cov_manifest(S, X, yv = rep(1,nrow(S)), k, q = NULL, mod = c("LM", "FM"),
tol = 10^-8, maxit = 1000, start = 0, mu = NULL, al = NULL,
be = NULL, si = NULL, rho = NULL, la = NULL, PI = NULL,
output = FALSE, out_se = FALSE)
```
Arguments

S  array of available configurations (n x TT) with categories starting from 0
X  array (n x TT x nc) of covariates with eventually includes lagged response (nc = number of covariates)
yv  vector of frequencies of the available configurations
k  number of latent states
q  number of support points for the AR(1) process
mod model ("LM" = Latent Markov with stationary transition, "FM" = finite mixture)
tol  tolerance for the convergence (optional) and tolerance of conditional probability
    if tol>1 then return
maxit  maximum number of iterations of the algorithm
start  type of starting values (0 = deterministic, 1 = random, 2 = initial values in input)
mu  starting value for mu (optional)
al  starting value for al (optional)
be  starting value for be (optional)
si  starting value for si when mod="FM" (optional)
rho  starting value for rho when mod="FM" (optional)
la  starting value for la (optional)
PI  starting value for PI (optional)
output to return additional output (PRED0, PRED1)
out_se  TRUE for computing information matrix and standard errors

Value

mu  vector of cutpoints
al  support points for the latent states
be  estimate of the vector of regression parameters
si  sigma of the AR(1) process (mod = "FM")
rho  parameter vector for AR(1) process (mod = "FM")
la  vector of initial probabilities
PI  transition matrix
lk  maximum log-likelihood
np  number of parameters
aic  value of AIC index
bic  value of BIC index
PRED0 prediction of latent state
PRED1 prediction of the overall latent effect
sebe  standard errors for the regression parameters be
selrho  standard errors for logit type transformation of rho
J1  information matrix
call  command used to call the function
Author(s)
Francesco Bartolucci, Silvia Pandolfi - University of Perugia (IT)

References


Examples

```r
## Not run:
# Example based on self-rated health status (SRHS) data

# load SRHS data
data(data_SRHS_long)
dataSRHS <- data_SRHS_long
head(dataSRHS)

res <- long2matrices(dataSRHS$id, X = cbind(dataSRHS$gender-1, 
dataSRHS$race == 2 | dataSRHS$race == 3, dataSRHS$education == 4, 
dataSRHS$education == 5, dataSRHS$age-50, (dataSRHS$age-50)^2/100), 
Y = dataSRHS$srhs)

X <- res$XX
S <- 5-res$YY

# *** fit stationary LM model
res0 <- vector("list", 10)
tol <- 10^-6;
for(k in 1:10){
  res0[[k]] <- est_lm_cov_manifest(S, X, k, 1, mod = "LM", tol)
  save.image("example_SRHS.RData")
}

# *** fit the mixture latent auto-regressive model
res <- vector("list",4)
k <- 1
q <- 51
res[[k]] <- est_lm_cov_manifest(S, X, k, q, mod = "FM", tol, output = TRUE)
for(k in 2:4) res[[k]] <- est_lm_cov_manifest(S, X, k, q = 61, mod = "FM", tol, output = TRUE)

## End(Not run)
```
est_lm_mixed  

Estimate mixed LM model

Description

Main function for estimating the mixed LM model with discrete random effect in the latent model.

The function is no longer maintained. Please look at lmestMixed function

Usage

```r
est_lm_mixed(S, yv = rep(1,nrow(S)), k1, k2, start = 0, tol = 10^-8, maxit = 1000,
  out_se = FALSE)
```

Arguments

- `S` array of available response configurations (n x TT x r) with categories starting from 0
- `yv` vector of frequencies of the available configurations
- `k1` number of latent classes
- `k2` number of latent states
- `start` type of starting values (0 = deterministic, 1 = random)
- `tol` tolerance level for convergence
- `maxit` maximum number of iterations of the algorithm
- `out_se` to compute standard errors

Value

- `la` estimate of the mass probability vector (distribution of the random effects)
- `Piv` estimate of initial probabilities
- `Pi` estimate of transition probability matrices
- `Psi` estimate of conditional response probabilities
- `lk` maximum log-likelihood
- `W` posterior probabilities of the random effect
- `np` number of free parameters
- `bic` value of BIC for model selection
- `call` command used to call the function

Author(s)

Francesco Bartolucci, Silvia Pandolfi - University of Perugia (IT)
References


Examples

```r
## Not run:
# Example based of criminal data

# load data
data(data_criminal_sim)
out <- long2wide(data_criminal_sim, "id", "time", "sex",
c("y1","y2","y3","y4","y5","y6","y7","y8","y9","y10"), aggr = T, full = 999)

XX <- out$XX
YY <- out$YY
freq <- out$freq
n1 <- sum(freq[XX[,1] == 1])
n2 <- sum(freq[XX[,1] == 2])
n <- sum(freq)

# fit mixed LM model only for females
YY <- YY[XX[,1] == 2,]
freq <- freq[XX[,1] == 2]
k1 <- 2
k2 <- 2
res <- est_lm_mixed(YY, freq, k1, k2, tol = 10^-8)
summary(res)
## End(Not run)
```

est_mc_basic

**Estimate basic Markov chain (MC) model**

**Description**

Main function for estimating the basic MC model.

The function is no longer maintained. Please look at `lmestMc` function.

**Usage**

```
est_mc_basic(S, yv, mod = 0, tol = 10^-8, maxit = 1000, out_se = FALSE)
```

**Arguments**

- `S`  
  matrix (n x TT) of available configurations of the response variable with categories starting from 0

- `yv`  
  vector of frequencies of the available configurations
mod: model on the transition probabilities (0 for time-heter., 1 for time-homog., from 2 to (TT-1) partial homog. of that order)

tol: tolerance level for convergence

maxit: maximum number of iterations of the algorithm

out_se: to compute the information matrix and standard errors

Value:

lk: maximum log-likelihood

piv: estimate of initial probability vector

Pi: estimate of transition probability matrices

np: number of free parameters

aic: value of AIC for model selection

bic: value of BIC for model selection

Fy: estimated marginal distribution of the response variable for each time occasion

sepiv: standard errors for the initial probabilities

sePi: standard errors for the transition probabilities

call: command used to call the function

Author(s):

Francesco Bartolucci, Silvia Pandolfi, University of Perugia (IT), http://www.stat.unipg.it/bartolucci

References:


Examples:

# Example of drug consumption data

# load data
data(data_drug)
data_drug <- as.matrix(data_drug)
S <- data_drug[,1:5]-1
yv <- data_drug[,6]

# fit of the Basic MC model
out <- est_mc_basic(S, yv, mod = 1, out_se = TRUE)
summary(out)
est_mc_cov

Estimate Markov chain (MC) model with covariates

Description

Main function for estimating the MC model with covariates.

The function is no longer maintained. Please look at lmestMc function.

Usage

est_mc_cov(S, X1 = NULL, X2 = NULL, yv = rep(1, nrow(S)), start = 0, tol = 10^-8, maxit = 1000, out_se = FALSE, output = FALSE, fort = TRUE)

Arguments

S matrix of available configurations of the response variable (n x TT) with categories starting from 0
X1 matrix of covariates affecting the initial probabilities (n x nc1)
X2 array of covariates affecting the transition probabilities (n x TT-1 x nc2)
yv vector of frequencies of the available configurations
start type of starting values (0 = deterministic, 1 = random)
tol tolerance level for checking convergence of the algorithm
maxit maximum number of iterations of the algorithm
out_se to compute the information matrix and standard errors
output to return additional output (PI, Piv)
fort to use fortran routine when possible (FALSE for not use fortran)

Value

lk maximum log-likelihood
Be estimated array of the parameters affecting the logit for the initial probabilities
Ga estimated array of the parameters affecting the logit for the transition probabilities
np number of free parameters
aic value of AIC for model selection
bic value of BIC for model selection
seBe standard errors for Be
seGa standard errors for Ga
Piv estimate of initial probability matrix
PI estimate of transition probability matrices
call command used to call the function
Author(s)
Francesco Bartolucci, Silvia Pandolfi, University of Perugia, http://www.stat.unipg.it/bartolucci

References

Examples

```r
## Not run:

# Example based on criminal data

# load criminal data
data(data_criminal_sim)

# We consider the response variable referring of crime of type 5
out <- long2wide(data_criminal_sim, "id", "time", "sex", "y5", aggr = T, full = 999)
XX <- out$XX-1
YY <- out$YY
freq <- out$freq
TT <- 6

X1 <- as.matrix(XX[,1])
X2 <- as.matrix(XX[,2:TT])
# estimate the model
res <- est_mc_cov(S = YY, yv = freq, X1 = X1, X2 = X2, output = TRUE)
summary(res)

# Initial probability for female
Piv0 <- round(colMeans(res$Piv[X1 == 0,]), 4)
# Initial probability for male
Piv1 <- round(colMeans(res$Piv[X1 == 1,]), 4)

## End(Not run)
```

LMbasic-class

Class 'LMbasic'

Description
An S3 class object created by `lmest` function for basic Latent Markov (LM) model.
Value

lk  maximum log-likelihood at convergence of the EM algorithm
piv estimate of initial probability vector
Pi  estimate of transition probability matrices (k x k x TT)
Psi  estimate of conditional response probabilities (mb x k x r)
np  number of free parameters
k  optimal number of latent states
aic  value of the Akaike Information Criterion for model selection
bic  value of the Bayesian Information Criterion for model selection
lkv  log-likelihood trace at every step
V  array containing the estimated posterior probabilities of the latent states for each response configuration and time occasion
n  number of observations in the data
TT  number of time occasions
modBasic  model on the transition probabilities: default 0 for time-heterogeneous transition matrices, 1 for time-homogeneous transition matrices, 2 for partial time homogeneity based on two transition matrices one from 2 to (TT-1) and the other for TT.
sepiv  standard errors for the initial probabilities
sePi  standard errors for the transition probabilities
sePsi  standard errors for the conditional response probabilities
Bic  vector containing the values of the BIC for each k
Aic  vector containing the values of the AIC for each k
call  command used to call the function
data  data.frame given in input

Author(s)

Francesco Bartolucci, Silvia Pandolfi, Fulvia Pennoni, Alessio Farcomeni, Alessio Serafini

See Also

lmest
LMbasiccont-class

Description

An S3 class object created by \texttt{lmestCont} function for the latent Markov (LM) model for continuous responses in long format.

Value

- \texttt{lk} maximum log-likelihood
- \texttt{piv} estimate of initial probability vector
- \texttt{Pi} estimate of transition probability matrices (k x k x TT)
- \texttt{Mu} estimate of conditional means of the response variables (r x k)
- \texttt{Si} estimate of var-cov matrix common to all states (r x r)
- \texttt{np} number of free parameters
- \texttt{k} optimal number of latent states
- \texttt{aic} value of the Akaike Information Criterion for model selection
- \texttt{bic} value of the Bayesian Information Criterion for model selection
- \texttt{lkv} log-likelihood trace at every step
- \texttt{V} array containing the posterior distribution of the latent states for each units and time occasion
- \texttt{n} number of observations in the data
- \texttt{TT} number of time occasions
- \texttt{modBasic} model on the transition probabilities: default 0 for time-heterogeneous transition matrices, 1 for time-homogeneous transition matrices, 2 for partial time homogeneity based on two transition matrices one from 2 to (TT-1) and the other for TT
- \texttt{sepiv} standard errors for the initial probabilities
- \texttt{sePi} standard errors for the transition probabilities
- \texttt{seMu} standard errors for the conditional means
- \texttt{seSi} standard errors for the var-cov matrix
- \texttt{Bic} vector containing the values of the BIC of the LM model with each k (latent states)
- \texttt{Aic} vector containing the values of the AIC of the LM model with each k (latent states)
- \texttt{call} command used to call the function
- \texttt{data} data frame given in input

Author(s)

Francesco Bartolucci, Silvia Pandolfi, Fulvia Pennoni, Alessio Farcomeni, Alessio Serafini
lmest

Estimate Latent Markov models

Description

Main function for estimating Latent Markov (LM) models for categorical responses.

Usage

lmest(responsesFormula = NULL, latentFormula = NULL,
      data, index, k = 1:4, start = 0,
      modSel = c("BIC", "AIC"), modBasic = 0,
      modManifest = c("LM", "FM"),
      paramLatent = c("multilogit", "difflogit"),
      weights = NULL, tol = 10^-8, maxit = 1000,
      out_se = FALSE, q = NULL, output = FALSE,
      parInit = list(piv = NULL, Pi = NULL, Psi = NULL,
                     Be = NULL, Ga = NULL, mu = NULL,
                     al = NULL, be = NULL, si = NULL,
                     rho = NULL, la = NULL, PI = NULL,
                     fixPsi = FALSE),
      fort = TRUE, seed = NULL)

Arguments

responsesFormula
  a symbolic description of the model to fit. A detailed description is given in the
  'Details' section
latentFormula
  a symbolic description of the model to fit. A detailed description is given in the
  'Details' section
data
  a data.frame in long format
index
  a character vector with two elements, the first indicating the name of the unit
  identifier, and the second the time occasions
k
  an integer vector specifying the number of latent states (default: 1:4)
start
  type of starting values (0 = deterministic, 1 = random, 2 = initial values in input)
modSel
  a string indicating the model selection criteria: "BIC" for Bayesian Information
  Criterion and "AIC" for Akaike Information Criterion
modBasic
  model on the transition probabilities (0 for time-heter., 1 for time-homog., from
  2 to (TT-1) partial homog. of that order)
modManifest
  model for manifest distribution ("LM" = Latent Markov with stationary transi-
  tion, "FM" = finite mixture)
paramLatent: type of parametrization for the transition probabilities ("multilogit" = standard multinomial logit for every row of the transition matrix, "difflogit" = multinomial logit based on the difference between two sets of parameters).

weights: an optional vector of frequencies of the available response configurations.

tol: tolerance level for convergence.

maxit: maximum number of iterations of the algorithm.

out_se: to compute the information matrix and standard errors (By default is set to FALSE).

q: number of support points for the AR(1) process (if modManifest = "FM").

output: to return additional output: PRED0, PRED1 for the LM model with covariates in the measurement model (LMmanifest-class) and V, PI, Piv, UL for the LM with covariates on the latent model (LMlatent-class).

parInit: list of initial model parameters when "start = 2". For the list of parameters look at LMBasic-class, LMlatent-class and LMmanifest-class.

fort: to use fortran routines when possible (By default is set to TRUE).

seed: an integer value with the random number generator state.

Details:

The function lmest is a general function for estimating LM models for categorical responses. The function requires data in long format and two additional columns indicating the unit identifier and the time occasions.

Covariates are allowed on manifest distribution (measurement model) or on the initial and transition probabilities (latent model). Two different formulas are employed to specify the different LM models, responsesFormula and latentFormula:

- **responsesFormula** is used to specify the measurement model:
  - responsesFormula = x1 + x2 ~ NULL
    the LM model without covariates and two responses (x1 and x2) is specified;
  - responsesFormula = NULL
    all the columns in the data except the "id" and "time" columns are used to estimate the LM model without covariates;
  - responsesFormula = x1 + x2 ~ x3 + x4
    the LM model with two responses (x1 and x2) and two covariates (x3 and x4) in the measurement model is specified;

- **latentFormula** is used to specify the LM model with covariates in the latent model:
  - responsesFormula = x1 + x2 ~ NULL
    latentFormula = ~ x3 + x4 | x5 + x6
    the LM model with two responses (x1 and x2) and two covariates affecting the initial probabilities (x3 and x4) and other two affecting the transition probabilities (x5 and x6) is specified;
  - responsesFormula = x1 + x2 ~ NULL
    latentFormula = ~ 1 | x3 + x4
    (or latentFormula = ~ NULL | x3 + x4)
    the covariates affect only the transition probabilities and an intercept is specified for the initial probabilities;
- \( \text{responsesFormula} = x_1 + x_2 \sim \text{NULL} \)
  \( \text{latentFormula} = \sim x_3 + x_4 \)
  the LM model with two covariates \( (x_3 \text{ and } x_4) \) affecting both the initial and transition probabilities is specified;

- \( \text{responsesFormula} = x_1 + x_2 \sim \text{NULL} \)
  \( \text{latentFormula} = \sim \text{NULL} | \text{NULL} \)
  \( \text{or} \ \text{latentFormula} = \sim 1 | 1 \)
  the LM model with only an intercept on the initial and transition probabilities is specified.

The function also allows us to deal with missing responses, including drop-out and non-monotonic missingness, under the missing-at-random assumption. Missing values for the covariates are not allowed. The LM model with individual covariates in the measurement model is estimated only for complete univariate responses.

For continuous outcomes see the function \texttt{lmestCont}.

Value

Returns an object of class `'LMbasic'` for the model without covariates (see \texttt{LMbasic-class}), or an object of class `'LMmanifest'` for the model with covariates on the manifest model (see \texttt{LMmanifest-class}), or an object of class `'LMlatent'` for the model with covariates on the latent model (see \texttt{LMlatent-class}).

Author(s)

Francesco Bartolucci, Silvia Pandolfi, Fulvia Pennoni, Alessio Farcomeni, Alessio Serafini

References


Examples

```r
### Basic LM model

data("data_SRHS_long")
SRHS <- data_SRHS_long[1:2400,]
# Categories rescaled to vary from 1 ("poor") to 5 ("excellent")
SRHS$srhs <- 5 - SRHS$srhs

out <- lmest(responsesFormula = srhs ~ NULL,
             index = c("id","t"),
             data = SRHS,
             k = 3,
             start = 1,
             modBasic = 1,
```
```r
## Basic LM model with model selection using BIC
out1 <- lmest(responsesFormula = srhs ~ NULL,
              index = c("id","t"),
              data = SRHS,
              k = 1:5,
              tol = 1e-8,
              modBasic = 1,
              seed = 123)
out1
out1$Bic

# Basic LM model with model selection using AIC
out2 <- lmest(responsesFormula = srhs ~ NULL,
              index = c("id","t"),
              data = SRHS,
              k = 1:5,
              tol = 1e-8,
              modBasic = 1,
              modSel = "AIC",
              seed = 123)
out2
out2$Aic

# Criminal data
data(data_criminal_sim)
data_criminal_sim = data.frame(data_criminal_sim)
responsesFormula <- lmestFormula(data = data_criminal_sim,
                                  response = "y")$responsesFormula
out3 <- lmest(responsesFormula = responsesFormula,
              index = c("id","time"),
              data = data_criminal_sim,
              k = 1:7,modBasic = 1,tol = 10^-4)
out3

# Example of drug consumption data
data("data_drug")
long <- data_drug[, -6] - 1
```
long <- data.frame(id = 1:nrow(long), long)
long <- reshape(long, direction = "long",
  idvar = "id",
  varying = list(2:ncol(long)))

out4 <- lmest(index = c("id","time"), k = 3, data = long,
  weights = data_drug[,6], modBasic = 1)

out4
summary(out4)

### LM model with covariates in the latent model
# Covariates: gender, race, educational level (2 columns), age and age^2

out5 <- lmest(responsesFormula = srhs ~ NULL,
  latentFormula = ~
    I(gender - 1) +
    I( 0 + (race == 2) + (race == 3)) +
    I(0 + (education == 4)) +
    I(0 + (education == 5)) +
    I(age - 50) + I((age-50)^2/100),
  index = c("id","t"),
  data = SRHS,
  k = 2,
  paramLatent = "multilogit",
  start = 0)

out5
summary(out5)

### LM model with the above covariates in the measurement model

out6 <- lmest(responsesFormula = srhs ~ -1 +
  I(gender - 1) +
  I( 0 + (race == 2) + (race == 3)) +
  I(0 + (education == 4)) +
  I(0 + (education == 5)) + I(age - 50) +
  I((age-50)^2/100),
  index = c("id","t"),
  data = SRHS,
  k = 2,
  modManifest = "LM",
  out_se = TRUE,
  tol = 1e-8,
  start = 1,
  seed = 123)

out6
summary(out6)

## End(Not run)
l mestCont

Estimate Latent Markov models for continuous responses

Description

Main function for estimating Latent Markov (LM) models for continuous responses.

Usage

l mestCont(responsesFormula = NULL, latentFormula = NULL,
  data, index, k = 1:4, start = 0,
  modSel = c("BIC", "AIC"), modBasic = 0,
  paramLatent = c("multilogit", "difflogit"),
  weights = NULL, tol = 10^-10,
  maxit = 5000, out_se = FALSE, output = FALSE,
  parInit = list(piv = NULL, Pi = NULL,
                 Mu = NULL, Si = NULL,
                 Be = NULL, Ga = NULL),
  fort = TRUE, seed = NULL)

Arguments

responsesFormula
  a symbolic description of the model to be fitted. A detailed description is given in the ‘Details’ section

latentFormula
  a symbolic description of the model to be fitted. A detailed description is given in the ‘Details’ section

data
  a data.frame in long format

index
  a character vector with two elements, the first indicating the name of the unit identifier, and the second the time occasions

k
  an integer vector specifying the number of latent states (default: 1:4)

start
  type of starting values (0 = deterministic, 1 = random, 2 = initial values in input)

modSel
  a string indicating the model selection criteria: "BIC" for Bayesian Information Criterion and "AIC" for Akaike Information Criterion Criterion

modBasic
  model on the transition probabilities (0 for time-heter., 1 for time-homog., from 2 to (TT-1) partial homog. of that order)

paramLatent
  type of parametrization for the transition probabilities ("multilogit" = standard multinomial logit for every row of the transition matrix, "difflogit" = multinomial logit based on the difference between two sets of parameters)

weights
  an optional vector of frequencies of the available response configurations

tol
  tolerance level for convergence

maxit
  maximum number of iterations of the algorithm

out_se
  to compute the information matrix and standard errors (By default is set to FALSE)
The function \texttt{lmestCont} is a general function for estimating LM models for continuous responses. The function requires data in long format and two additional columns indicating the unit identifier and the time occasions.

Covariates are allowed on the initial and transition probabilities (latent model). Two different formulas are employed to specify the different LM models, \texttt{responsesFormula} and \texttt{latentFormula}:

- \texttt{responsesFormula} is used to specify the measurement model:
  - \texttt{responsesFormula = x1 + x2 ~ NULL}
    the LM model without covariates and two responses (x1 and x2) is specified;
  - \texttt{responsesFormula = NULL}
    all the columns in the data except the "id" and "time" columns are used to estimate the LM model without covariates;

- \texttt{latentFormula} is used to specify the LM model with covariates in the latent model:
  - \texttt{responsesFormula = x1 + x2 ~ NULL}
    \texttt{latentFormula = ~ x3 + x4 | x5 + x6}
    the LM model with two responses (x1 and x2) and two covariates affecting the initial probabilities (x3 and x4) and other two affecting the transition probabilities (x5 and x6) is specified;
  - \texttt{responsesFormula = x1 + x2 ~ NULL}
    \texttt{latentFormula = ~ 1 | x3 + x4}
    (or \texttt{latentFormula = ~ NULL | x3 + x4})
    the covariates affect only the transition probabilities and an intercept is specified for the initial probabilities;
  - \texttt{responsesFormula = x1 + x2 ~ NULL}
    \texttt{latentFormula = ~ x3 + x4}
    the LM model with two covariates (x3 and x4) affecting both the initial and transition probabilities is specified;
  - \texttt{responsesFormula = x1 + x2 ~ NULL}
    \texttt{latentFormula = ~ NULL | NULL}
    (or \texttt{latentFormula = ~ 1 | 1})
    the LM model with only an intercept on the initial and transition probabilities is specified.

The function also allows us to deal with missing responses using the \texttt{mix} package for imputing the missing values. Missing values for the covariates are not allowed.

For categorical outcomes see the function \texttt{lmest}. 

\begin{itemize}
  \item \texttt{output} to return additional output (V, PI, Piv, Ul) (LMLatentcont-class)
  \item \texttt{parInit} list of initial model parameters when "start = 2". For the list of parameters look at LMBasiccont-class and LMLatentcont-class
  \item \texttt{fort} to use fortran routines when possible (By default is set to TRUE)
  \item \texttt{seed} an integer value with the random number generator state
\end{itemize}
Value

Returns an object of class 'LMbasiccont' for the model without covariates (see \texttt{LMbasiccont-class}),
or an object of class 'LMlatentcont' for the model with covariates on the latent model (see \texttt{LMlatentcont-class}).

Author(s)

Francesco Bartolucci, Silvia Pandolfi, Fulvia Pennoni, Alessio Farcomeni, Alessio Serafini

References


See Also

\texttt{lmestFormula}

Examples

```r
## Not run:
require(mmm)
data(multiLongGaussian)
t <- rep(1:4, times = max(multiLongGaussian$ID))
multiLongGaussian <- data.frame(t = t, multiLongGaussian)

# Basic LM model
out <- lmestCont(responsesFormula = resp1 + resp2 ~ NULL,
index = c("ID", "t"),
data = multiLongGaussian,
k = 3,
modBasic=1,
tol=10^-5)

out
summary(out)

# Basic LM model with model selection using BIC
out1 <- lmestCont(responsesFormula = resp1 + resp2 ~ NULL,
index = c("ID", "t"),
data = multiLongGaussian,
k = 1:5,
modBasic=1,
tol=10^-5)
```

out1
out1$Bic

# Basic LM model with model selection using AIC
out2 <- lmestCont(responsesFormula = resp1 + resp2 ~ NULL,
                   index = c("ID", "t"),
                   data = multiLongGaussian,
                   k = 1:5,
                   modBasic=1,
                   modSel = "AIC",
                   tol=10^-5)
out2
out2$Aic

# LM model with covariates in the latent model
out3 <- lmestCont(responsesFormula = resp1 + resp2 ~ NULL,
                   latentFormula = ~ X + time,
                   index = c("ID", "t"),
                   data = multiLongGaussian,
                   k = 3,
                   output=TRUE)
out3
summary(out3)

out4 <- lmestCont(responsesFormula = resp1 + resp2 ~ NULL,
                   latentFormula = ~ X + time | X + time,
                   index = c("ID", "t"),
                   data = multiLongGaussian,
                   k = 3,
                   output=TRUE)
out4
summary(out4)

## End(Not run)

---

**lmestData**

*Data for L. Mest functions*

**Description**

An object of class `lmestData` containing data in long format, some necessary information on the data structure and objects for the estimation functions.
Usage

```r
lmestData(data, id = NULL, time = NULL,
idAsFactor = TRUE, timeAsFactor = TRUE,
responsesFormula = NULL, latentFormula = NULL,
na.rm = FALSE, check.names = FALSE)
```

Arguments

data a matrix or data frame in long format of observation

id a numeric vector or a string indicating the column with the unit identifier. If
NULL, the first column is considered

time a numeric vector or a string indicating the column with the time occasions. If
NULL, the second column is considered, and if the id is not NULL, the function
will automatically add the column with the time occasions

idAsFactor a logical value indicating whether or not the column with the ids is converted to
a factor. (By default is set to TRUE)
timeAsFactor a logical value indicating whether or not the column with the time occasions is
converted in a factor. (By default is set to TRUE)

responsesFormula A detailed description is given in `lmest,lmestCont`

latentFormula A detailed description is given in `lmest,lmestCont`

na.rm a logical value indicating whether or not the observation with at least a missing
value is removed (By default is set to FALSE)

check.names a logical value indicating whether or not the names of the variables are syntacti-
cally valid, and adjusted if necessary. (By default is set to FALSE)

Value

An object of class 'lmestData' with the following objects:

data a data.frame object to use in the estimation functions

id a integer vector with the unit identifier

time a integer vector with the time occasions

n the number of observation

TT an integer value indicating number of time occasions

d an integer value indicating the number of variables (columns except id and
time)

Y the response variables

Xmanifest the variables affecting the measurement model if specified in responsesFormula

Xinitial the variables affecting the initial probabilities of the latent model if specified in
latentFormula

Xtrans the variables affecting the transition probabilities of the latent model if specified
in latentFormula
lmestData

Author(s)
Francesco Bartolucci, Silvia Pandolfi, Fulvia Pennoni, Alessio Farcomeni, Alessio Serafini

Examples

```r
require(mmm)
data(multiLongGaussian)
str(multiLongGaussian)

## Data with continuous responses

dt <- lmestData(data = multiLongGaussian, id = "ID")
str(dt)

## Summary of each variable and for each time
summary(dt)

## Summary of each variable
summary(dt, type = "cross")

## Summary of each variable by time
summary(dt, type = "year")

plot(dt)
plot(dt, typePlot = "sh")

#######################
## Not run:
data("data_criminal_sim")
dt1 <- lmestData(data = data_criminal_sim, id = "id", time = "time")
str(dt1)

summary(dt1, varType = rep("d", ncol(dt1$Y)))

dt2 <- lmestData(data = data_criminal_sim, id = "id", time = "time",
responsesFormula = y1 + y2 - y3, latentFormula = ~ y7 + y8 | y9 + y10)
str(dt2)

## Summary for responses, covariates on the manifest distribution,
## covariates on initial and transition probabilities
summary(dt2, dataSummary = "responses", varType = rep("d", ncol(dt2$Y)))
summary(dt2, dataSummary = "manifest", varType = rep("d", ncol(dt2$Xmanifest)))
summary(dt2, dataSummary = "initial", varType = rep("d", ncol(dt2$Xinitial)))
summary(dt2, dataSummary = "transition", varType = rep("d", ncol(dt2$Xtrans)))
```
lmestDecoding

Perform local and global decoding

Description

Function that performs local and global decoding (Viterbi algorithm) from the output of lmest, lmestCont, and lmestMixed.

Usage

lmestDecoding(est, sequence = NULL, fort = TRUE, ...)

## S3 method for class 'LMbasic'
# S3 method for class 'LMbasic'

## S3 method for class 'LMmanifest'
# S3 method for class 'LMmanifest'

## S3 method for class 'LMlatent'
# S3 method for class 'LMlatent'

## S3 method for class 'LMbasiccont'
# S3 method for class 'LMbasiccont'

## S3 method for class 'LMmixed'
# S3 method for class 'LMmixed'

lmestDecoding(est, sequence = NULL, fort = TRUE, ...)

Arguments

est an object obtained from a call to lmest, lmestCont, and lmestMixed
sequence an integer vector indicating the units for the decoding. If NULL the whole observations are considered. (By default is set to NULL)
fort to use fortran routines when possible (By default is set to TRUE)
... further arguments

Value

U1 matrix of local decoded states corresponding to each row of Y
Ug matrix of global decoded states corresponding to each row of Y

Author(s)

Francesco Bartolucci, Silvia Pandolfi, Fulvia Pennoni, Alessio Farcomeni, Alessio Serafini
References


Examples

# Decoding for basic LM model

data("data_drug")
long <- data_drug[,6]-1
long <- data.frame(id = 1:nrow(long),long)
long <- reshape(long,direction = "long",
idvar = "id",
 varying = list(2:ncol(long)))
est <- lmest(index = c("id","time"),k = 3, data = long,
weights = data_drug[,6], modBasic = 1)

# Decoding for a single sequence
out1 <- lmestDecoding(est, sequence = 1)
out2 <- lmestDecoding(est, sequence = 1:4)

# Decoding for all sequences
out3 <- lmestDecoding(est)

### Not run:
# Decoding for LM model with covariates on the initial and transition probabilities

data("data_SRHS_long")
SRHS <- data_SRHS_long[1:2400,]
# Categories rescaled to vary from 1 ("poor") to 5 ("excellent")
SRHS$srh <- 5 - SRHS$srh

est2 <- lmest(responsesFormula = srhs ~ NULL,
 latentFormula = ~
I(gender - 1) +
I(0 + (race == 2) + (race == 3)) +
I(0 + (education == 4)) +
I(0 + (education == 5)) +
I(age - 50) + I((age-50)^2/100),
index = c("id","t"),
data = SRHS,
k = 2,
# Decoding for a single sequence
out3 <- lmestDecoding(est2, sequence = 1)

# Decoding for the first three sequences
out4 <- lmestDecoding(est2, sequence = 1:3)

# Decoding for all sequences
out5 <- lmestDecoding(est2)

## End(Not run)

---

**lmestFormula**

Formulas for LMest functions

### Description
Building formulas for `lmest, lmestCont, lmestMixed,` and `lmestMc`.

### Usage

```r
lmestFormula(data, 
             response, manifest = NULL, 
             LatentInitial = NULL, LatentTransition = NULL, 
             AddInterceptManifest = FALSE, 
             AddInterceptInitial = TRUE, 
             AddInterceptTransition = TRUE, responseStart = TRUE, 
             manifestStart = TRUE, LatentInitialStart = TRUE, 
             LatentTransitionStart = TRUE)
```

### Arguments
- **data** a data.frame or a matrix of data
- **response** a numeric or character vector indicating the column indices or the names for the response variables
- **manifest** a numeric or character vector indicating the column indices or the names for the covariates affecting the measurement model
- **LatentInitial** a numeric or character vector indicating the column indices or the names for the covariates affecting the initial probabilities
- **LatentTransition** a numeric or character vector indicating the column indices or the names for the covariates affecting the transition probabilities
lmestFormula

AddInterceptManifest
a logical value indicating whether the intercept is added to the covariates affecting the measurement model

AddInterceptInitial
a logical value indicating whether the intercept is added to covariates affecting the initial probabilities

AddInterceptTransition
a logical value indicating whether the intercept is added to covariates affecting the transition probabilities

responseStart
a logical value indicating whether the response variables names start with response argument

manifestStart
a logical value indicating whether the covariates names start with manifest argument

LatentInitialStart
a logical value indicating whether the covariates names start with LatentInitial argument

LatentTransitionStart
a logical value indicating whether the covariates names start with LatentTransition argument

Details
Generates formulas for responsesFormula and latentFormula to use in lmest, lmestCont, lmestMixed, and lmestMc.

Value
Returns a list with responsesFormula and latentFormula objects.

Author(s)
Francesco Bartolucci, Silvia Pandolfi, Fulvia Pennoni, Alessio Farcomeni, Alessio Serafini

Examples

data(data_SRHS_long)
names(data_SRHS_long)
# Formula with response srhs and covariates for both initial and transition
# gender, race, educational, age.

## With intercept
fm <- lmestFormula(data = data_SRHS_long,
                   response = "srhs",
fmm

## Without intercept
fm <- lmestFormula(data = data_SRHS_long,
response = "srhs",
LatentInitial = 3:6, LatentTransition = 3:6,
AddInterceptInitial = FALSE, AddInterceptTransition = FALSE)

fm

#####

data(data_criminal_sim)
str(data_criminal_sim)

# Formula with only the responses from y1 to y10
fm <- lme4Formula(data = data_criminal_sim, response = "y")$responsesFormula
fm

# Formula with only the responses from y1 to y10 and intercept for manifest
fm <- lme4Formula(data = data_criminal_sim, 
    response = "y", AddInterceptManifest = TRUE)$responsesFormula
fm

#####

require(mmm)
data(multiLongGaussian)
names(multiLongGaussian)

# Formula with response resp1, resp2, covariate for manifest,
# X covariates for initail and time covariate for transition
fm <- lme4Formula(data = multiLongGaussian, 
    response = c("resp"),
    LatentInitial = "X", LatentTransition = "time")
fm

## Wrong model because two variable start with X.
## Check the starts arguments. For the right model:

fm <- lme4Formula(data = multiLongGaussian, 
    response = c("resp"),
    LatentInitial = "X", LatentTransition = "time",
    LatentInitialStart = FALSE)
fm

## or
fm <- lme4Formula(data = multiLongGaussian, 
    response = c("resp"),
    LatentInitial = 4, LatentTransition = "time",
    LatentInitialStart = FALSE)
fm

## Not run:
data(data_criminal_sim)
data_criminal_sim <- data.frame(data_criminal_sim)
# Estimate mixed LM model for females

```r
responsesFormula <- lmestFormula(data = data_criminal_sim,
                                response = "y")$responsesFormula

out <- lmest(responsesFormula = responsesFormula,
             index = c("id","time"),
             data = data_criminal_sim,
             k = 2)
```

## End(Not run)

---

**lmestMc**

*Estimate Markov Chain models*

**Description**

Main function for estimating Markov Chain (MC) models for categorical responses with or without covariates.

**Usage**

```r
lmestMc(responsesFormula = NULL,
        data, index, start = 0,
        modBasic = 0, weights = NULL,
        tol = 10^-8, maxit = 1000,
        out_se = FALSE, output = FALSE, fort = TRUE, seed = NULL)
```

**Arguments**

- **responsesFormula**
  - a symbolic description of the model to fit. A detailed description is given in the 'Details' section
- **data**
  - a data.frame in long format
- **index**
  - a character vector with two elements, the first indicating the name of the unit identifier, and the second the time occasions
- **start**
  - type of starting values (0 = deterministic, 1 = random, 2 = initial values in input)
- **modBasic**
  - model on the transition probabilities (0 for time-heter., 1 for time-homog., from 2 to (TT-1) partial homog. of that order)
- **weights**
  - an optional vector of frequencies of the available response configurations
- **tol**
  - tolerance level for convergence
- **maxit**
  - maximum number of iterations of the algorithm
- **out_se**
  - to compute the information matrix and standard errors (FALSE is the default option)
- **output**
  - to return additional output (PI,Piv) (**MCcov-class**)
- **fort**
  - to use fortran routines when possible (By default is set to TRUE)
- **seed**
  - An integer value with the random number generator state.
Details

The function `lmestMc` estimates the basic MC model and the MC model with covariates for categorical responses. The function requires data in long format and two additional column indicating the unit identifier and the time occasions.

`responsesFormula` is used to specify the basic MC models and the model with covariates:

- `responsesFormula = x1 + x2 ~ NULL`  
  the MC model without covariates and two responses (`x1` and `x2`) is specified;
- `responsesFormula = NULL`  
  all the columns in the data except the "id" and "time" columns are used to estimate MC without covariates;
- `responsesFormula = x1 ~ x2 + x3 | x4 + x5`  
  the MC model with one response (`x1`), two covariates affecting the initial probabilities (`x2` and `x3`) and other two different covariates affecting the transition probabilities (`x4` and `x5`) is specified;
- `responsesFormula = x1 ~ x2 + x3`  
  the MC model with one response (`x1`) and two covariates (`x2` and `x3`) affecting both the initial and transition probabilities is specified.

Missing responses are not allowed.

Value

Returns an object of class 'MCbasic' for the basic model without covariates (see `MCbasic-class`), or an object of class 'MCcov' for the model with covariates (see `MCcov-class`).

Author(s)

Francesco Bartolucci, Silvia Pandolfi, Fulvia Pennoni, Alessio Farcomeni, Alessio Serafini

References


Examples

```r
## Not run:
# Basic Markov Chain model
data("RLMSlong")

# Categories rescaled from 1 "absolutely unsatisfied" to 5 "absolutely satisfied"
RLMSlong$value <- 5 - RLMSlong$value

out <- lmestMc(responsesFormula = value ~ NULL,
```
index = c("id","time"),
modBasic = 1,
data = RLMSlong)

out
summary(out)

# Example of drug consumption data
data("data_drug")
long <- data_drug[,,-6]
long <- data.frame(id = 1:nrow(long),long)
long <- reshape(long,direction = "long",
               idvar = "id",
               varying = list(2:ncol(long)))

out1 <- lmestMc(index = c("id","time"), data = long,
               weights = data_drug[,6], modBasic = 1, out_se = TRUE)
out1

### MC model with covariates
### Covariates: gender, race, educational level (2 columns), age and age^2
data("data_SRHS_long")
SRHS <- data_SRHS_long[1:2400,]

# Categories of the responses rescaled from 1 “poor” to 5 “excellent"
SRHS$srhs <- 5 - SRHS$srhs

out2 <- lmestMc(responsesFormula = srhs ~
               I( 0 + (race==2) + (race == 3)) +
               I(0 + (education == 4)) +
               I(0 + (education == 5)) +
               I(age - 50) +
               I((age-50)^2/100),
               index = c("id","t"),
data = SRHS)

out2
summary(out2)

# Criminal data
data(data_criminal_sim)
data_criminal_sim = data.frame(data_criminal_sim)

out3 <- lmestMc(responsesFormula = y5~sex,
               index = c("id","time"), data = data_criminal_sim, output = TRUE)
lmestMixed

Estimate mixed Latent Markov models

Description
Main function for estimating the mixed latent Markov (LM) models for categorical responses with discrete random effects in the latent model.

Usage

```r
lmestMixed(responsesFormula = NULL, 
            data, index, k1, k2, start = 0, 
            weights = NULL, tol = 10^-8, maxit = 1000, 
            out_se = FALSE, seed = NULL)
```

Arguments
- `responsesFormula`: a symbolic description of the model to fit. A detailed description is given in the 'Details' section
- `data`: a `data.frame` in long format
- `index`: a character vector with two elements, the first indicating the name of the unit identifier, and the second the time occasions
- `k1`: number of latent classes
- `k2`: number of latent states
- `start`: type of starting values (0 = deterministic, 1 = random, 2 = initial values in input)
- `weights`: an optional vector of frequencies of the available response configurations
- `tol`: tolerance level for convergence
- `maxit`: maximum number of iterations of the algorithm
- `out_se`: to compute the information matrix and standard errors (FALSE is the default option)
- `seed`: an integer value with the random number generator state

Details
The function `lmestMixed` estimates the mixed LM for categorical data. The function requires data in long format and two additional columns indicating the unit identifier and the time occasions. `responsesFormula` is used to specify the responses of the mixed LM model:
• responsesFormula = x1 + x2 ~ NULL
  the mixed LM model with two categorical responses (x1 and x2) is specified;
• responsesFormula = NULL
  all the columns in the data except the "id" and "time" columns are used to estimate the mixed LM.

Missing responses are not allowed.

Value

Returns an object of class 'LMmixed' (see LMmixed-class).

Author(s)

Francesco Bartolucci, Silvia Pandolfi, Fulvia Pennoni, Alessio Farcomeni, Alessio Serafini

References


Examples

```r
## Not run:
# Example based on criminal data

data(data_criminal_sim)
data_criminal_sim <- data.frame(data_criminal_sim)
# Estimate mixed LM model for females
responsesFormula <- lmestFormula(data = data_criminal_sim,
                                  response = "y")$responsesFormula

# fit mixed LM model only for females
out <- lmestMixed(responsesFormula = responsesFormula,
                  index = c("id","time"),
                  k1 = 2,
                  k2 = 2,
                  data = data_criminal_sim[data_criminal_sim$sex == 2,])
out
summary(out)

## End(Not run)
```
lmestSearch

Search for the global maximum of the log-likelihood

Description

Function that searches for the global maximum of the log-likelihood of different models and selects the optimal number of states.

Usage

```r
lmestSearch(responsesFormula = NULL, latentFormula = NULL, data, index, k, 
version = c("categorical", "continuous"), 
weights = NULL, nrep = 2, tol1 = 10^-5, 
tol2 = 10^-10, out.se = FALSE, seed = NULL, ...)
```

Arguments

- `responsesFormula` a symbolic description of the model to fit. A detailed description is given in the 'Details' section of `lmest`
- `latentFormula` a symbolic description of the model to fit. A detailed description is given in the 'Details' section of `lmest`
- `data` a data.frame in long format
- `index` a character vector with two elements, the first indicating the name of the unit identifier, and the second the time occasions
- `k` a vector of integer values for the number of latent states
- `weights` an optional vector of frequencies of the available response configurations
- `version` type of responses for the LM model: "categorical" and "continuous"
- `nrep` number of repetitions of each random initialization
- `tol1` tolerance level for checking convergence of the algorithm in the random initializations
- `tol2` tolerance level for checking convergence of the algorithm in the last deterministic initialization
- `out_se` to compute the information matrix and standard errors (FALSE is the default option)
- `seed` an integer value with the random number generator
- `...` additional arguments to be passed to functions `lmest` or `lmestCont`
Details

The function combines deterministic and random initializations strategy to reach the global maximum of the model log-likelihood. It uses one deterministic initialization (\texttt{start=0}) and a number of random initializations (\texttt{start=1}) proportional to the number of latent states. The tolerance level is set equal to $10^{-5}$. Starting from the best solution obtained in this way, a final run is performed (\texttt{start=2}) with a default tolerance level equal to $10^{-10}$.

Missing responses are allowed according to the model to be estimated.

Value

Returns an object of class \texttt{"LMsearch"} with the following components:

- \textbf{out.single} Output of every LM model estimated for each number of latent states given in input
- \textbf{Aic} Values the Akaike Information Criterion for each number of latent states given in input
- \textbf{Bic} Values of the Bayesian Information Criterion for each number of latent states given in input
- \textbf{lkv} Values of log-likelihood for each number of latent states given in input.

Author(s)

Francesco Bartolucci, Silvia Pandolfi, Fulvia Pennoni, Alessio Farcomeni, Alessio Serafini

References


Examples

```r
### Example with data on drug use in wide format

data("data_drug")
long <- data_drug[, -6]

# add labels referred to the identifier
long <- data.frame(id = 1:nrow(long), long)

# reshape data from the wide to the long format
long <- reshape(long, direction = "long",
               idvar = "id",
               varying = list(2:ncol(long)))
```
out <- lmestSearch(data = long, 
                  index = c("id","time"),
                  version = "categorical",
                  k = 1:3,
                  weights = data_drug[,6],
                  modBasic = 1,
                  seed = 123)

out
summary(out$out.single[[3]])

## Not run:
### Example with data on self rated health

# LM model with covariates in the measurement model

data("data_SRHS_long")
SRHS <- data_SRHS_long[1:1000,]

# Categories rescaled to vary from 1 ("poor") to 5 ("excellent")
SRHS$srhs <- 5 - SRHS$srhs

out1 <- lmestSearch(data = SRHS,
                    index = c("id","t"),
                    version = "categorical",
                    responsesFormula = srhs ~ -1 +
                        I(gender - 1) +
                        I( 0 + (race == 2) + (race == 3)) +
                        I(0 + (education == 4)) +
                        I(0 + (education == 5)) + I(age - 50) +
                        I((age-50)^2/100),
                        k = 1:2,
                        out_se = TRUE,
                        seed = 123)

summary(out1)
summary(out1$out.single[[2]])

## End(Not run)

---

**LMlatent-class**

An S3 class object created by `lmest` for Latent Markov (LM) model with covariates in the latent model.
Value

- `lk`: maximum log-likelihood
- `Be`: estimated array of the parameters affecting the logit for the initial probabilities
- `Ga`: estimated array of the parameters affecting the logit for the transition probabilities
- `Piv`: estimate of initial probability matrix. The first state is used as reference category when `param = "multilogit"`
- `PI`: estimate of transition probability matrices. State `u` is used as reference category when `paramLatent = "multilogit"`
- `Psi`: estimate of conditional response probabilities (mb x k x r)
- `np`: number of free parameters
- `k`: optimal number of latent states
- `aic`: value of the Akaike Information Criterion for model selection
- `bic`: value of the Bayesian Information Criterion for model selection
- `lkv`: log-likelihood trace at every step of the EM algorithm
- `n`: number of observations in the data
- `TT`: number of time occasions
- `paramLatent`: type of parametrization for the transition probabilities ("multilogit" = standard multinomial logit for every row of the transition matrix, "difflogit" = multinomial logit based on the difference between two sets of parameters)
- `V`: array containing the posterior distribution of the latent states for each response configuration and time occasion
- `Ul`: matrix containing the predicted sequence of latent states by the local decoding method
- `sePsi`: standard errors for the conditional response matrix
- `seBe`: standard errors for `Be`
- `seGa`: standard errors for `Ga`
- `Bic`: vector containing the values of the BIC for each `k`
- `Aic`: vector containing the values of the AIC for each `k`
- `call`: command used to call the function
- `data`: Data frame given in input

Author(s)

Francesco Bartolucci, Silvia Pandolfi, Fulvia Pennoni, Alessio Farcomeni, Alessio Serafini

See Also

lmest
LMLatentcont-class

Class 'LMLatentcont'

Description

An S3 class object created by \texttt{lmestCont} for the Latent Markov (LM) model for continuous responses in long format with covariates in the latent model.

Value

- \texttt{lk}: maximum log-likelihood
- \texttt{Be}: estimated array of the parameters affecting the logit for the initial probabilities
- \texttt{Ga}: estimated array of the parameters affecting the logit for the transition probabilities
- \texttt{Mu}: estimate of conditional means of the response variables
- \texttt{Si}: estimate of var-cov matrix common to all states
- \texttt{np}: number of free parameters
- \texttt{k}: optimal number of latent states
- \texttt{aic}: value of the Akaike Information Criterion for model selection
- \texttt{bic}: value of the Bayesian Information Criterion for model selection
- \texttt{lkv}: log-likelihood trace at every step
- \texttt{n}: number of observations in the data
- \texttt{TT}: number of time occasions
- \texttt{paramLatent}: type of parametrization for the transition probabilities ("multilogit" = standard multinomial logit for every row of the transition matrix, "difflogit" = multinomial logit based on the difference between two sets of parameters)
- \texttt{seMu}: standard errors for the conditional means
- \texttt{seSi}: standard errors for the var-cov matrix
- \texttt{seBe}: standard errors for \texttt{Be}
- \texttt{seGa}: standard errors for \texttt{Ga}
- \texttt{PI}: estimate of transition probability matrices
- \texttt{Piv}: estimate of initial probability matrix
- \texttt{Ul}: matrix containing the predicted sequence of latent states by the local decoding method
- \texttt{Bic}: vector containing the values of the BIC of the LM model with each \texttt{k} (latent states)
- \texttt{Aic}: vector containing the values of the AIC of the LM model with each \texttt{k} (latent states)
- \texttt{call}: command used to call the function
- \texttt{data}: data frame given in input
**LMmanifest-class**

**Author(s)**
Francesco Bartolucci, Silvia Pandolfi, Fulvia Pennoni, Alessio Farcomeni, Alessio Serafini

**See Also**
lmestCont

---

**LMmanifest-class**  
Class 'LMmanifest'

**Description**
An S3 class object created by lmest for Latent Markov (LM) model with covariates in the measurement model.

**Value**
- **mu**: vector of cut-points
- **al**: support points for the latent states
- **be**: estimate of the vector of regression parameters
- **si**: sigma of the AR(1) process (mod = "FM")
- **rho**: parameter vector for AR(1) process (mod = "FM")
- **la**: vector of initial probabilities
- **PI**: transition matrix
- **lk**: maximum log-likelihood
- **np**: number of parameters
- **k**: optimal number of latent states
- **aic**: value of the Akaike Information Criterion
- **bic**: value of Bayesian Information Criterion
- **n**: number of observations in the data
- **TT**: number of time occasions
- **modManifest**: for LM model with covariates on the manifest model: "LM" = Latent Markov with stationary transition, "FM" = finite mixture model where a mixture of AR(1) processes is estimated with common variance and specific correlation coefficients
- **sebe**: standard errors for the regression parameters be
- **selrho**: standard errors for logit type transformation of rho
- **J1**: information matrix
- **PRED0**: prediction of latent state
- **PRED1**: prediction of the overall latent effect
- **Bic**: vector containing the values of the BIC for each k
- **Aic**: vector containing the values of the AIC for each k
- **call**: command used to call the function
- **data**: data frame given in input
LMmixed-class

Author(s)
Francesco Bartolucci, Silvia Pandolfi, Fulvia Pennoni, Alessio Farcomeni, Alessio Serafini

See Also
lmest

LMmixed-class  Class 'LMmixed'

Description
An S3 class object created by lmestMixed for the mixed latent Markov (LM) models for categorical data in long format.

Value
- la: estimate of the mass probability vector (distribution of the random effects)
- Piv: estimate of initial probabilities
- Pi: estimate of transition probability matrices
- Psi: estimate of conditional response probabilities
- lk: maximum log-likelihood
- W: posterior probabilities of the random effect
- np: number of free parameters
- k1: number of support points (latent classes) of the latent variable defining the unobserved clusters
- k2: number of support points (latent states) of the latent variable defining the first-order Markov process
- bic: value of the Akaike Information Criterion for model selection
- aic: value of the Akaike Information Criterion for model selection
- n: number of observations in the data
- TT: number of time occasions
- sela: standard errors for la
- sePiv: estimate of initial probability matrix
- sePi: standard errors for the transition probabilities
- sePsi: standard errors for the conditional response matrix
- call: command used to call the function
- data: the input data

Author(s)
Francesco Bartolucci, Silvia Pandolfi, Fulvia Pennoni, Alessio Farcomeni, Alessio Serafini
long2matrices

From data in the long format to data in array format

Description
Function that transforms data in the long format to data in array format.

Usage
long2matrices(id, time = NULL, X = NULL, Y)

Arguments
id vector of subjects id
time vector of time occasions
X matrix of covariates in long format
Y matrix of responses in long format

Value
XX array of covariates (n x TT x nc)
YY array of responses (n x TT x r)

Author(s)
Francesco Bartolucci, Silvia Pandolfi, University of Perugia (IT), http://www.stat.unipg.it/bartolucci

Examples
# Example based on SRHS data

# load SRHS data
data(data_SRHS_long)
dataSRHS <- data_SRHS_long[1:1600,]
head(dataSRHS)
X <- cbind(dataSRHS$gender - 1, dataSRHS$race == 2 | dataSRHS$race == 3,
dataSRHS$education == 4, dataSRHS$education == 5, dataSRHS$age - 50,
(dataSRHS$age - 50)^2/100)
Y <- dataSRHS$srhs
res <- long2matrices(dataSRHS$id, X = X, Y = Y)
long2wide  From data in the long format to data in the wide format

Description
Function that transforms data in the long format to data in the wide format.

Usage
long2wide(data, nameid, namet, colx, coly, aggr = T, full = 999)

Arguments
- data: matrix of data
- nameid: name of the id column
- namet: name of the t column
- colx: vector of the names of the columns of the covariates
- coly: vector of the names of the columns of the responses
- aggr: if wide aggregated format is required
- full: number to use for missing data

Value
- listid: list of id for every unit
- listt: list of the time occasions
- data_wide: data in wide format
- XX: array of the covariates
- YY: array of the responses
- freq: vector of the corresponding frequencies

Author(s)
Francesco Bartolucci, Silvia Pandolfi, University of Perugia (IT), http://www.stat.unipg.it/bartolucci

Examples
# Example based on criminal data
# load criminal data
data(data_criminal_sim)
# consider only the first 1000 records to shorten time
out <- long2wide(data_criminal_sim[1:1000,], "id", "time", "sex", c("y1","y2","y3","y4","y5","y6","y7","y8","y9","y10"), aggr = TRUE, full = 999)
matrices2long          From data in array format to data in long format

Description

Function to convert data with array format in data with long format.

Usage

matrices2long(Y, X1 = NULL, X2 = NULL)

Arguments

Y    array of responses (n x TT x r)
X1   array of covariates (n x TT x nc1)
X2   array of covariates (n x TT x nc2)

Details

Y, X1 and X2 must have the same number of observations.

Value

Returns a data.frame with data in long format. The first column indicates the name of the unit identifier, and the second column indicates the time occasions.

Author(s)

Francesco Bartolucci, Silvia Pandolfi, Fulvia Pennoni, Alessio Farcomeni, Alessio Serafini

Examples

### Example with data on self rated health

data(data_SRHS_long)
SRHS <- data_SRHS_long[1:1600,]

# Covariates
X <- cbind(SRHS$gender-1,
           SRHS$race == 2 | SRHS$race == 3,
           SRHS$education == 4,
           SRHS$education == 5,
           SRHS$age-50,
           (SRHS$age-50)^2/100)

# Responses
Y <- SRHS$srhs

res <- long2matrices(SRHS$id, X = X, Y = Y)

long <- matrices2long(Y = res$YY, X1 = res$XX)

---

**MCbasic-class**

*Class 'MCbasic'*

---

**Description**

An S3 class object created by `lmestMc` function for the Markov chain (MC) model without covariates.

**Value**

- **lk**: maximum log-likelihood
- **piv**: estimate of initial probability vector
- **Pi**: estimate of transition probability matrices
- **np**: number of free parameters
- **aic**: value of the Akaike Information Criterion for model selection
- **bic**: value of the Bayesian Information Criterion for model selection
- **Fy**: estimated marginal distribution of the response variable ats each time occasion
- **n**: number of observations in the data
- **TT**: number of time occasions
- **modBasic**: model on the transition probabilities: default 0 for time-heterogeneous transition matrices, 1 for time-homogeneous transition matrices, 2 for partial time homogeneity based on two transition matrices one from 2 to (TT-1) and the other for TT
- **sepiv**: standard errors for the initial probabilities
- **sePi**: standard errors for the transition probabilities
- **call**: command used to call the function
- **data**: data frame given in input

**Author(s)**

Francesco Bartolucci, Silvia Pandolfi, Fulvia Pennoni, Alessio Farcomeni, Alessio Serafini

**See Also**

*lmestMc*
**MCcov-class**

*Class 'MCcov'*

**Description**

An S3 class object created by `lmestMc` function for Markov chain (MC) model for categorical responses in long format with covariates.

**Value**

- `lk` maximum log-likelihood
- `Be` estimated array of the parameters affecting the logit for the initial probabilities
- `Ga` estimated array of the parameters affecting the logit for the transition probabilities
- `np` number of free parameters
- `aic` value of the Akaike Information Criterion (AIC) for model selection
- `bic` value of the Bayesian Information Criterion (BIC) for model selection
- `n` number of observations in the data
- `TT` number of time occasions
- `seBe` standard errors for `Be`
- `seGa` standard errors for `Ga`
- `Piv` estimate of initial probability matrix
- `PI` estimate of transition probability matrices
- `call` command used to call the function
- `data` data frame given in input

**Author(s)**

Francesco Bartolucci, Silvia Pandolfi, Fulvia Pennoni, Alessio Farcomeni, Alessio Serafini

**See Also**

`lmestMc`
Description

Given the output, it is written in a readable form

Usage

```r
## S3 method for class 'LMbasic'
print(x, ...)
## S3 method for class 'LMbasiccont'
print(x, ...)
## S3 method for class 'LMLatent'
print(x, ...)
## S3 method for class 'LMLatentcont'
print(x, ...)
## S3 method for class 'LMmanifest'
print(x, ...)
## S3 method for class 'LMmixed'
print(x, ...)
## S3 method for class 'MCbasic'
print(x, ...)
## S3 method for class 'MCcov'
print(x, ...)
## S3 method for class 'LMsearch'
print(x, modSel = "BIC", ...)
```

Arguments

- `x` output from `lmest,lmestCont,lmestMixed`, and `lmestMc`
- `modSel` a string indicating the model selection criteria: "BIC" (default) for Bayesian Information Criterion and "AIC" for Akaike Information Criterion Criterion
- `...` further arguments passed to or from other methods

Author(s)

Francesco Bartolucci, Silvia Pandolfi, Fulvia Pennoni, Alessio Farcomeni, Alessio Serafini
Description

Longitudinal dataset deriving from the Russia Longitudinal Monitoring Survey (RLMS) about job satisfaction measured by an ordinal variable at seven different occasions with five categories, 1 for “absolutely satisfied”, 2 for “mostly satisfied”, 3 for “neutral”, 4 for “not very satisfied”, and 5 for “absolutely unsatisfied”.

Usage

data(RLMSdat)

Format

A data frame with 1718 observations on the following 7 variables.

- IKSJQ reported job satisfaction at the 1st occasion
- IKSJR reported job satisfaction at the 2nd occasion
- IKSJS reported job satisfaction at the 3rd occasion
- IKSJT reported job satisfaction at the 4th occasion
- IKSJU reported job satisfaction at the 5th occasion
- IKSJV reported job satisfaction at the 6th occasion
- IKSJW reported job satisfaction at the 7th occasion

Source


References

Russia Longitudinal Monitoring survey, RLMS-HSE, conducted by Higher School of Economics and ZAO "Demoscope" together with Carolina Population Center, University of North Carolina at Chapel Hill and the Institute of Sociology RAS

Examples

data(RLMSdat)
Description

Longitudinal dataset in long format deriving from the Russia Longitudinal Monitoring Survey (RLMS) about job satisfaction measured by an ordinal variable at seven different occasions with five categories, 1 for “absolutely satisfied”, 2 for “mostly satisfied”, 3 for “neutral”, 4 for “not very satisfied”, and 5 for “absolutely unsatisfied”.

Usage

data(RLMSlong)

Format

A data frame with 1718 observations on the following 7 variables.

time occasion of observation.
id subject id.
rlms see RLMSdat.
value reported job satisfaction at different time occasions coded as 1 for “absolutely satisfied”, 2 for “mostly satisfied”, 3 for “neutral”, 4 for “not very satisfied”, 5 for “absolutely unsatisfied”.

Source


References

Russia Longitudinal Monitoring survey, RLMS-HSE, conducted by Higher School of Economics and ZAO "Demoscope" together with Carolina Population Center, University of North Carolina at Chapel Hill and the Institute of Sociology RAS

Examples

data(RLMSlong)
Function to compute standard errors for the parameter estimates.

Usage

```r
se(est, ...)  # S3 method for class 'LMbasic'
se(est, ...)  # S3 method for class 'LMbasiccont'
se(est, ...)  # S3 method for class 'LMlatent'
se(est, ...)  # S3 method for class 'LMlatentcont'
```

Arguments

- `est`: an object obtained from a call to `lmest` and `lmestCont`
- `...`: further arguments

Value

Standard errors for estimates in `est` object.

Author(s)

Francesco Bartolucci, Silvia Pandolfi, Fulvia Pennoni, Alessio Farcomeni, Alessio Serafini

Examples

```r
## Not run:
data("data_SRHS_long")
SRHS <- data_SRHS_long[1:2400,]

# Categories rescaled to vary from 1 ("poor") to 5 ("excellent")
SRHS$srh <- 5 - SRHS$srh

out <- lmest(responsesFormula = srhs ~ NULL,
             index = c("id","t"),
data = SRHS,
k = 3,
modBasic = 1,
out_se = FALSE)
```
search.model.LM

Search for the global maximum of the log-likelihood

```r
out.se <- se(out)

out1 <- lmest(responsesFormula = srhs ~ NULL,
              index = c("id","t"),
              data = SRHS,
              k = 3,
              modBasic = 1,
              out_se = TRUE)
out1.se <- se(out1)

out2 <- lmest(responsesFormula = srhs ~ NULL,
              latentFormula = ~
              I(gender - 1) +
              I( 0 + (race == 2) + (race == 3)) +
              I(0 + (education == 4)) +
              I(0 + (education == 5)) +
              I(age - 50) + I((age-50)^2/100),
              index = c("id","t"),
              data = SRHS,
              k = 2,
              paramLatent = "multilogit",
              start = 0)
out2.se <- se(out2)

require(mmm)
data(multiLongGaussian)
t <- rep(1:4, times = max(multiLongGaussian$ID))
multiLongGaussian <- data.frame(t = t, multiLongGaussian)

out3 <- lmestCont(responsesFormula = resp1 + resp2 ~ NULL,
                  index = c("ID", "t"),
                  data = multiLongGaussian,
                  k =3,
                  modBasic = 1,
                  tol = 10^-5)
out3.se <- se(out3)

out4 <- lmestCont(responsesFormula = resp1 + resp2 ~ NULL,
                  latentFormula = ~ X + time | X + time,
                  index = c("ID", "t"),
                  data = multiLongGaussian,
                  k = 3,
                  output = TRUE)
out4.se <- se(out4)

## End(Not run)
```
**Description**

Function that searches for the global maximum of the log-likelihood of different models given a vector of possible number of states to try for.

The function is no longer maintained. Please look at `lmestSearch` function.

**Usage**

```r
search.model.LM(version = c("basic","latent","manifest","basic.cont","latent.cont"),
                 kv, ..., nrep = 2, tol1 = 10^-5, tol2 = 10^-10, out_se = FALSE)
```

**Arguments**

- `version`: model to be estimated ("basic" = basic LM model (est_lm_basic function); "latent" = LM model with covariates in the distribution of the latent process (est_lm_cov_latent function); "manifest" = LM model with covariates in the measurement model (est_lm_cov_manifest function); "basic.cont" = basic LM model for continuous outcomes (est_lm_basic_cont function); "latent.cont" = LM model for continuous outcomes with covariates in the distribution of the latent process (est_lm_cov_latent_cont function))
- `kv`: vector of possible number of latent states
- `...`: additional arguments to be passed based on the model to be estimated (see details)
- `nrep`: number of repetitions of each random initialization
- `tol1`: tolerance level for checking convergence of the algorithm in the random initializations
- `tol2`: tolerance level for checking convergence of the algorithm in the last deterministic initialization
- `out_se`: TRUE for computing information matrix and standard errors

**Details**

The function combines deterministic and random initializations strategy to reach the global maximum of the model log-likelihood. It uses one deterministic initialization (start=0) and a number of random initializations (start=1) proportional to the number of latent states. The tolerance level is set equal to $10^{-5}$. Starting from the best solution obtained in this way, a final run is performed (start=2) with a default tolerance level equal to $10^{-10}$.

Arguments in `...` depend on the model to be estimated. They match the arguments to be passed to functions `est_lm_basic`, `est_lm_cov_latent`, `est_lm_cov_manifest`, `est_lm_basic_cont`, or `est_lm_cov_latent_cont`.

**Value**

- `out.single`: output of each single model (as from `est_lm_basic`, `est_lm_cov_latent` or `est_lm_cov_manifest`) for each k in `kv`
- `aicv`: value of AIC index for each k in `kv`
summary

bicv value of BIC index for each k in kv
lkv value of log-likelihood for each k in kv

Author(s)

Francesco Bartolucci, Silvia Pandolfi, University of Perugia (IT), http://www.stat.unipg.it/bartolucci

Examples

## Not run:

# example for est_lm_basic
data(data_drug)
data_drug <- as.matrix(data_drug)
S <- data_drug[,1:5]-1
yv <- data_drug[,6]
n <- sum(yv)
# Search Basic LM model
res <- search.model.LM("basic", kv = 1:4, S, yv, mod = 1)
summary(res)

## End(Not run)

summary

Summary of LM fits

Description

Summary methods

Usage

## S3 method for class 'LMbasic'
summary(object, ...)
## S3 method for class 'LMbasiccont'
summary(object, ...)
## S3 method for class 'LMlatent'
summary(object, ...)
## S3 method for class 'LMlatentcont'
summary(object, ...)
## S3 method for class 'LMmanifest'
summary(object, ...)
## S3 method for class 'LMmixed'
summary(object, ...)
## S3 method for class 'MCbasic'
summary(object, ...)
Arguments

object
...  output from `lmest`, `lmestCont`, `lmestMixed`, and `lmestMc`
  further arguments passed to or from other methods

Author(s)

Francesco Bartolucci, Silvia Pandolfi, Fulvia Pennoni, Alessio Farcomeni, Alessio Serafini

Description

Methods for `lmestData` object providing basic descriptive statistics (summary) and plots.

Usage

## S3 method for class 'lmestData'
summary(object, type = c("all", "cross", "year"),
dataSummary = c("all", "responses", "manifest", "initial", "transition"),
varType = rep("c", x$d), digits = getOption("digits"),
maxsum = 10, maxobs = 20, ...)

## S3 method for class 'lmestData'
plot(x, typePlot = c("s", "sh"),
dataPlots = c("all", "responses", "manifest", "initial", "transition"),
...)

## S3 method for class 'lmestData'
print(x, ...)

Arguments

object
x
type  an object of class `lmestData`
  an object of class `lmestData`
  type of summary to print. all prints a summary for each variable, and a summary for each variables by time. cross prints a summary for each variable. year prints a summary for each variable by time. The summary is adapted according to varType (By default is set to all)
dataSummary a string indicating whether summary is returned: all for the entire data, responses for the responses, manifest for covariates on the manifest distribution, initial for the covariate affecting the initial probabilities, and transition for the covariates affecting the transition probabilities. (By default is set to all)

varType a string vector of length equal to the number of variables, "c" for continuous and "d" for discrete, indicating which variables are continuous and which are discrete

digits the number of significant digits

maxsum an integer value indicating the maximum number of levels to print

maxobs an integer value indicating the maximum number of observations in which the summary statistics are reported for each observation

typePlot a string indicating the type of plot. "s" plots a scatterplot matrix. "sh" plots a scatterplot matrix with the histogram for each variable in the diagonal

dataPlots a string indicating whether the plot is returned: all for the entire data, responses for the responses, manifest for covariates on the manifest distribution, initial for the covariate affecting the initial probabilities, transition for the covariates affecting the transition probabilities. (By default is set to all)

... further arguments

Author(s)
Francesco Bartolucci, Silvia Pandolfi, Fulvia Pennoni, Alessio Farcomeni, Alessio Serafini
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