

Package ‘pleLMA’

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Type Package

Title Pseudo-Likelihood Estimation of Log-Multiplicative Association Models

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Author Carolyn J. Anderson

Maintainer Carolyn J. Anderson <cja@illinois.edu>

Description Log-multiplicative association models (LMA) are models for cross-classifications of categorical variables where interactions are represented by products of category scale values and an association parameter. Maximum likelihood estimation (MLE) fails for moderate to large numbers of categorical variables. The 'pleLMA' package overcomes this limitation of MLE by using pseudo-likelihood estimation to fit the models to small or large cross-classifications dichotomous or multi-category variables. Originally proposed by Besag (1974, <[doi:10.1111/j.2517-6161.1974.tb00999.x](https://doi.org/10.1111/j.2517-6161.1974.tb00999.x)>), pseudo-likelihood estimation takes large complex models and breaks it down into smaller ones. Rather than maximizing the likelihood of the joint distribution of all the variables, a pseudo-likelihood function, which is the product likelihoods from conditional distributions, is maximized. LMA models can be derived from a number of different frameworks including (but not limited to) graphical models and uni-dimensional and multi-dimensional item response theory models. More details about the models and estimation can be found in the vignette.

License GPL (>= 3)

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Description

For the nominal model, convergence statistics are computed for each item, as well as the algorithm as a whole. The main argument is the history or log from fitting item regressions. The convergence statistics are the differences between current values of the log likelihoods and item parameter estimates and those from the previous iteration. The maximum over item of the differences of the log likelihood values is used to determine convergence of the pseudo-likelihood algorithm. This function is used internally, but it can also be used after fitting a model to examine how many iterations are required for parameter estimates to get close to the final values and whether any item parameters are still changing.

Usage

```
convergence.stats(item.log, nitems, nless, LambdaName, NuName)
```

Arguments

<code>item.log</code>	Iteration history of items' log likelihoods and parameter estimates
<code>nitems</code>	Number of items
<code>nless</code>	Number of unique marginal terms (i.e., lambdas) and unique category scale values(i.e., nus)
<code>LambdaName</code>	Names of lambdas in item regressions
<code>NuName</code>	Names of nu in item regressions

Value

`diff.last` Differences between item loglikes & parameters on last two iterations
`criterion.loglike` Maximum over items of the absolute value of LogLike differences
`criterion.items` Sum of item differences of item parameters

Examples

```
# 9 items from dass data for 250 cases
data(dass)
inData <- dass[1:250,c("d1", "d2", "d3", "a1","a2","a3","s1","s2","s3")]

#--- input for uni-dimensional
inTraitAdj <- matrix(1, nrow=1, ncol=1)
inItemTraitAdj <- matrix(1, nrow=9, ncol=1)

#--- Uni-dimensional Nominal Model
n1 <- ple.lma(inData, model.type="nominal", inItemTraitAdj,inTraitAdj, tol=1e-02)

# Since this function is internal to fit.nominal, need to also run
s <- set.up(inData, model.type='nominal', inTraitAdj, inItemTraitAdj)

convergence.stats(n1$item.log, n1$nitems, n1$nless, s$LambdaName, s$NuName)
```

```

#--- Multidimensional models
#--- re-define inTraitAdj and inItemTraitAdj for 3 dimensional models
  inTraitAdj <- matrix(1, nrow=3, ncol=3)

  dpres <- matrix(c(1,0,0), nrow=3, ncol=3, byrow=TRUE)
  anxiety <- matrix(c(0,1,0), nrow=3, ncol=3, byrow=TRUE)
  stress <- matrix(c(0,0,1), nrow=3, ncol=3, byrow=TRUE)
  das <- list(dpres, anxiety, stress)
  inItemTraitAdj <- rbind(das[[1]], das[[2]], das[[3]])

#--- 3 dimensional nominal
  n3 <- ple.lma(inData, model.type="nominal", inItemTraitAdj, inTraitAdj, tol=1e-03)
  s <- set.up(inData, model.type='nominal', inTraitAdj, inItemTraitAdj)
  convergence.stats(n3$item.log, n3$nitems, n3$nless, s$LambdaName, s$NuName)

```

convergenceGPCM	<i>Computes statistics to assess convergence for generalized partial credit models</i>
-----------------	--

Description

For the generalized partial credit model, convergence statistics are computed for each item, as well as the algorithm as a whole. The convergence statistics are the differences between current values of the log likelihoods and item parameter estimates and those from the previous iteration. The maximum over items' differences of the log likelihood values is used to determine convergence of the pseudo-likelihood algorithm. This function is used internally, but it can also be used after fitting a model to examine how many iterations are required for parameter estimates to get close to the final values and whether any item parameters are still changing.

Usage

```
convergenceGPCM(item.log, nitems, ncat, nless, LambdaName)
```

Arguments

item.log	Iteration history of items' log likelihoods and parameter estimates
nitems	Number of items
ncat	Number of categories
nless	Number of unique lambdas
LambdaName	Names of lambdas in formula used to fit item regressions (internal to fit_gpcm)

Value

diff.last Differences between item's log likelihoods and parameters for each item
 criterion.loglike Maximum overs item of the absolute value of differences between item LogLike values
 criterions.items Sum of item differences of their parameters

Examples

```
# 9 items from dass data for 250 cases
data(dass)
inData <- dass[1:250,c("d1", "d2", "d3", "a1","a2","a3","s1","s2","s3")]

#--- input for uni-dimensional
inTraitAdj <- matrix(1, nrow=1, ncol=1)
inItemTraitAdj <- matrix(1, nrow=9, ncol=1)

#--- fit Unidiemsional gpcm Model
g1<- ple.lma(inData, model.type="gpcm",inItemTraitAdj,inTraitAdj, tol= 1e-03)

# Since convergenceGPCM is internal to fit.gpcm, need to get 'Lambdaname'
s <- set.up(inData, model.type='gpcm', inTraitAdj, inItemTraitAdj)

convergenceGPCM(g1$item.log, g1$nitems, g1$ncat, g1$nless, s$LambdaName)

#--- Multidimensional models
#--- re-define inTraitAdj and inItemTraitAdj for 3 dimensional models
inData <- dass[1:250,c("d1", "d2", "d3", "a1","a2","a3","s1","s2","s3")]
inTraitAdj <- matrix(1, nrow=3, ncol=3)
dpress <- matrix(c(1,0,0), nrow=3, ncol=3, byrow=TRUE)
anxiety <- matrix(c(0,1,0), nrow=3, ncol=3, byrow=TRUE)
stress <- matrix(c(0,0,1), nrow=3, ncol=3, byrow=TRUE)
das <- list(dpress, anxiety, stress)
inItemTraitAdj <- rbind(das[[1]], das[[2]], das[[3]])

#--- 3 dimensional gpcm
g3 <- ple.lma(inData, model.type="gpcm", inItemTraitAdj, inTraitAdj, tol=1e-03)
s <- set.up(inData, model.type='gpcm', inTraitAdj, inItemTraitAdj)
convergenceGPCM(g3$item.log, g3$nitems, g3$ncat, g3$nless, s$LambdaName)
```

dass	<i>Dateframe of responses to items from depression, anxiety, and stress scales</i>
------	--

Description

The dass data are responses from a random sample of 1,000 individuals collected during the period 2017 – 2019. The data were retrieved July 2020. The items included here are on scales designed to measure depression (14 items), anxiety (13 items), and stress (15 items). The 42 items were presented online and in random order. Respondents were instructed to consider the last week when responding to the items using the following categories: (1) Did not apply to me at all; (2) Applied to me to some degree, or some of the time; (3) Applied to me to a considerable degree, or a good part of the time; (4) Applied to me very much, or most of the time.

Usage

dass

Format

A data frame with 1,000 rows (respondents) and 42 columns (items):

- d1** I couldn't seem to experience any positive feeling at all.
- d2** I just couldn't seem to get going
- d3** I felt that I had nothing to look forward to
- d4** I felt sad and depressed
- d5** I felt that I had lost interest in just about everything
- d6** I felt I wasn't worth much as a person
- d7** I felt that life wasn't worthwhile
- d8** I couldn't seem to get any enjoyment out of the things I did
- d9** I felt down-hearted and blue
- d10** I was unable to become enthusiastic about anything
- d11** I felt I was pretty worthless
- d12** I could see nothing in the future to be hopeful about
- d13** I felt that life was meaningless
- d14** I found it difficult to work up the initiative to do things
- a1** I was aware of dryness of my mouth
- a2** I experienced breathing difficulty (eg, excessively rapid breathing, breathlessness in the absence of physical exertion)
- a3** I had a feeling of shakiness (eg, legs going to give way)
- a4** I felt that I was using a lot of nervous energy
- a5** I had a feeling of faintness
- a6** I perspired noticeably (eg, hands sweaty) in the absence of high temperatures or physical exertion
- a7** I felt scared without any good reason
- a8** I had difficulty in swallowing
- a9** I was aware of the action of my heart in the absence of physical exertion (eg, sense of heart rate increase, heart missing a beat)
- a10** I felt I was close to panic
- a11** I felt terrified
- a12** I was worried about situations in which I might panic and make a fool of myself
- a13** I experienced trembling (eg, in the hands)
- s1** I found myself getting upset by quite trivial things
- s2** I tended to over-react to situations
- s3** I found it difficult to relax

- s4 I found myself in situations that made me so anxious I was most relieved when they ended
- s5 I found myself getting upset rather easily
- s6 I found myself getting impatient when I was delayed in any way (eg, elevators, traffic lights, being kept waiting)
- s7 I felt that I was rather touchy
- s8 I found it hard to wind down
- s9 I found that I was very irritable
- s10 I found it hard to calm down after something upset me
- s11 I feared that I would be thrown off by some trivial but unfamiliar task
- s12 I found it difficult to tolerate interruptions to what I was doing
- s13 I was in a state of nervous tension
- s14 I was intolerant of anything that kept me from getting on with what I was doing
- s15 I found myself getting agitated

Source

<https://openpsychometrics.org>

Examples

```
data(dass)
head(dass)
```

error.check

Checks for basic errors in input to the 'ple.lma' function

Description

This function looks at the input to the main function (ple.lma) and checks for 11 different possible errors. If an error is detected, the function issues a warning and stops any further execution. This function is internal to 'ple.lma' but can be used outside of the wrapper function.

Usage

```
error.check(inData, model.type, inTraitAdj = NULL, inItemTraitAdj = NULL)
```

Arguments

inData	Data frame with columns corresponding to categorical variables and rows to the number of cases
model.type	Type of model that will be fit to data
inTraitAdj	Trait x Trait adjacency matrix (not required for independence)
inItemTraitAdj	Item x Trait adjacency matrix (not required for independence)

Value

Message whether error was detected in input, and if so the nature of the error

Examples

```
#--- some data
data(dass)
inData <- dass[1:250,c("d1", "d2", "d3", "a1","a2","a3","s1","s2","s3")]

#--- no errors
error.check(inData, model.type="independence")

#--- for unidimensional
inTraitAdj <- matrix(1, nrow=1, ncol=1)
inItemTraitAdj <- matrix(1, nrow=9, ncol=1)

#--- no errors
error.check(inData, model.type="rasch", inTraitAdj, inItemTraitAdj)
error.check(inData, model.type="gpcm", inTraitAdj, inItemTraitAdj)
error.check(inData, model.type="nominal", inTraitAdj, inItemTraitAdj)
```

fit.gpcm

*Fits LMA model where category scale values equal $a_{im} * x_j$*

Description

Function estimates the parameters of LMA models with fixed category scores multiplied by an item weight parameter. This function can be used to estimate the LMA model corresponding to is a generalized partial credit model for multi-category items and the 2 parameter logistic model for dichotomous items. The function sets up log objects and model formula. In the case of unidimensional models, the function iterates over item regressions; whereas, for multidimensional models, the function iterates between the item and phi regressions. This function is called from 'ple.lma', but can be run outside of 'ple.lma'.

Usage

```
fit.gpcm(
  Master,
  Phi.mat,
  PersonByItem,
  TraitByTrait,
  item.by.trait,
  tol,
  npersons,
  nitens,
  ncat,
```



```

nless,
ntraits,
Maxnphi,
pq.mat,
starting.sv,
ItemNames,
LambdaName,
LambdaNames,
PhiNames
)

```

Arguments

Master	Master data set in long format
Phi.mat	Matrix of starting values of association parameters
PersonByItem	Person by item matrix of responses (same as inData)
TraitByTrait	Trait by trait adjacency matrix (same as inTraitAdj)
item.by.trait	Item by trait vector indicating trait item load on (same as inItemTraitAdj)
tol	Criterion used to determine convergence
npersons	Number of persons
nitems	Number of items
ncat	Number of categories per item
nless	Number of categories minus 1 (i.e., unique lambdas)
ntraits	Number of latent traits
Maxnphi	Number of phi parameters to be estimated
pq.mat	Used to compute rest-scores and totals
starting.sv	Fixed category scores
ItemNames	Names of items needed label output
LambdaName	Names of lambdas needed for formula of the item regressions
LambdaNames	Names of lambdas needed for formula of the stacked regression
PhiNames	Name of phi parameters (Null for uni-dimensional models)

Value

item.log History over iterations of the algorithm for items' log likelihood, lambda, and a parameter
phi.log History over iterations of the algorithm for log likelihood, lambdas and phi parameters
criterion Current value of the convergence statistic which is the maximum of items' absolute differences between the current and previous value of the log likelihood
estimates An item by parameter matrix of estimated item parameter where the first column are items' log likelihood
Phi.mat Estimated matrix of association parameters
fitem Formula for item data

fstack Formula for stacked data
 item.mlogit Summary from final run of mlogit for item regressions for each item
 phi.mlogit Summary from final run mlogit for stacked regression
 mpl.item Value of maximum of log ple function from fitting items (i.e., sum of logLike)
 mpl.phi Value of maximum of log ple function from stacked regression to get phi estimates
 AIC Akaike information criterion for pseudo-likelihood (smaller is better)
 BIC Bayesian information criterion for pseudo-likelihood (smaller is better)

Examples

```

data(dass)
inData <- dass[1:250,c("d1", "d2", "a1", "a2", "s1", "s2")]
#--- unidimensional
inTraitAdj <- matrix(1, nrow=1, ncol=1)
inItemTraitAdj <- matrix(1, nrow=6, ncol=1)

# Need to set up data
s <- set.up(inData, model.type='gpcm', inTraitAdj, inItemTraitAdj, tol=1e-03)

g <- fit.gpcm(s$Master, s$Phi.mat, s$PersonByItem, s$TraitByTrait,
             s$item.by.trait, s$tol, s$npersons, s$nititems, s$ncat,
             s$nlless, s$ntraits, s$Maxnphi, s$pq.mat, s$starting.sv,
             s$ItemNames, s$LambdaName, s$LambdaNames, s$PhiNames)

```

fit.independence *Fits the log-linear model of independence*

Description

This function fits by the log-linear model of independence (i.e., only includes marginal effect terms) using pseudo-likelihood estimation. This provides a baseline model with which to compare other models. The independence maximum of the loglikelihood can be used as a measure of no association. The input to the function is only the Master data set and the names of marginal effect terms and items, all of which are created by the 'set.up' function. This function is called from 'ple.lma' or can be run output of wrapper.

Usage

```
fit.independence(Master, LambdaNames, LambdaName, ItemNames)
```

Arguments

Master	Master data set from set.up
LambdaNames	Needed to define formula
LambdaName	Used for column names of matrix estimates
ItemNames	Used for row names of number of item by parameter matrix of estimated Lambda parameters

Value

phi.mlogit Parameters estimates and mlpl = logLike output from mnlogit
 fstack Formula used in stacked regression
 estimates Item by parameter estimates matrix
 mlpl.phi Maximum of log pseudo-likelihood from stacked regression
 AIC Akaike information criterion for pseudo-likelihood (smaller is better)
 BIC Bayesian information criterion for pseudo-likelihood (smaller is better)

Examples

```
#--- data and set-up
data(dass)
inData <- dass[1:250,c("d1", "d2", "d3", "a1","a2","a3","s1","s2","s3")]
s <- set.up(inData, model.type='independence')

#--- fit independence model
ind <- fit.independence(s$Master, s$LambdaNames, s$LambdaName, s$ItemNames)
```

fit.nominal

Fits the nominal model

Description

Function estimates the parameters of LMA models where the category scale are estimated. The function can be used to estimate the parameters of the LMA model corresponding the nominal model (for multi-category items) and the 2 parameter logistic model for dichotomous items. The function sets up log object(s) and model formula. In the case of unidimensional models, the function iterates over item regressions; whereas, for multidimensional models, the function iterates between the item and phi regressions. This function is called from 'ple.lma', but can be run outside of 'ple.lma'.

Usage

```
fit.nominal(
  Master,
  Phi.mat,
  starting.sv,
  pq.mat,
  tol,
  PersonByItem,
  TraitByTrait,
  ItemByTrait,
  item.by.trait,
  ItemNames,
  LambdaNames,
```

```

    NuNames,
    LambdaName,
    NuName,
    PhiNames,
    npersons,
    nitems,
    ncat,
    nless,
    ntraits,
    Maxnphi
  )

```

Arguments

Master	Master data set in long format
Phi.mat	Matrix of starting values of the association parameters
starting.sv	Matrix starting values category scale values
pq.mat	Array used compute rest scores and total scores
tol	Value used to determine convergence of algorithm
PersonByItem	Same as inData (rows are response patterns)
TraitByTrait	Same as inTraitAdj (trait x trait adjacency)
ItemByTrait	Same as inItemTraitAdj (item x trait adjacency)
item.by.trait	One dimensional array indicating trait item loads on
ItemNames	Names of items in inData (i.e. columns names of categorical variables)
LambdaNames	Lambda names used in the Master and stacked data frames
NuNames	Nu names in Master data frame
LambdaName	Lambda names in formula for items
NuName	Nu names in formula for item regressions
PhiNames	Association parameter names for stacked regression
npersons	Number of persons
nitems	Number of items
ncat	Number of categories per item
nless	ncat-1 = number unique lambda and unique nus
ntraits	Number of traits
Maxnphi	Number of association parametets

Value

item.log Iteration history of LogLike, lambda, and item parameters
 phi.log Iteration history of LogLike, lambdas and phi parameters
 criterion Current value of the convergence statistic
 estimates Item x parameter matrix: LogLike, lambda and scale values

Phi.mat Estimated conditional correlation matrix
 fitem Formula for item data
 fstack Formula for stacked data
 item.mlogit Summaries from final run of mlogit for item regressions
 phi.mlogit Summary from final run of mlogit for stacked regression
 mlpl.item Max log pseudo-likelihood function from item regressions
 mlpl.phi Maximum of log pseudo-likelihood function from stacked regression
 AIC Akaike information criterion for pseudo-likelihood (smaller is better)
 BIC Bayesian information criterion for pseudo-likelihood (smaller is better)

Examples

```
data(dass)
inData <- dass[1:250,c("d1", "d2", "d3", "a1","a2","a3","s1","s2","s3")]
#--- unidimensional
inTraitAdj <- matrix(1, nrow=1, ncol=1)
inItemTraitAdj <- matrix(1, nrow=9, ncol=1)
s <- set.up(inData, model.type='nominal', inTraitAdj, inItemTraitAdj,
            tol=1e-02)

n1 <- fit.nominal(s$Master, s$Phi.mat, s$starting.sv, s$pq.mat, s$tol,
                 s$PersonByItem, s$TraitByTrait, s$ItemByTrait, s$item.by.trait,
                 s$ItemNames, s$LambdaNames, s$NuNames, s$LambdaName, s$NuName,
                 s$PhiNames, s$npersons, s$nitens, s$ncat,s$ nless, s$ntraits,
                 s$Maxnphi)
```

 fit.rasch

Fits an LMA using fixed category scores

Description

The LMA model with fixed category scores is fit by this function and the model corresponds to models in the Rasch family of item response models. The category scores can be set by either the user or the package defaults. The default category scores are equally spaced, sum to zero, and sum of squares equal 1. Scores can be set by user by specifying them in the item by category matrix of 'starting.sv'. The pseudo-likelihood algorithm only runs a single stacked regression. This function is called from 'ple.lma' but can also be run outside of the main wrapper function.

Usage

```
fit.rasch(
  Master,
  npersons,
  nitens,
  ncat,
```

```

nless,
Maxnphi,
pq.mat,
starting.sv,
LambdaNames,
PhiNames,
ItemNames,
LambdaName,
ntraits
)

```

Arguments

Master	Master data set in long format
npersons	Number of persons
nitems	Number of items
ncat	Number of categories
nless	Number of unique Lambdas (i.e., ncat-1)
Maxnphi	Number of phi parameters
pq.mat	One dimensional array to compute rest-scores
starting.sv	Fixed category scores
LambdaNames	Names of lambda paramters in Master and formula for stacked regression
PhiNames	Names of association parameters
ItemNames	Names of items
LambdaName	Names of lambdas used in output
ntraits	Number of traits

Value

estimates An item by parameter matrix of the maximum of the log likelihood, estimated item parameters (i.e., Lambdas), and the values of the fixed category scores.

fstack Formula for stacked regression

phi.mlogit Results from mlogit for stacked regression

estimates An item x parameter estimate matrix and fixed category scores used

Phi.mat Estimated phi parameters

mlpl.phi Value of maximum of log pseudo-likelihood function from the stacked regression

AIC Akaike information criterion for pseudo-likelihood (smaller is better)

BIC Bayesian information criterion for pseudo-likelihood (smaller is better)

Examples

```
#-- data(dass)
inData <- dass[1:250,c("d1", "d2", "d3", "a1","a2","a3","s1","s2","s3")]
#-- unidimensional
inTraitAdj <- matrix(1, nrow=1, ncol=1)
inItemTraitAdj <- matrix(1, nrow=9, ncol=1)

s <- set.up(inData, model.type='rasch', inTraitAdj, inItemTraitAdj)

r <- fit.rasch(s$Master, s$npersons, s$nititems, s$ncat, s$nless, s$Maxnphi,
              s$pq.mat, s$starting.sv, s$LambdaNames, s$PhiNames, s$ItemNames,
              s$LambdaName, s$ntraits)
```

FitStack

*Up-dates association parameters of the nominal model***Description**

Discrete choice model (conditional multinomial logistic regression model) is fit to stacked data to up-date the matrix of association parameters of the LMA that corresponds to the nominal item response model. This is a function internal to 'fit.nominal' and is used for multi-dimensional models. The function is similar to 'fit.StackGPCM'. This function is unlikely to be run outside of 'fit.nominal' or 'ple.lma'.

Usage

```
FitStack(
  Master,
  item.log,
  phi.log,
  fstack,
  TraitByTrait,
  pq.mat,
  npersons,
  nititems,
  ncat,
  nless,
  ntraits,
  Maxnphi,
  PhiNames,
  LambdaNames
)
```

Arguments

Master Master data set from which stacked data is created

item.log	Last row contains current scale values (item.history)
phi.log	Last row contains current estimates of phi
fstack	Formula for stacked regression
TraitByTrait	inTraitAdj matrix
pq.mat	Summing array to get rest scores and totals
npersons	Number of persons
nitems	Number of items
ncat	Number of categories per item
nless	Number of categories less 1 (unique lambdas & unique nus)
ntraits	Number of latent traits
Maxnphi	Number of phis to be estimated
PhiNames	Names of the Phi parameters
LambdaNames	Names of lambdas that correspond to those in Master

Value

Phi.mat Matrix of up-dated estimates of association (phi) parameters

phi.log History of iterations log likelihood and estimates of lambda and phi parameters

fitStackGPCM	<i>Up-dates association parameters of the GPCM by fitting model to stacked data</i>
--------------	---

Description

Discrete choice model (conditional multinomial logistic regression) is fit to stacked data to update matrix of association parameters of the LMA that corresponds to the generalized partial credit model. This function is called from 'fit.gpcm', which is called from 'ple.lma'. It is unlikely that it would be run outside of these wrappers. It is only slightly different from 'fitStack' for nominal models.

Usage

```
fitStackGPCM(
  Master,
  item.log,
  phi.log,
  fstack,
  TraitByTrait,
  starting.sv,
  npersons,
  nitems,
  ncat,
```



```

    nless,
    ntraits,
    Maxnphi,
    pq.mat,
    LambdaNames,
    PhiNames
  )

```

Arguments

Master	Master data set from which stacked data is created
item.log	Needed to get most recent values of scale values (item.log)
phi.log	History of estimates parameters from stacked regression
fstack	Forumla for stacked regression
TraitByTrait	inTraitAdj matrix
starting.sv	Fixed category scores
npersons	Number of persons
nitems	Number of items
ncat	Number of categories per item
nless	Number of unique lambdas and unique nus per item
ntraits	Number of latent traits
Maxnphi	Number of phi parameters to bet estimated (NULL for 1 dimensional)
pq.mat	Used to compute rest-scores and totals
LambdaNames	Needed for formula and data for up-dating phi (stacked regresson)
PhiNames	Null for 1D models

Value

Phi.mat Up-dated matrix of phi parameters
 item.log of iterations for LogLike, Lambda and phi parameters

item.gpcm	<i>Estimates item parameters of LMA with linear restrictions on category scores</i>
-----------	---

Description

This function is internal to the function 'fit.gpcm' and performs the item regressions. It is a core function of the pseudo-likelihood algorithm for items of the GPCM. The function calls function 'itemGPCM.data' to create the data for input into 'mlogit', which is use to fit a conditional multinomial model for each item. The up-dated scale values are put into the Master data frame and the 'item.log' array. It generally would not run outside of 'fit.gpcm' or 'ple.lma'.

Usage

```

item.gpcm(
  Master,
  item.log,
  Phi.mat,
  fitem,
  TraitByTrait,
  PersonByItem,
  npersons,
  nitems,
  ncat,
  nless,
  ntraits,
  Maxnphi,
  pq.mat,
  starting.sv,
  LambdaName
)

```

Arguments

Master	Master data frame
item.log	History over iterations of items' log likelihood and estimates of lambda, and item parameters
Phi.mat	Starting value of matrix of association parameters (optional)
fitem	Formula for item regressions
TraitByTrait	Trait adjacency matrix (same as inTraitAdj)
PersonByItem	Same as inData
npersons	Number of persons
nitems	Number of items
ncat	Number of categories per item
nless	Number of unique lambdas and unique nus per item
ntraits	Number of latent traits
Maxnphi	Number of phi parameters to bet estimated (NULL for 1 dimensional)
pq.mat	Used to compute rest-scores and totals
starting.sv	Fixed category scores
LambdaName	Lambda names for formula for items item regressions

Value

Master Master data frame with up-dated category scores for items
item.log Up-dated history array over iterations of the algorithm of items' log likelihood and estimated lambda and alpha parameters

ItemData	<i>Prepares data for up-dating scale value parameters of nominal model</i>
----------	--

Description

This function creates a data frame, 'item data', to be used in the item regressions for nominal models. It computes weighted rest scores and totals, including correlated traits. This function is internal to 'ItemLoop' and it is unlikely to be run outside of 'fit.nominal' or 'ple.lma'.

Usage

```
ItemData(
  Master,
  ItemID,
  Phi.mat = Phi.mat,
  npersons,
  nitems,
  ntraits,
  ncat,
  nless,
  TraitByTrait,
  pq.mat,
  LambdaName,
  NuName
)
```

Arguments

Master	Master data frame
ItemID	The item for which scale values are being up-dated
Phi.mat	Current estimate conditional covariance matrix (i.e., association paramters)
npersons	Number of persons
nitems	Number of items
ntraits	Number of traits
ncat	Number of categories
nless	Number of unique lambdas and unique nus
TraitByTrait	Same as inTraitAdj
pq.mat	One dimemsinal array used to get rest and totals scores
LambdaName	Name of lambdas for in item regression
NuName	Name of nus in item regression

Value

ItemFit Data frame used to up-date scale values

ItemGPCM.data	<i>Creates data frame up-dating phi parameters of the gpcm.</i>
---------------	---

Description

This function creates a data frame, 'gpcm.item.data', to be used in the item regressions of LMA models where category scales values are fixed. Sets up data for up-dating alpha parameters of the LMA that corresponds to the GPCM. This function is internal to 'item.gpcm' and it is unlikely to be run outside of 'fit.gpcm' or 'ple.lma'.

Usage

```
ItemGPCM.data(
  Master,
  ItemID,
  Phi.mat,
  TraitByTrait,
  pq.mat,
  starting.sv,
  npersons,
  nitens,
  ncat,
  nless,
  ntraits,
  LambdaName
)
```

Arguments

Master	Data frame of all data in long format
ItemID	Specifies the item for which a data frame is created to be input into an item regression
Phi.mat	Starting value of matrix of association parameters
TraitByTrait	Trait by trait adjacency matrix (same as inTraitAdj)
pq.mat	Array used to compute rest scores
starting.sv	Matrix of item category scores that are fixed
npersons	Number of persons
nitens	Number of items
ncat	Number of categories
nless	Number of unique lambdas (ncat-1)
ntraits	Number of latent traits
LambdaName	Names for lambda for item regression

Value

gpcm.item.data Data frame for item to be used up-dated in an item regression for specified item

ItemLoop	<i>loops through items and up-dates estimates of scale values for each item in Nominal Model</i>
----------	--

Description

This is a core function of the pseudo-likelihood algorithm for items of the nominal model. The function calls function 'ItemData' to create the data frame for input into 'mlogit', which is use to fit a conditional multinomial model (i.e., a discrete choice model) for each item. The up-dated scale are put into the Master data frame and added to the item.log array. Generally the function would not run outside of 'fit.nominal' or 'ple.lma'.

Usage

```
ItemLoop(
  Master,
  item.log,
  Phi.mat = Phi.mat,
  PersonByItem,
  npersons,
  nitems,
  ntraits,
  ncat,
  nless,
  TraitByTrait,
  pq.mat,
  LambdaName,
  NuName,
  fitem
)
```

Arguments

Master	Current master frame
item.log	Iteration history for the items parameters
Phi.mat	Current estimate of Phi.mat
PersonByItem	Person by item adjacency matrix (same as inData)
npersons	Number of persons
nitems	Number of items
ntraits	Number of traits
ncat	Number of categories

nless	Number of unique lambda and unique nus (ncat-1)
TraitByTrait	TraitsByTrait adjacency matrix (sam as TraitAdj)
pq.mat	One dimensional array for computing rest-scores
LambdaName	Marginal effect names used in formula and item data frame for item regressions
NuName	Scale values names in used in formula and item data frame for item regressions
fitem	Formula for item regression

Value

Master Master data frame up-dated scale values for all items
 item.log Iteration history of item parameters where the last row showing results from the current iteration

iterationPlot	<i>Plots estimated parameters by iteration for the gpcm and nominal models</i>
---------------	--

Description

This is a utility function that plots the estimated item parameters by iterations. The plots can be used to determine how many iterations are required to get close to final values. This functions can be used uni- or multi-dimensional gpcm and models. The number of pages equals the number of items and each page has the plots of marginal effects (left side) and category scale values or alph parameters (right).

Usage

```
iterationPlot(model.fit)
```

Arguments

model.fit Object from fitting nominal or gpcm model to data

Value

Plots of estimated parameters by iteration

Examples

```
data(dass)
inData <- dass[1:250,c("d1", "d2", "d3", "a1","a2","a3","s1","s2","s3")]
#--- input for uni-dimensional
inTraitAdj <- matrix(1, nrow=1, ncol=1)
inItemTraitAdj <- matrix(1, nrow=9, ncol=1)
```

```
#--- generalized partial credit model
g1 <- ple.lma(inData, model.type="gpcm", inItemTraitAdj, inTraitAdj)
iterationPlot(g1)

#--- nominal response model
n1 <- ple.lma(inData, model.type="nominal", inItemTraitAdj,inTraitAdj)
iterationPlot(n1)

#--- Multidimensional models
inTraitAdj <- matrix(1, nrow=3, ncol=3)

dpress <- matrix(c(1,0,0), nrow=3, ncol=3, byrow=TRUE)
anxiety <- matrix(c(0,1,0), nrow=3, ncol=3, byrow=TRUE)
stress <- matrix(c(0,0,1), nrow=3, ncol=3, byrow=TRUE)
das <- list(dpress, anxiety, stress)
inItemTraitAdj <- rbind(das[[1]], das[[2]], das[[3]])

g3 <- ple.lma(inData, model.type="gpcm", inItemTraitAdj, inTraitAdj)
iterationPlot(g3)

n3 <- ple.lma(inData, model.type="nominal", inItemTraitAdj, inTraitAdj)
iterationPlot(n3)
```

lma.summary

Produces a summary of results

Description

This utility function creates a summary list with five elements. The first is a 'report' that contains a summary of characteristics of the data, the model specification, convergence information, and fit statistics. The second and third elements complete the model specification and are the trait adjacency matrix ('TraitByTrait') and the item x trait adjacency matrix ('ItemByTrait'), respectively. The fourth element, 'estimates', contains a matrix of item parameters, and the fifth element, 'phi.mat' contains association parameter estimates.

Usage

```
lma.summary(model.fit)
```

Arguments

model.fit A list object from fitting a model to data

Value

results A list with summary information

Examples

```
#--- 3 items from depression, anxiety and stress scales of
# the daass for 250 cases
data(dass)
inData <- dass[1:250,c("d1", "d2", "d3", "a1","a2","a3","s1","s2","s3")]

#--- log-linear model of independence
ind <- ple.lma(inData, model.type="independence")
noquote(lma.summary(ind))

#--- input for uni-dimensional
inTraitAdj <- matrix(1, nrow=1, ncol=1)
inItemTraitAdj <- matrix(1, nrow=9, ncol=1)

#--- rasch family
r1 <- ple.lma(inData, model.type="rasch", inItemTraitAdj, inTraitAdj)
lma.summary(r1)
#--- Or if specific output is desired
noquote(lma.summary(r1)$report)
lma.summary(r1)$TraitByTrait
lma.summary(r1)$ItemByTrait
lma.summary(r1)$estimates
lma.summary(r1)$phi

#--- generalized parial credit model
g1 <- ple.lma(inData, model.type="gpcm", inItemTraitAdj, inTraitAdj, tol=1e-03)
lma.summary(g1)$report
lma.summary(g1)$estimates
lma.summary(g1)$phi

#--- nominal response model
n1 <- ple.lma(inData, model.type="nominal", inItemTraitAdj, inTraitAdj, tol=1e-03)
noquote(lma.summary(n1))
```

ple.lma

Main function for estimating parameters of LMA models

Description

This function is a wrapper function that checks for errors in the input (i.e., ‘error.check’), sets up required objects and data (i.e., ‘set.up’), calls function to fit specified model (either ‘fit.independence’, ‘fit.rasch’, ‘fit.gpcm’, or ‘fit.nomial’), and outputs an extensive list of details and results. The required input for all models consist of a data frame where elements are consecutive integers (1, 2, ...) indicating the category chosen by each case/individual (rows) for each variable (columns), and the model type. For the LMA models that correspond to item response theory models require an Item x Trait adjacency matrix (‘inItemTraitAdj’) and a Trait x Trait adjacency matrix (‘inTraitAdj’).

Optional input include the tolerance value ('tol') which is used to for determine whether the pseudo-likelihood algorithm has converged for a gpcm or nominal model default=1e-6). Additional optional input ('starting.sv') is an item by category a matrix of starting scale values for the nominal model or fixed category scores for the gpcm and rasch models. The default category scale values/scores are equally spaced, centered at zero, and the sum of squared values equals 1. The final optional input is a trait x trait ('starting.phi') matrix of starting values for the association parameter matrix (default=identity matrix).

Usage

```
ple.lma(
  inData,
  model.type,
  inItemTraitAdj = NULL,
  inTraitAdj = NULL,
  tol = NULL,
  starting.sv = NULL,
  starting.phi = NULL
)
```

Arguments

<code>inData</code>	A person x item data matrix or data frame with elements equal to reponse options chosen by an individual.
<code>model.type</code>	Model to be fit (nominal, gpcm, rasch, independence) to data.
<code>inItemTraitAdj</code>	An Item x Trait adjacency matrix indicating what trait an item loads on.
<code>inTraitAdj</code>	A Trait x Trait adjacency matrix indicating relationship among traits.
<code>tol</code>	Convergence criterion, default = 1e-6
<code>starting.sv</code>	Starting category scale values/fixed scores
<code>starting.phi</code>	Starting matrix of phi parameters (i.e., conditional covariance matrix)

Value

`model.type` The model (nominal, gpcm, rash, or independence) that was fit to data

`TraitByTrait` The Trait x Trait adjacency matrix used.

`ItemByTrait` The Item x Trait adjacency matrix.

`item.by.trait` One dimensional version of `ItemByTrait` that gives the number of trait.

`ItemNames` Names of items in `inData`

`PhiNames` Names of the association parameters (i.e., phi)

`formula.item` Formula used to up-date item parameters via item regressions.

`formula.phi` Formula used to up-date association parameters via stacked regression.

`npersons` Number of persons in data set.

`nitems` Number of items.

`ncat` Number of categories per item.

nless Number of unique marginal effects & unique scale values.
 Maxnphi Number of association parameters estimated.
 ntraits Number of traits.
 starting.sv Starting scale values for nominal model or fixed scores for rasch or gpcm.
 tol Used to determine convergence default= 1e-7
 criterion Final value criterion at convergence
 item.log Item iteration history plus maximum of the LogLike for each item
 phi.log Association parameter iteration history
 estimates Item x Parameter matrix where 1st column is max LogLike for each item and remaining columns are item parameter estimate
 Phi.mat Estimated conditional correlation matrix
 item.mlogit Output from final mlogit fit to items
 phi.mlogit Output form final mlogit fit to stacked data
 mpl.item Max Log(pseudo-likelihood) function from item models (i.e. sum of first column of estimates)
 mpl.phi Max Log(pseudo-likelihood) function from stacked regression(s).
 AIC Akaike information criterion for pseudo-likelihood (smaller is better)
 BIC Bayesian information criterion for pseudo-likelihood (smaller is better)

Examples

```
#--- some data, 3 items from dpression, anxiety and stress scales
#   and only 250 cases out of possible 1000
data(dass)
inData <- dass[1:250,c("d1", "d2", "d3", "a1","a2","a3","s1","s2","s3")]

#--- log-linear model of independence
ind <- ple.lma(inData, model.type="independence")

#--- input for uni-dimensional
inTraitAdj <- matrix(1, nrow=1, ncol=1)
inItemTraitAdj <- matrix(1, nrow=9, ncol=1)

#--- rasch family
r1 <- ple.lma(inData, model.type="rasch", inItemTraitAdj, inTraitAdj)

#--- rasch with alternative scores
scores <- matrix(c(0,1,2,3),nrow=9,ncol=4,byrow=TRUE)
r1b <- ple.lma(inData, model.type="rasch", inItemTraitAdj,
               inTraitAdj, starting.sv=scores)

#--- generalized partial credit model
g1 <- ple.lma(inData, model.type="gpcm", inItemTraitAdj, inTraitAdj)

#--- gpcm with alternative scores
```

```

scores <- matrix(c(0,1,2,3),nrow=9,ncol=4,byrow=TRUE)
g1b <- ple.lma(inData, model.type="gpcm", inItemTraitAdj, inTraitAdj, starting.sv=scores)

#--- nominal response model
n1 <- ple.lma(inData, model.type="nominal", inItemTraitAdj,inTraitAdj)

#--- re-run nominal model with input starting values and phi
#   and setting stronger convergence criterion.
sv <- n1$estimates[, 6:9]
phi <- n1$Phi.mat
n1b <- ple.lma(inData, model.type="nominal", inItemTraitAdj,
              inTraitAdj, starting.sv=sv, starting.phi=phi, tol=1e-8)

#--- Multidimensional models
#--- re-define inTraitAdj and inItemTraitAdj for 3 dimensional models
inTraitAdj <- matrix(1, nrow=3, ncol=3)

dpress <- matrix(c(1,0,0), nrow=3, ncol=3, byrow=TRUE)
anxiety <- matrix(c(0,1,0), nrow=3, ncol=3, byrow=TRUE)
stress <- matrix(c(0,0,1), nrow=3, ncol=3, byrow=TRUE)
das <- list(dpress, anxiety, stress)
inItemTraitAdj <- rbind(das[[1]], das[[2]], das[[3]])

#--- 3 dimensional rasch
r3 <- ple.lma(inData, model.type="rasch", inItemTraitAdj, inTraitAdj)

#--- 3 dimensional gpcm
g3 <- ple.lma(inData, model.type="gpcm", inItemTraitAdj, inTraitAdj)

#--- 3 dimensional nominal
n3 <- ple.lma(inData, model.type="nominal", inItemTraitAdj, inTraitAdj)

#--- 2 parameter logistic IRT model fit to responses to
#   10 dichotomous Vocabulary items from from 2018 GSS
#   by 1309 respondents
data(vocab)
inItemTraitAdj <- matrix(1, nrow=10, ncol=1)
inTraitAdj <- matrix(1, nrow=1, ncol=1)

#--- rasch irt
rasch <- ple.lma(inData=vocab, model.type="rasch", inItemTraitAdj, inTraitAdj, tol=1e-03)

#--- 2 pl as a gpcm model
g.2pl <- ple.lma(inData=vocab, model.type="gpcm", inItemTraitAdj, inTraitAdj, tol=1e-03)

#--- 2 pl as a nominal model
n.2pl <- ple.lma(inData=vocab, model.type="nominal", inItemTraitAdj, inTraitAdj, tol=1e-03)

```

reScaleItem	<i>Re-scales the category scale values and Phi after convergence of the nominal model</i>
-------------	---

Description

This auxillary function only applies to nominal models after estimating the parameters of the model. During estimation that scaling identification constraint is put on conditional variances (i.e., phi_mm) such that they equal 1. This function provide an alternative identification constraint after the algorithm has converged. This function allow a user to tease apart the strength and structure of associations. The alternative scaling identification constraint is to set the sum of category scale values equals 0 and the sum of squares equal to 1. The phi parameters are adjusted accordingly. Only one item per trait should be selected for the identification constraint and this is indicated by the object anchor.

Usage

```
reScaleItem(model.fit, anchor)
```

Arguments

model.fit	Model object for a nominal model
anchor	Indicator of item(s) to place scaling constraint on.

Value

sNu Re-scaled category scale values
sPhi.mat Re-scale phi matrix (conditional covariance matrix)

Examples

```
#--- 3 items from depression, anxiety, and stress scales
#   for 250 cases out of possible 1000
data(dass)
inData <- dass[1:250,c("d1", "d2", "d3", "a1","a2","a3","s1","s2","s3")]
inTraitAdj <- matrix(1, nrow=1, ncol=1)
inItemTraitAdj <- matrix(1, nrow=9, ncol=1)
#--- nominal response model
n1 <- ple.lma(inData, model.type="nominal",inItemTraitAdj,inTraitAdj,tol=1e-03)
anchor <- c(1,0,0,0,0,0,0,0,0)
reScaleItem(model.fit=n1, anchor)

#--- Multidimensional models
inTraitAdj <- matrix(1, nrow=3, ncol=3)
dpress <- matrix(c(1,0,0), nrow=3, ncol=3, byrow=TRUE)
anxiety <- matrix(c(0,1,0), nrow=3, ncol=3, byrow=TRUE)
```

```

stress <- matrix(c(0,0,1), nrow=3, ncol=3, byrow=TRUE)
das <- list(dpress, anxiety, stress)
inItemTraitAdj <- rbind(das[[1]], das[[2]], das[[3]])

n3 <- ple.lma(inData, model.type="nominal", inItemTraitAdj, inTraitAdj, tol=1e-03)
anchor <- c(1,0,0, 0,1,0, 1,0,0)
reScaleItem(model.fit=n3, anchor)

```

Scale	<i>Imposes scaling constraint to identify parameters of the LMA (nominal) model</i>
-------	---

Description

Scaling is internal to the function 'fit.nominal', which corresponds to the nominal item response theory model. It imposes the required scaling identification constraint by transforming the conditional covariance matrix 'Phi.mat' to a conditional correlation matrix (i.e., set $\phi_{mm}=1$ for all m). The inverse transformation is applied to the current category scale value estimates and these are put back into the Master data frame so that data are ready for the next iteration of the algorithm.

Usage

```

Scale(
  Master,
  item.log,
  Phi.mat,
  PersonByItem,
  npersons,
  nitems,
  ncat,
  nless,
  ntraits,
  item.by.trait
)

```

Arguments

Master	Current Master data frame.
item.log	Iteration history of LogLike, lambda, and item parameters
Phi.mat	Current phi matrix
PersonByItem	inData
npersons	Number of persons
nitems	Number of items

<code>ncat</code>	Number of categories
<code>nless</code>	Number of unique nus (<code>ncat-1</code>)
<code>ntraits</code>	Number of (latent) dimensions
<code>item.by.trait</code>	Indicates the trait an item load on.

Value

Master	Master frame with re-scaled scale values
Phi.mat	Re-scaled matrix of association parameters

ScaleGPCM

Imposes scaling constraint to identify parameters of LMA (GPCM)

Description

Scaling is internal to the function 'fit.gpcm', which fits the GPCM version of the LMA. It imposes the required scaling identification constraint by transforming the conditional covariance matrix 'Phi.mat' to a conditional correlation matrix. The inverse transformation is applied to the current estimates of the slope or 'a' parameters. Category scale values are recomputed using the re-scale slopes (i.e., $\text{nu} = a * x$) and these are put back into the Master data set so that data are ready for the next iteration of the algorithm.

Usage

```
ScaleGPCM(
  Master,
  item.log,
  Phi.mat,
  PersonByItem,
  npersons,
  nitems,
  ncat,
  nless,
  ntraits,
  starting.sv,
  item.by.trait
)
```

Arguments

Master	Master/main data set
item.log	Iteration history array, last row are current parameters
Phi.mat	Current phi matrix
PersonByItem	inData (response patterns)
npersons	Number of persons

nitems	Number of items
ncat	Number of categories
nless	Number of unique lambdas (ncat-1)
ntraits	Number of latent traits
starting.sv	Matrix of fixed category scores (nitems x ncat)
item.by.trait	Object that indicates which trait item loads on

Value

Master Master data set with re-scaled scale values

Phi.mat Re-scaled matrix of association parameters

scalingPlot	<i>Graphs estimated scale values by integers of the LMA (nominal) model</i>
-------------	---

Description

This function plots the estimated item scale values (i.e, nus) by integers to see shape of scaling of the categories. A linear regression is overlaid in the plot to help assess linearity. The dashed red line overlaid in the plot is the linear regression line of the scale values on integers.

Usage

```
scalingPlot(model.fit)
```

Arguments

model.fit Output from a nominal model

Value

plots of estimated scale values by integers

Examples

```
#--- some data, 2 items from depression, anxiety and stress scales
#   for 250 cases out of possible 1000
data(dass)
inData <- dass[1:250,c("d1", "d2", "a1", "a2", "s1", "s2")]
inTraitAdj <- matrix(1, nrow=1, ncol=1)
inItemTraitAdj <- matrix(1, nrow=6, ncol=1)
n1 <- ple.lma(inData, model.type="nominal", inItemTraitAdj, inTraitAdj, tol=1e-03)
scalingPlot(n1)
```

 set.up

Sets up the data based on input data and model specifications

Description

This function sets up the data and sets constants that are essentially the same for all models. This is used within the main wrapper function 'ple.lma', but can also be run independently. If a user wants to run the functions 'fit.independence', 'fit.rasch', 'fit.gpcm', or 'fit.nominal', the set up function should be run prior to using these functions to create required input. Such an approach can speed up replication studies because 'set.up' would only need to be run once and the response vector (i.e., named 'y') in the Master data frame be replaced by a new one.

Usage

```
set.up(
  inData,
  model.type,
  inTraitAdj = NULL,
  inItemTraitAdj = NULL,
  tol = NULL,
  starting.sv = NULL,
  starting.phi = NULL
)
```

Arguments

inData	A person x item Data frame with response patterns
model.type	Type of model to be fit
inTraitAdj	Trait x Trait adjacency matrix (NULL for independence)
inItemTraitAdj	Item x Trait adjacency matrix (NULL for independence)
tol	Tolerance for determining convergence (default: 1e-06)
starting.sv	Starting category scale values/fixed scores (default: sum equal to zero and sum of squares equal to 1)
starting.phi	optional: Starting phi matrix (default: identity matrix)

Value

PersonByItem inData (rows are response patterns)
 TraitByTrait Trait x Trait adjacency matrix
 ItemByTrait Item x Trait adjacency matrix
 item.by.trait Need for re-scaling phi.mat
 starting.sv An item by number of category matrix with starting values for scale values for nominal model and fixed category scores for gpcm and rasch models
 ItemNames Names of items in inData and PersonByItem

LambdaName Short list of lambda names needed for item regressions
 NuName Short list of nu names needed for item regressions
 LambdaNames Long list of lambdas using in Master data set
 NuNames Long list of nu using in Master data set
 PhiNames Names of the unique phi parameters
 npersons Number of individual or persons in data
 nitems Number of items
 ncat Number of categories
 nless Number of unique lambdas and unique nus
 ntraits Number of traits
 Maxnphi Number of phis to estimate
 Nstack Length of master data set
 pq.mat An array used to computed (weighted) rest-scores
 Phi.mat A number of traits x number of traits Phi matrix (default: the identity matrix)
 Master Master data set formatted for input to to mlogit
 tol Tolerance for determining convergence

Examples

```

data(dass)
inData <- dass[1:250,c("d1", "d2", "d3", "a1","a2","a3","s1","s2","s3")]

#--- to set data up for model of independence
ind.setup <- set.up(inData, model.type="independence")

#--- for model specification for uni-dimensional models
inTraitAdj <- matrix(1, nrow=1, ncol=1)
inItemTraitAdj <- matrix(1, nrow=9, ncol=1)

i.setup <- set.up(inData, model.type='independence')

r.setup <- set.up(inData, model.type='rasch', inTraitAdj,
                 inItemTraitAdj)

g.setup <- set.up(inData, model.type='gpcm', inTraitAdj,
                 inItemTraitAdj)

n.setup <- set.up(inData, model.type='nominal', inTraitAdj,
                 inItemTraitAdj)

```

StackData	<i>Prepares data for up-dating association parameters of a multidimensional nominal LMA</i>
-----------	---

Description

Prepares data frame for input to 'mnllogit' for the stacked regression to obtain association parameters of the multidimensional LMA models corresponding to the Nominal item response model. This function is called from 'fit.nominal'. It generally would not run outside of either 'fit.nominal' or 'ple.lma'.

Usage

```
StackData(
  Master,
  item.log,
  phi.log,
  pq.mat,
  npersons,
  nitems,
  ncat,
  nless,
  ntraits,
  Maxnphi,
  PhiNames,
  LambdaNames
)
```

Arguments

Master	Master data frame from which stacked data is created
item.log	Last row contains current scale values (item.history)
phi.log	Last row contains current estimates of phi
pq.mat	Summing array to get rest scores and totals
npersons	Number of persons
nitems	Number of items
ncat	Number of categories per item
nless	Number of categories less 1 (i.e., unique lambdas and unique nus)
ntraits	Number of latent traits
Maxnphi	Number of phis to be estimated
PhiNames	Names of the Phi parameters
LambdaNames	Names of lambdas that correspond to those in Master

Value

Phi.mat Up-dated matrix of phi parameters

phi.log History of iterations for LogLike, Lambda and phi parameters

StackDataGPCM	<i>Prepares data for up-dating association parameters of LMA (GPCM) model</i>
---------------	---

Description

Prepares data frame for input to 'mnlogit' for the stacked regression to obtain association parameters of the multidimensional LMA models corresponding to the GPCM. This function is called from 'fit.gpcm'. It generally would not run outside of 'fit.nominal' or 'ple.lma'.

Usage

```
StackDataGPCM(
  Master,
  item.log,
  starting.sv,
  npersons,
  nitems,
  ncat,
  nless,
  Maxnphi,
  pq.mat,
  LambdaNames,
  PhiNames
)
```

Arguments

Master	Current master data frame
item.log	Current history of iterations from which currenata parameters are drawn
starting.sv	Fixed category scores
npersons	Number of persons
nitems	Number of items
ncat	Number of categories
nless	Number of unique lambdas
Maxnphi	Number of estimated phi parameters
pq.mat	Array needed for rest-total scores
LambdaNames	Names of lambdas in Master/Stacked data set
PhiNames	Names of phi parameters

Value

stack.data Formats data for input to mnlogit to up-date phi parameters

theta.estimates	<i>Computes estimates of theta (values on latent trait(s)) for all LMA models</i>
-----------------	---

Description

The final estimates of the item scale values and the conditional covariance matrix (i.e, Phi.mat) are used to compute values on latent traits for each individual or case. The estimated thetas are the (conditinal) mean values of response patterns. The correlations between the estimated thetas equal the marginal correlations.

Usage

```
theta.estimates(inData, model.fit)
```

Arguments

inData	Matrix of response patterns
model.fit	Object containing output from running ple.lma

Value

theta.est A person by trait matrix of values on the latent traits

Examples

```
data(dass)
inData <- dass[1:250,c("d1", "d2", "d3", "a1","a2","a3","s1","s2","s3")]
inTraitAdj <- matrix(1, nrow=1, ncol=1)
inItemTraitAdj <- matrix(1, nrow=9, ncol=1)

r1 <- ple.lma(inData, model.type="rasch", inItemTraitAdj, inTraitAdj)
theta.r1 <- theta.estimates(inData, r1)

g1 <- ple.lma(inData, model.type="gpcm", inItemTraitAdj, inTraitAdj)
theta.g1 <- theta.estimates(inData, g1)

n1 <- ple.lma(inData, model.type="nominal", inItemTraitAdj,inTraitAdj)
theta.n1 <- theta.estimates(inData, n1)
```

vocab

Dataframe of response to vocabulary items from the 2018 General Social Survey

Description

These data are responses to 10 vocabulary items from the GSS collected in 2018 and retrieved July 2019 from <https://gss.norc.org>. These data are provided as an example of binary items and how the package can fit two parameter logistic models as either a GPCM or nominal model. Both models should give the same results. There are 10 words and responses to them were either correct or incorrect. There are 1309 respondents in the data who gave answers to all items. The specific words used are not released due to test security reasons. The instructions given to answering these items are as follows: "We would like to know something about how people go about guessing words they do not know. On this card are listed some words—you may know some of them, and you may not know quite a few of them. On each line the first word is in capital letters – like BEAST. Then there are five other words. Tell me the number of the word that comes closest to the meaning of the word in capital letters. For example, if the word in capital letters is BEAST, you would say "4" since "animal" comes closer to BEAST than any of the other words. If you wish, I will read the words to you. These words are difficult for almost everyone– just give me your best guess if you are not sure of the answer. CIRCLE ONE CODE NUMBER FOR EACH ITEM BELOW."

Usage

vocab

Format

A data frame with 1309 rows and 10 columns (items):

wordA word A

wordB word B

wordC word C

wordD word D

wordE word E

wordF word F

wordG word G

wordH word H

wordI word I

wordJ word J

Source

<https://gss.norc.org>

Examples

```
data(vocab)  
head(vocab)
```

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