Package ‘randomLCA’

June 22, 2023

Type Package
Title Random Effects Latent Class Analysis
Version 1.1-3
Date 2023-06-20
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Description Fits standard and random effects latent class models. The single level random effects model is described in Qu et al <doi:10.2307/2533043> and the two level random effects model in Beath and Heller <doi:10.1177/1471082X0800900302>. Examples are given for their use in diagnostic testing.
Depends R(>= 3.2.0), lattice
Suggests R.rsp
VignetteBuilder R.rsp
Imports boot, fastGHQuad, Matrix, Rfast, parallel, doParallel, doRNG, foreach
LazyLoad yes
LazyData yes
NeedsCompilation yes
License GPL (>= 2)
Repository CRAN
Date/Publication 2023-06-22 13:22:35 UTC

R topics documented:

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AIC

AIC for randomLCA object

Description

Returns AIC for a randomLCA object.

Usage

```r
## S3 method for class 'randomLCA'
AIC(object, ..., k = 2)
```

Arguments

- `object`: randomLCA object
- `...`: additional argument; currently none is used.
- `k`: penalty per parameter

Value

- `AIC`
AIC3

Author(s)

Ken Beath

Examples

pap.lca2 <- randomLCA(pap[, 1:10], freq = pap$Freq, nclass = 2, cores = 1)
print(AIC(pap.lca2))

Description

Returns AIC with penalty 3 for a randomLCA object.

Usage

AIC3(object)

Arguments

object randomLCA object

Value

AIC3.

Author(s)

Ken Beath

Examples

pap.lca2 <- randomLCA(pap[, 1:10], freq = pap$Freq, nclass = 2, cores = 1)
print(AIC3(pap.lca2))
### BIC

**BIC for randomLCA object**

**Description**

Returns BIC for a randomLCA object.

**Usage**

```r
## S3 method for class 'randomLCA'
BIC(object, ...)
```

**Arguments**

- `object`: randomLCA object
- `...`: additional argument; currently none is used.

**Value**

BIC

**Author(s)**

Ken Beath

**Examples**

```r
pap.lca2 <- randomLCA(pap[, 1:10], freq = pap$Freq, nclass = 2, cores = 1)
print(BIC(pap.lca2))
```

---

### calcCond2Prob

**Calculate Conditional Outcome Probabilities for 2 Level Models**

**Description**

The conditional probabilities are obtained integrating over the period random effect.

**Usage**

```r
calcCond2Prob(object, conditionalp = 0.5)
```

**Arguments**

- `object`: RandomLCA object
- `conditionalp`: the percentiles for the random effect
calcCondProb

Value

Returns a data frame containing class, block, outcome, outcomep (outcome probability) and perc (percentiles of the random effect) if conditionalp is specified. For example a conditionalp of 0.5 is the 50th percentile or the median corresponding to a random effect of zero. 0.025 and 0.975 correspond to the 2.5th and 97.5th percential, so the region between them is 95% of the variation in the data.

Author(s)

Ken Beath <kenbeath@mq.edu.au>

Examples

```r
symptoms.lca2random2 <- randomLCA(symptoms[,1:16], freq = symptoms$Freq, random = TRUE, level2 = TRUE, nclass = 2, level2size = 4, constload = FALSE, cores = 1)
print(calcCond2Prob(symptoms.lca2random2))
```

calcCondProb

Calculate Conditional Outcome Probabilities

Description

Calculates the conditional outcome probabilities for random effects models or for standard latent class returns the outcome probabilities. For random effects, the outcome probabilities may be calculated for various percentiles of the random effect.

Usage

```r
calcCondProb(object, conditionalp = 0.5)
```

Arguments

- **object**: RandomLCA object
- **conditionalp**: the percentiles for the random effect

Value

Returns a data frame containing class, block, outcome, outcomep (outcome probability) and perc (percentiles of the random effect) if conditionalp is specified. For example a conditionalp of 0.5 is the 50th percentile or the median corresponding to a random effect of zero. 0.025 and 0.975 correspond to the 2.5th and 97.5th percential, so the region between them is 95% of the variation in the data.

Author(s)

Ken Beath <ken.beath@mq.edu.au>
Examples

dentistry.lcarandom <- randomLCA(dentistry[, 1:5], freq = dentistry$freq,
random = TRUE, probit = TRUE, cores = 1)
print(calcCondProb(dentistry.lcarandom))

calcMargProb

Calculates Marginal Outcome Probabilities

Description

Calculates the marginal outcome probabilities for a random effects latent class model, by integrating
the outcome probability over the random effect. This is performed using Gauss-Hermite quadrature
with the number of quadrature points specified for the model fitting.

Usage

calcMargProb(object)

Arguments

object randomLCA object

Value

Returns a data frame containing class, block, outcome, outcomep (outcome probability).

Author(s)

Ken Beath

Examples

dentistry.lcarandom <- randomLCA(dentistry[, 1:5], freq = dentistry$freq,
random = TRUE, probit = TRUE, cores = 1)
print(calcMargProb(dentistry.lcarandom))
classProbs

Determines class probabilities for fitted model

Description
The class probabilities for the model are returned.

Usage
classProbs(object)

Arguments
object randomLCA object

Details
Simply extracts the corresponding variable from the randomLCA object.

Value
A vector of class probabilities for each class.

Author(s)
Ken Beath

Examples

pap.lca2 <- randomLCA(pap[, 1:10], freq = pap$Freq, nclass = 2, cores = 1)
print(classProbs(pap.lca2))

dentistry

Dental X-ray data

Description
Six dentists evaluated dental x-rays for incipient caries in Handelman et al (1986), data consists of 5 of the dentists analysed by Espeland and Handelman (1989) using a latent class model. Further analysis incorporating a random effects latent class model by Qu et al (1996), and by Albert and Dodd (2004)

Usage
dentistry
Format

A data frame with 32 observations on the following 6 variables.

V1  Dentist 1
V2  Dentist 2
V3  Dentist 3
V4  Dentist 4
V5  Dentist 5
freq Number of subjects

Source

Espeland and Handelman (1989)

References


Examples

```r
# fit LCR model from Qu et al (1996)
dentistry.lca <- randomLCA(dentistry[, 1:5], freq = dentistry$freq, cores = 1)
# start with constant loading
dentistry.lcarandom <- randomLCA(dentistry[, 1:5], freq = dentistry$freq, random = TRUE, probit = TRUE, cores = 1)
# allow loading to vary by dentist
dentistry.lcarandomunequal <- randomLCA(dentistry[, 1:5], freq = dentistry$freq, random = TRUE, constload = FALSE, probit = TRUE, cores = 1)
```
**Description**

Extract fitted values for randomLCA object.

**Usage**

```r
## S3 method for class 'randomLCA'
fitted(object, ...)
```

**Arguments**

- `object`: randomLCA object
- `...`: additional argument; currently none is used.

**Value**

A data frame. The first columns of the data frame correspond to the patterns, followed by the frequency of each pattern, and then the fitted number for each pattern.

**Author(s)**

Ken Beath <ken.beath@mq.edu.au>

**Examples**

```r
dentistry.lcarandom <- randomLCA(dentistry[, 1:5], freq = dentistry$freq, random = TRUE, probit = TRUE, cores = 1)
print(fitted(dentistry.lcarandom))
```

---

**genderrole**

*Gender Role Opinion Items*

**Description**

Opinions collected on gender roles in a study by Felling et al (1987). This was originally published in Heinen (1996) and subsequently in Galindo Garre and Vermunt (2006).

**Usage**

`genderrole`
Format

A data frame with 16 observations on the following 5 variables.

Q1 Women’s liberation sets women against men.
Q2 It’s better for a wife not to have a job because that always poses problems in the household, especially if there are children.
Q3 The most natural situation occurs when the man is the breadwinner and the woman runs the household and takes care of the children.
Q4 It isn’t really as important for a girl to get a good education as it is for a boy.
Q5 A woman is better suited to raise small children than a man.
Freq Number of subjects

Source

Galindo Garre and Vermunt (2006)

References


Examples

# standard latent class
genderrole.lca1 <- randomLCA(genderrole[,1:5], freq = genderrole$Freq, nclass = 1, cores = 1)
genderrole.lca2 <- randomLCA(genderrole[,1:5], freq = genderrole$Freq, cores = 1)
genderrole.lca3 <- randomLCA(genderrole[,1:5], freq = genderrole$Freq, nclass = 3, cores = 1)

# repeat with random effect with constant loading
# increase quadrature points and/or use higher penalty to obtain
# convergence

genderrole.lca1random <- randomLCA(genderrole[,1:5], freq = genderrole$Freq, nclass = 1, random = TRUE, cores = 1)
genderrole.lca2random <- randomLCA(genderrole[,1:5], freq = genderrole$Freq, random = TRUE, penalty = 0.1, quadpoints = 61, cores = 1)
genderrole.lca3random <- randomLCA(genderrole[,1:5], freq = genderrole$Freq, nclass = 3, random = TRUE, penalty = 0.1, quadpoints = 61, cores = 1)

# improved BIC for 1 class random
print(c(BIC(genderrole.lca1), BIC(genderrole.lca2), BIC(genderrole.lca3)))

# can also repeat fits without constant loading to give mixture of IRT models

genderrole.lca1random2 <- randomLCA(genderrole[,1:5], freq = genderrole$Freq, nclass = 1, random = TRUE, constload = FALSE, cores = 1)
genderrole.lca2random2 <- randomLCA(genderrole[,1:5], freq = genderrole$Freq, random = TRUE, constload = FALSE, quadpoints = 61, penalty = 0.1, cores = 1)
genderrole.lca3random2 <- randomLCA(genderrole[, 1:5], freq = genderrole$Freq, 
nclass = 3, random = TRUE, constload = FALSE, quadpoints = 61, penalty = 0.1, cores = 1) 
# no improvement in fit 
print(c(BIC(genderrole.lca1random2), BIC(genderrole.lca2random2), 
BIC(genderrole.lca3random2)))

hivtests

HIV testing data

Description

Serum samples are tested for HIV by 4 different biossays in Alvord et al (1988) and sensitivity and specificity determined using latent class analysis. Qu et al (1996) repeat the analysis using a model incorporating a random effect.

Usage

hivtests

Format

A data frame with 16 observations on the following 5 variables.

V1  Test 1
V2  Test 2
V3  Test 3
V4  Test 4
freq Number of subjects

Source

Qu, Tan and Kutner (1989)

References


Examples

# fit standard latent class
hivtests.lca2 <- randomLCA(hivtests[, 1:4], freq = hivtests$freq, cores = 1)
# with random effect and constant loading
hivtests.lca2random <- randomLCA(hivtests[, 1:4], freq = hivtests$freq, random = TRUE,
    quadpoints = 101, penalty = 1.0, cores = 1)
# with random effect and variable loading
# for this model there are 13 parameters fitted to 16 observations, so model is fairly unstable
hivtests.lca2random2 <- randomLCA(hivtests[, 1:4], freq = hivtests$freq, random = TRUE,
    constload = FALSE, quadpoints = 101, penalty = 1.0, cores = 1)
# BIC shows best model is random effects with constant loading
print(c(BIC(hivtests.lca2), BIC(hivtests.lca2random), BIC(hivtests.lca2random2)))

logLik

log Likelikelihood for randomLCA object

Description

Returns log Likelihood for a randomLCA object.

Usage

## S3 method for class 'randomLCA'
logLik(object, ...)

Arguments

object randomLCA object

... additional argument; currently none is used.

Value

The loglikelihood.

Author(s)

Ken Beath

Examples

pap.lca2 <- randomLCA(pap[, 1:10], freq = pap$Freq, nclass = 2, cores = 1)
print(logLik(pap.lca2))
maxPostClass

Determines class with maximum posterior class probability for each observation

Description
For each observation the posterior class probability is determined for each class, and then the class with the maximum posterior class probability is returned.

Usage
maxPostClass(object)

Arguments
object randomLCA object

Details
Returns the class with the maximum posterior class probability for each observation.

Value
A data frame. The first columns of the data frame correspond to the patterns, followed by the frequency of each pattern, and then the class with the maximum posterior class probability. The returned result is for the summarised data. If raw data is used, that is no frequencies, and it is required to calculated the posterior class probability for each observation then it is simply required to merge the maximum class with the raw data, possibly removing any variable "Freq" in the raw data.

Author(s)
Ken Beath

Examples
pap.lca2 <- randomLCA(pap[, 1:10], freq = pap$Freq, nclass = 2, cores = 1)
maxClass.lca2 <- maxPostClass(pap.lca2)
names(maxClass.lca2)[length(names(maxClass.lca2))] <- "maxProb.lca2"
pap.lca3 <- randomLCA(pap[, 1:10], freq = pap$Freq, nclass = 3, cores = 1)
maxClass.lca3 <- maxPostClass(pap.lca3)
names(maxClass.lca3)[length(names(maxClass.lca3))] <- "maxProb.lca3"

maxClass <- merge(maxClass.lca2, maxClass.lca3)
# aggregate because there is more than one record for each combination
# shows the relationship between the 2 and 3 class models
print(aggregate(maxClass$Freq, list(maxProb2 = maxClass$maxProb.lca2, maxProb3 = maxClass$maxProb.lca3)))
Description

Four tests were performed on hospital patients to determine if a myocardial infarction had occurred.

Usage

myocardial

Format

A data frame with 32 observations on the following 6 variables.

- Q.wave  result from ECG test
- History  clinical history
- LDH flipped, enzyme related to tissue breakdown
- CPK high, creatine kinase or creatine phosphokinase, related to muscle damage
- freq  Number of subjects

Source

Rindskopf and Rindskopf (1986)

References


Examples

# fit 2 class model from Rindskopf and Rindskopf (1986)
myocardial.lca2 <- randomLCA(myocardial[, 1:4], freq = myocardial$freq, cores = 1)
outcomeProbs

Extract outcome probabilities for randomLCA object

Description

Extract outcome probabilities and confidence intervals for a randomLCA object.

Usage

```r
## S3 method for class 'randomLCA'
outcomeProbs(object, level = 0.95, boot=FALSE, type="perc", R=999,
              scale=c("prob","raw"), cores = max(detectCores() %/% 2, 1), ...)
```

Arguments

- **object**: randomLCA object
- **level**: confidence interval
- **boot**: use parametric bootstrap to obtain confidence interval
- **type**: type of bootstrap confidence intervals to use, with "perc" or "norm" valid, see boot.ci for description.
- **R**: replications for parametric bootstrap
- **scale**: either "prob" where probabilities are returned, the default, or "raw" where the probabilities are returned on the logit or probit scale, depending on which scale was selected in the textttrandomLCA function
- **cores**: number of cores to use when bootstrapping. Should be at least 1 less than available cores
- **...**: additional argument; currently none is used.

Details

Confidence intervals are calculated based on asymptotic normality of the estimates transformed by either the inverse of the probit or logistic, or using parametric bootstrap. The asymptotic confidence intervals are currently only available for models without random effects. For the confidence intervals obtained from the parametric bootstrap, the bootstrap is performed on the data that has been transformed to the logit or probit scale, as appropriate.

Value

Data frame consisting of outcome probabilities and confidence intervals. One for each class.

Author(s)

Ken Beath
Examples

```r
# standard latent class with 2 classes
dentistry.lca2 <- randomLCA(dentistry[, 1:5], freq = dentistry$freq, nclass = 2, cores = 1)
print(outcomeProbs(dentistry.lca2))
# print on the default logit scale
print(outcomeProbs(dentistry.lca2, scale = "raw"))
# convert back to probabilities
print(1.0/(1.0+exp(-outcomeProbs(dentistry.lca2, scale = "raw")[[1]])))
print(1.0/(1.0+exp(-outcomeProbs(dentistry.lca2, scale = "raw")[[2]])))
```

---

**Positive Action program implementation**

**Description**

The Positive Action program is a series of interventions designed to reduce negative behaviours in elementary-school students. In a study in Hawaii (Beets et al, 2006) information was recorded from students in the treatment group about whether the various parts of the program were implemented. While it is useful to describe the proportion of students experiencing implementation of each part of the program, latent class analysis will reveal if there are specific patterns to the implementation of the program (Alcock, 2008).

**Usage**

pap

**Format**

A data frame with 606 observations summarising the answers for 1566 students on the following 11 variables. For each variable the data has been dichotomized so that a 0 represents no implementation and a 1 represents some implementation.

- **Q1** you receive stickers from your teacher for doing positive actions?
- **Q2** you receive a word of the week card from your teacher?
- **Q3** you put notes in an icu box?
- **Q4** your teacher read notes about you from the icu box?
- **Q5** your teacher read your notes from the icu box?
- **Q6** your class receive a token for meeting your classroom goals?
- **Q7** you participate in a positive action assembly?
- **Q8** your class receive a balloon in an assembly for achieving their classroom goals?
- **Q9** your class participate in whole school positive action celebrations?
- **Q10** most weeks were you taught a positive action lesson?

Freq  Number of subjects
Source
Alcock (2008)

References


Examples

```r
# standard latent class
pap.lca1 <- randomLCA(pap[, 1:10], freq = pap$Freq, nclass = 1, cores = 1)
pap.lca2 <- randomLCA(pap[, 1:10], freq = pap$Freq, nclass = 2, cores = 1)

# standard latent class
pap.lca3 <- randomLCA(pap[, 1:10], freq = pap$Freq, nclass = 3, cores = 1)
pap.lca4 <- randomLCA(pap[, 1:10], freq = pap$Freq, nclass = 4, cores = 1)
pap.lca5 <- randomLCA(pap[, 1:10], freq = pap$Freq, nclass = 5, cores = 1)

# repeat with random effect with constant loading
# once BIC increases fitting further models is unnecessary
pap.lca1random <- randomLCA(pap[, 1:10],
freq = pap$Freq, nclass = 1, random = TRUE, cores = 1)
pap.lca2random <- randomLCA(pap[, 1:10],
freq = pap$Freq, nclass = 2, random = TRUE, cores = 1)
pap.lca3random <- randomLCA(pap[, 1:10],
freq = pap$Freq, nclass = 3, random = TRUE, cores = 1)

# can also repeat fits without constant loading to give mixture of IRT models
pap.lca1random2 <- randomLCA(pap[, 1:10],
freq = pap$Freq, nclass = 1, random = TRUE, constload = FALSE, cores = 1)
pap.lca2random2 <- randomLCA(pap[, 1:10],
freq = pap$Freq, nclass = 2, random = TRUE, constload = FALSE, cores = 1)
pap.lca3random2 <- randomLCA(pap[, 1:10],
freq = pap$Freq, nclass = 3, random = TRUE, constload = FALSE, cores = 1)

# produce table of BIC values
# shows 4 class best of standard latent class
# but 2 class latent class with constant loading has better BIC
pap.bic <- data.frame(bic = c(BIC(pap.lca1), BIC(pap.lca2), BIC(pap.lca3),
BIC(pap.lca4), BIC(pap.lca5)),
bic2 = c(BIC(pap.lca1random),
BIC(pap.lca2random), BIC(pap.lca3random), NA, NA),
bic3 = c(BIC(pap.lca1random2),
BIC(pap.lca2random2), BIC(pap.lca3random2), NA, NA))
print(pap.bic)
# plot 4 class standard
plot(pap.lca4, type = "b")
```
# plot 2 class standard
plot(pap.lca2random, type = "b")

## S3 method for class 'randomLCA'
plot(x, ..., graphtype = ifelse(x$random, "marginal", "conditional"),
     conditionalp = 0.5, classhorizontal = TRUE)

x randomLCA object
graphtype Type of graph
conditionalp For a conditional graph the percentile corresponding to the random effect at
which the outcome probability is to be calculated
classhorizontal classes to be plotted across the page
... additional parameters to xyplot

Author(s)
Ken Beath <ken.beath@mq.edu.au>

See Also
calcCondProb, calcMargProb

Examples

# standard latent class with 2 classes
uterinecarcinoma.lca2 <- randomLCA(uterinecarcinoma[, 1:7], freq = uterinecarcinoma$freq, cores = 1)
plot(uterinecarcinoma.lca2)
uterinecarcinoma.lcarandom2 <- randomLCA(uterinecarcinoma[, 1:7],
                                           freq = uterinecarcinoma$freq, random = TRUE, probit = TRUE, quadpoints = 61, cores = 1)
# default for random effects models is marginal
postClassProbs

Determines posterior class probabilities for fitted model

### Description
The posterior class probabilities for each observed pattern and class is determined. These are returned as a data frame together with the patterns for each observation. If class = 0 is requested then all classes are returned, otherwise only the selected class.

### Usage
postClassProbs(object, class = 0)

### Arguments
- **object**: randomLCA object
- **class**: class to be returned. Zero returns all classes.

### Value
A data frame. The first columns of the data frame correspond to the patterns, followed by the frequency of each pattern, and then the posterior class probabilities for either the selected class or for all classes. The returned result is for the summarised data. If raw data is used, that is no frequencies, and it is required to calculate the posterior class probability for each observation then it is simply required to merge the class probabilities with the raw data, possibly removing any variable "freq" in the raw data.

### Author(s)
Ken Beath

### Examples
```
pap.lca2 <- randomLCA(pap[, 1:10], freq = pap$Freq, nclass = 2, cores = 1)
print(postClassProbs(pap.lca2))
```
**randomLCA**

* Fits a Latent Class Model including a Random Effect

**Description**

Fit latent class models, which may include a random effect.

**Usage**

```r
randomLCA(patterns, freq = NULL, nclass = 2, calcSE = TRUE, notrials = 20,
random = FALSE, byclass = FALSE, quadpoints = 21, constload = TRUE,
blocksize = dim(patterns)[2], level2 = FALSE, probit = FALSE,
level2size = blocksize, qniterations = 5, penalty = 0.01, EMtol = 1.0e-5,
verbose = FALSE, seed = as.integer(runif(1, 0, .Machine$integer.max)),
cores = max(detectCores() %/% 2, 1))
```

**print.randomLCA**

* print for randomLCA object

**Description**

Prints a randomLCA object. Prints summary.

**Usage**

```r
## S3 method for class 'randomLCA'
print(x, ...)
```

**Arguments**

- **x**: randomLCA object
- **...**: additional argument; currently none is used.

**Author(s)**

Ken Beath

**Examples**

```r
pap.lca1 <- randomLCA(pap[, 1:10], freq = pap$Freq, nclass = 1, cores = 1)
pap.lca1
# or
print(pap.lca1)
```
randomLCA

Arguments

patterns  Data frame or matrix of 0 and 1 defining the outcome patterns. May also include missing values, with randomLCA using maximum likelihood to fit the models using all available data.
freq  Frequency for each outcome pattern, if missing this is calculated from the patterns, and the patterns are summarised to remove duplicate values.
nclass  Number of classes to be fitted
calcSE  Calculate standard errors for parameters. Useful for bootstrapping.
notrials  For a standard latent class model, the number of random starting values used
random  Include random effect?
byclass  Vary random effect loading(s) by class?
quadpoints  Number of quadrature points for adaptive quadrature
constload  Outcome loadings are constant for random effects model?
blocksize  Where a random effects (single level) model is broken into blocks, that is the loadings are repeated, this defines the size of the blocks
probit  Probit model for random effect?
level2  Fit 2 level random effects model (further details to follow)?
level2size  Size of level 2 blocks if fitting 2 level models
qnterations  Number of Quasi-Newton iterations within each EM/adaptive cycle. Decrease if there is a failure to converge
penalty  penalty applied to likelihood for outcome probabilities. Shrinks outcome probabilities in slightly and can prevent extreme values. Setting penalty to 0 will produce an unpenalized fit.
EMtol  convergence tolerance for EM algorithm for fixed effect latent class
verbose  Prints fit progress if true
seed  Initial random seed for generating starting values. This can be set to guarantee that the fit is the same each time, including the order of the classes.
cores  Number of cores to be used for parallel evaluation of starting values

Details

The structure of the patterns is assumed to be a number of blocks of different outcomes each of level2size, allowing outcomes to be repeated. Each outcome is assumed to have it’s own loading. An example is the width of the patterns is n and the level2size is n, resulting in n outcomes and therefore n loadings. Alternatively if the level2size is 1, then there are n repeats of the same outcome (but with different probabilities) with the same loading. In practice they may not be the same type of outcome, but usually will be.

The algorithm used is EM for the standard latent class and adaptive (in the sense of moving the location of the quadrature points) Gauss-Hermite quadrature for the random effects models. The number of quadrature points defaults to 21.
randomLCA object This contains

- **fit**: Fit object from optim
- **nclass**: Number of classes
- **classp**: Class probabilities
- **outcomep**: Outcome probability
- **lambdacoef**: Loadings
- **se**: Standard errors corresponding to results returned by optim
- **np**: Number of parameters
- **nobs**: Number of observations in total
- **logLik**: log likelihood for fitted model
- **penlogLik**: Penalised log likelihood for fitted model
- **observed**: Observed numbers corresponding to each pattern
- **fitted**: Fitted number corresponding to each pattern
- **deviance**: Deviance
- **classprob**: Posterior class probability for each pattern
- **bics**: BIC obtained for each trial when fitting initial latent class models
- **call**: call to randomLCA
- **random**: random parameter to randomLCA
- **constload**: constload parameter to randomLCA
- **level2**: level2 parameter to randomLCA
- **level2size**: level2size parameter to randomLCA
- **byclass**: byclass parameter to randomLCA
- **probit**: probit parameter to randomLCA
- **quadpoints**: quadpoints parameter to randomLCA
- **blocksize**: blocksize parameter to randomLCA
- **freq**: frequency of each pattern
- **qniterations**: qniterations parameter to randomLCA
- **penalty**: penalty parameter to randomLCA

**Note**

In the returned object there are fields for patterns and frequencies. If frequencies are not supplied then the patterns and frequencies are constructed. If frequencies are supplied then zero rows are removed. When frequencies are supplied it is assumed that the data has been simplified. The returned fitted, posterior class probabilities etc, all correspond to the simplified patterns, not to the original data.

**Author(s)**

Ken Beath
ranef

References


Examples

# standard latent class with 2 classes
dentistry.lca2 <- randomLCA(dentistry[, 1:5], freq = dentistry$freq, nclass = 2, cores = 1)
# random effects model with constant random effect loading
dentistry.lca2random <- randomLCA(dentistry[, 1:5], freq = dentistry$freq, nclass = 2, random = TRUE, constload = TRUE, probit = TRUE, cores = 1)
# allow loading to vary by dentist
# this is the 2LCR model from Qu et al (1996)
dentistry.lca2random1 <- randomLCA(dentistry[, 1:5], freq = dentistry$freq, nclass = 2, random = TRUE, constload = FALSE, probit = TRUE, cores = 1)

ranef

Extract random effects from a randomLCA object

Description

Extracts the Empirical Bayes estimates of the random effects.

Usage

## S3 method for class 'randomLCA'
ranef(object, ...)

Arguments

object randomLCA object with a random effect

... additional argument; currently none is used.

Value

A matrix with the first column containing the random effects and the second column the standard error of the random effects.

Author(s)

Ken Beath

Examples

pap.lca2random <- randomLCA(pap[, 1:10], freq = pap$freq, random = TRUE, nclass = 2, cores = 1)
print(ranef(pap.lca2random))
Description

Refits a randomLCA object using new data. This is useful when fitting simulated data, for example using a bootstrap.

Usage

```r
## S3 method for class 'randomLCA'
refit(object, newpatterns, newfreq, useinit = FALSE, ...)
```

Arguments

- **object**: randomLCA object
- **newpatterns**: the new patterns that are to be fitted using the existing model
- **newfreq**: the frequencies corresponding to the patterns if required
- **useinit**: use initial values from randomLCA object
- **...**: additional argument; currently none is used.

Details

The useunit parameter determines whether the parameter estimates from the supplied model are used as initial values or whether the complete model fitting process is repeated. If the initial values are used then fitting will be faster, and the fitted classes will be similar to those in the original model. If the data was not generated from the original model there is an increased risk that the fit will not find the global maxima. For this reason when performing a bootstrap Likelihood ratio test it is better to use useinit = FALSE. However when using useinit = FALSE there may be label switching, where the estimated classes are similar, but in a different order. Unless the estimated parameters are assigned to the correct classes this will invalidate the results of a parametric bootstrap for parameter confidence intervals.

Value

The fitted model to the new data.

Author(s)

Ken Beath
Examples

```r
myocardial.lca1 <- randomLCA(myocardial[, 1:4], freq = myocardial$freq, nclass = 1, cores = 1)
myocardial.lca2 <- randomLCA(myocardial[, 1:4], freq = myocardial$freq, cores = 1)
# calculate observed lrt
obslrt <- 2*(logLik(myocardial.lca2)-logLik(myocardial.lca1))

print(obslrt)

nsims <- 999
# generate the simulations
thesims <- simulate(myocardial.lca1, nsims)
# for each simulation determin lrt
simlrt <- rep(NA, nsims)
for (isim in 1:nsims) {
  submodel <- refit(myocardial.lca1, newpatterns = thesims[[isim]])
  fullmodel <- refit(myocardial.lca2, newpatterns = thesims[[isim]])
  simlrt[isim] <- 2*(logLik(fullmodel)-logLik(submodel))
  print(c(isim, simlrt[isim]))
}
# calculate p value as proportion of simulated lrt greater than observed,
# corrected by adding one to numerator and denominator
print((sum(simlrt >= obslrt)+1)/(nsims+1))
```

---

### simulate

**Simulate**

Simulate data from a fitted randomLCA model

#### Usage

```r
## S3 method for class 'randomLCA'
simulate(object, nsim, seed, ...)
```

#### Arguments

- `object`: randomLCA object
- `nsim`: number of data sets to be simulated
- `seed`: random seed
- `...`: additional optional arguments.

#### Details

Generates random data from the supplied object.
Value
A simulated data frame or a list of simulated data frames.

Author(s)
Ken Beath

Examples

```r
myocardial.lca1 <- randomLCA(myocardial[, 1:4], freq = myocardial$freq, nclass = 1, cores = 1)
myocardial.lca2 <- randomLCA(myocardial[, 1:4], freq = myocardial$freq, cores = 1)
# calculate observed lrt
obslrt <- 2*(logLik(myocardial.lca2)-logLik(myocardial.lca1))

print(obslrt)

nsims <- 999
# generate the simulations
thesims <- simulate(myocardial.lca1, nsims)
# for each simulation determine lrt
simlrt <- rep(NA, nsims)
for (isim in 1:nsims) {
  submodel <- refit(myocardial.lca1, newpatterns = thesims[[isim]])
  fullmodel <- refit(myocardial.lca2, newpatterns = thesims[[isim]])
  simlrt[isim] <- 2*(logLik(fullmodel)-logLik(submodel))
  print(c(isim, simlrt[isim]))
}
# calculate p value as proportion of simulated lrt greater than observed,
# corrected by adding one to numerator and denominator
print((sum(simlrt >= obslrt)+1)/(nsims+1))
```

summary.randomLCA

Summary for randomLCA object

Description
Summarises the fit of a randomLCA object.

Usage

```r
## S3 method for class 'randomLCA'
summary(object, ...)
```

Arguments

- `object` randomLCA object
- `...` additional argument; currently none is used.
*symptoms*

**Value**

<table>
<thead>
<tr>
<th>Value</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>logLik</td>
<td>Log Likelihood</td>
</tr>
<tr>
<td>AIC</td>
<td>AIC</td>
</tr>
<tr>
<td>BIC</td>
<td>BIC</td>
</tr>
<tr>
<td>AIC3</td>
<td>AIC with penalty of 3</td>
</tr>
<tr>
<td>nclass</td>
<td>no of classes</td>
</tr>
<tr>
<td>probit</td>
<td>link is probit</td>
</tr>
<tr>
<td>classp</td>
<td>class probabilities</td>
</tr>
<tr>
<td>outcomep</td>
<td>outcome probabilities (conditional)</td>
</tr>
<tr>
<td>margoutcomep</td>
<td>outcome probabilities (marginal), if model contains random effects</td>
</tr>
<tr>
<td>random</td>
<td>model includes random effects</td>
</tr>
<tr>
<td>level2</td>
<td>model has 2 level hierarchy</td>
</tr>
<tr>
<td>constload</td>
<td>loadings are constant by outcome</td>
</tr>
<tr>
<td>byclass</td>
<td>lambda and tau vary by class</td>
</tr>
<tr>
<td>lambdacoef</td>
<td>lambda coefficients</td>
</tr>
<tr>
<td>taucoef</td>
<td>tau coefficients</td>
</tr>
</tbody>
</table>

**Author(s)**

Ken Beath

**Examples**

```r
pap.lca1 <- randomLCA(pap[, 1:10], freq = pap$Freq, nclass = 1, cores = 1)
summary(pap.lca1)
```

---

**symptoms**

*Symptoms data*

**Description**

This is the data for Beath and Heller (2009).

Allergy and respiratory symptoms for infants 0 to 2 years in six month periods. Outcome is presence or absence of symptom in the six months. Original data was collected at Visits 1-7 over the 2 year period which were summarised to six month periods.

Note that these models can be slow to fit, with the "symptoms.lca2random2" model taking about 1-2 hours.

Thanks to the investigators of the CAPS study for making the data available.
Usage

symptoms

Format

A data frame with 444 observations on the following 17 variables.

- **Nightcough.13**: Night cough in visits 1-3
- **Wheeze.13**: Wheeze in visits 1-3
- **Itchyrash.13**: Itchy rash in visits 1-3
- **FlexDerma.13**: Flexural Dermatitis in visits 1-3
- **Nightcough.45**: Night cough in visits 1-3
- **Wheeze.45**: Wheeze in visits 4-5
- **Itchyrash.45**: Itchy rash in visits 4-5
- **FlexDerma.45**: Flexural Dermatitis in visits 4-5
- **Nightcough.6**: Night cough in visit 6
- **Wheeze.6**: Wheeze in visit 6
- **Itchyrash.6**: Itchy rash in visit 6
- **FlexDerma.6**: Flexural Dermatitis in visits 1-3
- **Nightcough.7**: Night cough in visit 7
- **Wheeze.7**: Wheeze in visit 7
- **Itchyrash.7**: Itchy rash in visit 7
- **FlexDerma.7**: Flexural Dermatitis in visit 7
- **Freq**: Number of subjects

Source

Mihrshai et al (2001)

References

Mihrshahi, S., Peat, J.K., Webb, K., Tovey, R.E., Marks, G.B., Mellis, C.M. and Leeder S.R. (2001) The Childhood Asthma Prevention Study (CAPS): Design and research protocol of a randomized trial for the primary prevention of asthma. Control led Clinical Trials, **22**:333–354.


Examples

```r
symptoms.lca2 <- randomLCA(symptoms[, 1:16], freq = symptoms$Freq, nclass = 2, cores = 1)
symptoms.lca2random <- randomLCA(symptoms[, 1:16], freq = symptoms$Freq, random = TRUE, nclass = 2, blocksize = 4, constload = FALSE, cores = 1)
```
uterinecarcinoma

symptoms.lca2random2 <- randomLCA(symptoms[, 1:16], freq = symptoms$Freq, random = TRUE, level2 = TRUE, nclass = 2, level2size = 4, constload = FALSE, penalty = 0.1, cores = 1)

uterinecarcinoma Uterine Carcinoma Data

**Description**

Classification of 118 histology samples by 118 pathologists. Original classification in Holmquist et al (1967) was to one of five categories, this has been reduced to two. Analysed by a number of authors, with a random effects model in Qu et al (1996).

**Usage**

uterinecarcinoma

**Format**

A data frame with 20 observations on the following 8 variables.

V1 Pathologist 1
V2 Pathologist 2
V3 Pathologist 3
V4 Pathologist 4
V5 Pathologist 5
V6 Pathologist 6
V7 Pathologist 7
freq Number of observed pattern

**Source**

Qu et al (1996)

**References**


Examples

uterinecarcinoma.lcarandom2 <- randomLCA(uterinecarcinoma[, 1:7],
    freq = uterinecarcinoma$freq, random = TRUE, probit = TRUE, quadpoints = 61, cores = 1)
# LCR1 model of Que et al. This is fairly unstable and
# is also slow and doesn’t improve the model fit
uterinecarcinoma.lcarandom2by <- randomLCA(uterinecarcinoma[, 1:7], freq = uterinecarcinoma$freq,
    byclass = TRUE, random = TRUE, probit = TRUE, quadpoints = 71, cores = 1)
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