

# Package ‘multinomialLogitMix’

May 9, 2026

**Type** Package

**Title** Clustering Multinomial Count Data under the Presence of Covariates

**Version** 1.1

**Date** 2023-07-13

**Maintainer** Panagiotis Papastamoulis <papapast@yahoo.gr>

**Description** Methods for model-based clustering of multinomial counts under the presence of covariates using mixtures of multinomial logit models, as implemented in Papastamoulis (2023) <[DOI:10.1007/s11634-023-00547-5](https://doi.org/10.1007/s11634-023-00547-5)>. These models are estimated under a frequentist as well as a Bayesian setup using the Expectation-Maximization algorithm and Markov chain Monte Carlo sampling (MCMC), respectively. The (unknown) number of clusters is selected according to the Integrated Completed Likelihood criterion (for the frequentist model), and estimating the number of non-empty components using overfitting mixture models after imposing suitable sparse prior assumptions on the mixing proportions (in the Bayesian case), see Rousseau and Mengersen (2011) <[DOI:10.1111/j.1467-9868.2011.00781.x](https://doi.org/10.1111/j.1467-9868.2011.00781.x)>. In the latter case, various MCMC chains run in parallel and are allowed to switch states. The final MCMC output is suitably post-processed in order to undo label switching using the Equivalence Classes Representatives (ECR) algorithm, as described in Papastamoulis (2016) <[DOI:10.18637/jss.v069.c01](https://doi.org/10.18637/jss.v069.c01)>.

**License** GPL-2

**Imports** Rcpp (>= 1.0.8.3), MASS, doParallel, foreach, label.switching, ggplot2, coda, matrixStats, mvtnorm, RColorBrewer

**LinkingTo** Rcpp, RcppArmadillo

**NeedsCompilation** yes

**Author** Panagiotis Papastamoulis [aut, cre] (ORCID: <<https://orcid.org/0000-0001-9468-7613>>)

**Repository** CRAN

**Date/Publication** 2023-07-17 05:00:02 UTC

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multinomialLogitMix-package

*Clustering Multinomial Count Data under the Presence of Covariates*

---

## Description

Methods for model-based clustering of multinomial counts under the presence of covariates using mixtures of multinomial logit models, as implemented in Papastamoulis (2023) <DOI:10.1007/s11634-023-00547-5>. These models are estimated under a frequentist as well as a Bayesian setup using the Expectation-Maximization algorithm and Markov chain Monte Carlo sampling (MCMC), respectively. The (unknown) number of clusters is selected according to the Integrated Completed Likelihood criterion (for the frequentist model), and estimating the number of non-empty components using overfitting mixture models after imposing suitable sparse prior assumptions on the mixing proportions (in the Bayesian case), see Rousseau and Mengersen (2011) <DOI:10.1111/j.1467-9868.2011.00781.x>. In the latter case, various MCMC chains run in parallel and are allowed to switch states. The final MCMC output is suitably post-processed in order to undo label switching using the Equivalence Classes Representatives (ECR) algorithm, as described in Papastamoulis (2016) <DOI:10.18637/jss.v069.c01>.

## Details

The DESCRIPTION file:

```

Package:      multinomialLogitMix
Type:         Package
Title:        Clustering Multinomial Count Data under the Presence of Covariates
Version:      1.1
Date:         2023-07-13
Authors@R:   c(person(given = "Panagiotis", family = "Papastamoulis", email = "papapast@yahoo.gr", role = c("aut", "cre"))
Maintainer:   Panagiotis Papastamoulis <papapast@yahoo.gr>

```

Description: Methods for model-based clustering of multinomial counts under the presence of covariates using mixtures of  
 License: GPL-2  
 Imports: Rcpp (>= 1.0.8.3), MASS, doParallel, foreach, label.switching, ggplot2, coda, matrixStats, mvtnorm, RColorBrewer  
 LinkingTo: Rcpp, RcppArmadillo  
 Author: Panagiotis Papastamoulis [aut, cre] (<<https://orcid.org/0000-0001-9468-7613>>)

#### Index of help topics:

dealWithLabelSwitching	Post-process the generated MCMC sample in order to undo possible label switching.
expected_complete_LL	Expected complete LL
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gibbs_mala_sampler_ppt	Prior parallel tempering scheme of hybrid Gibbs/MALA MCMC samplers for the multinomial logit mixture.
log_dirichlet_pdf	Log-density function of the Dirichlet distribution
mala_proposal	Proposal mechanism of the MALA step.
mixLoglikelihood_GLM	Log-likelihood of the multinomial logit.
mix_mnm_logistic	EM algorithm
multinomialLogitMix	Main function
multinomialLogitMix-package	Clustering Multinomial Count Data under the Presence of Covariates
multinomial_logistic_EM	Part of the EM algorithm for multinomial logit mixture
myDirichlet	Simulate from the Dirichlet distribution
newton_raphson_mstep	M-step of the EM algorithm
shakeEM_GLM	Shake-small EM
simulate_multinomial_data	Synthetic data generator
splitEM_GLM	Split-small EM scheme.

See the main function of the package: [multinomialLogitMix](#), which wraps automatically calls to the MCMC sampler [gibbs\\_mala\\_sampler\\_ppt](#) and the EM algorithm [mix\\_mnm\\_logistic](#).

#### Author(s)

NA

Maintainer: Panagiotis Papastamoulis <[papapast@yahoo.gr](mailto:papapast@yahoo.gr)>

## References

- Papastamoulis, P. Model based clustering of multinomial count data. *Advances in Data Analysis and Classification* (2023). <https://doi.org/10.1007/s11634-023-00547-5>
- Papastamoulis, P. and Iliopoulos, G. (2010). An Artificial Allocations Based Solution to the Label Switching Problem in Bayesian Analysis of Mixtures of Distributions. *Journal of Computational and Graphical Statistics*, 19(2), 313-331. <http://www.jstor.org/stable/25703571>
- Papastamoulis, P. (2016). label.switching: An R Package for Dealing with the Label Switching Problem in MCMC Outputs. *Journal of Statistical Software, Code Snippets*, 69(1), 1-24. <https://doi.org/10.18637/jss.v069.c01>
- Rousseau, J. and Mengersen, K. (2011), Asymptotic behaviour of the posterior distribution in over-fitted mixture models. *Journal of the Royal Statistical Society: Series B (Statistical Methodology)*, 73: 689-710. <https://doi.org/10.1111/j.1467-9868.2011.00781.x>

## See Also

[multinomialLogitMix](#), [gibbs\\_mala\\_sampler\\_ppt](#), [mix\\_mnm\\_logistic](#)

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dealWithLabelSwitching

*Post-process the generated MCMC sample in order to undo possible label switching.*

---

## Description

This function implements the Equivalence Classes Representatives (ECR) algorithm from the label.switching package in order to undo the label switching phenomenon.

## Usage

```
dealWithLabelSwitching(gs, burn, thin = 10, zPivot = NULL, returnRaw = FALSE, maxM = NULL)
```

## Arguments

gs	An object generated by the main function of the package.
burn	Number of draws that will be discarded as burn-in.
thin	Thinning of the MCMC sample.
zPivot	Optional vector of allocations that will be used as the pivot of the ECR algorithm. If this is not supplied, the pivot will be selected as the allocation vector that corresponds to the iteration that maximized the log-likelihood of the model.
returnRaw	Boolean. If true, the function will also return the raw output.
maxM	Not used.

## Details

See Papastamoulis (2016).

**Value**

`cluster` Single best clustering of the data, according to the Maximum A Posteriori rule.  
`nClusters_posterior` Estimated posterior distribution of the number of clusters.  
`mcmc` Post-processed mcmc output.  
`posteriorProbabilities` Estimated posterior membership probabilities.

**Author(s)**

Panagiotis Papastamoulis

**References**

Papastamoulis, P. (2016). `label.switching`: An R Package for Dealing with the Label Switching Problem in MCMC Outputs. *Journal of Statistical Software*, 69(1), 1-24.

---

`expected_complete_LL` *Expected complete LL*

---

**Description**

This function is not used at the moment.

**Usage**

```
expected_complete_LL(y, X, b, w, pr)
```

**Arguments**

`y` count data.  
`X` design matrix.  
`b` Logit coefficients.  
`w` mixing proportions.  
`pr` mixing proportions.

**Value**

Complete log-likelihood of the model.

**Author(s)**

Panagiotis Papastamoulis

---

gibbs_mala_sampler	<i>The core of the Hybrid Gibbs/MALA MCMC sampler for the multinomial logit mixture.</i>
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---

### Description

This function implements Gibbs sampling to update the mixing proportions and latent allocations variables of the mixture model. The coefficients of the logit model are updated according to Metropolis-Hastings type move, based on a Metropolis adjusted Langevin (MALA) proposal.

### Usage

```
gibbs_mala_sampler(y, X, tau = 3e-05, nu2, K, mcmc_iter = 100,
alpha_prior = NULL, start_values = "EM", em_iter = 10,
thin = 10, verbose = FALSE, checkAR = NULL,
probsSave = FALSE, ar_low = 0.4, ar_up = 0.6)
```

### Arguments

y	matrix of counts.
X	design matrix (including constant term).
tau	the variance of the normal prior distribution of the logit coefficients.
nu2	scale of the MALA proposal (positive).
K	number of components of the (overfitting) mixture model.
mcmc_iter	Number of MCMC iterations.
alpha_prior	Parameter of the Dirichlet prior distribution for the mixing proportions.
start_values	Optional list of starting values. Random initialization is used if this is not provided.
em_iter	Maximum number of iterations if an EM initialization is enabled.
thin	optional thinning of the generated MCMC output.
verbose	Boolean.
checkAR	Number of iterations to adjust the scale of the proposal in MALA mechanism during the initial warm-up phase of the sampler.
probsSave	Optional.
ar_low	Lowest threshold for the acceptance rate of the MALA proposal (optional).
ar_up	Highest threshold for the acceptance rate of the MALA proposal (optional).

### Value

nClusters	sampled values of the number of clusters (non-empty mixture components).
allocations	sampled values of the latent allocation variables.
logLikelihood	Log-likelihood values per MCMC iteration.

mixing_proportions	sampled values of mixing proportions.
coefficients	sampled values of the coefficients of the multinomial logit.
complete_logLikelihood	Complete log-likelihood values per MCMC iteration.
class_probs	Classification probabilities per iteration (optional).
AR	Acceptance rate of the MALA proposal.

**Note**

This function is used inside the prior tempering scheme, which is the main function.

**Author(s)**

Panagiotis Papastamoulis

**See Also**

[gibbs\\_mala\\_sampler\\_ppt](#)

**Examples**

```
# Generate synthetic data
K <- 2
p <- 2
D <- 2
n <- 2
set.seed(116)
simData <- simulate_multinomial_data(K = K, p = p, D = D, n = n, size = 20, prob = 0.025)

gs <- gibbs_mala_sampler(y = simData$count_data, X = simData$design_matrix,
  tau = 0.00035, nu2 = 100, K = 2, mcmc_iter = 3,
  alpha_prior = rep(1,K), start_values = "RANDOM",
  thin = 1, verbose = FALSE, checkAR = 100)
```

---

gibbs\_mala\_sampler\_ppt

*Prior parallel tempering scheme of hybrid Gibbs/MALA MCMC samplers for the multinomial logit mixture.*

---

**Description**

The main MCMC scheme of the package. Multiple chains are run in parallel and swaps between are proposed. Each chain uses different parameters on the Dirichlet prior of the mixing proportion. The smaller concentration parameter should correspond to the first chain, which is the one that used for inference. Subsequent chains should have larger values of concentration parameter for the Dirichlet prior.

**Usage**

```
gibbs_mala_sampler_ppt(y, X, tau = 3e-05, nu2, K,
mcmc_cycles = 100, iter_per_cycle = 10, dirPriorAlphas,
start_values = "EM", em_iter = 10, nChains = 4, nCores = 4,
warm_up = 100, checkAR = 50, probsSave = FALSE,
showGraph = 50, ar_low = 0.4, ar_up = 0.6, withRandom = TRUE)
```

**Arguments**

y	matrix of counts.
X	design matrix (including constant term).
tau	the variance of the normal prior distribution of the logit coefficients.
nu2	scale of the MALA proposal (positive).
K	number of components of the (overfitting) mixture model.
mcmc_cycles	Number of MCMC cycles. At the end of each cycle, a swap between chains is attempted.
iter_per_cycle	Number of iterations per cycle.
dirPriorAlphas	Vector of concentration parameters for the Dirichlet priors in increasing order.
start_values	Optional list of start values. Randomly generated values are used if this is not provided.
em_iter	Maximum number of iterations if an EM initialization is enabled.
nChains	Total number of parallel chains.
nCores	Total number of CPU cores for parallel processing of the nChains.
warm_up	Initial warm-up period of the sampler, in order to adaptively tune the scale of the MALA proposal (optional).
checkAR	Number of iterations to adjust the scale of the proposal in MALA mechanism during the initial warm-up phase of the sampler.
probsSave	Optional.
showGraph	Optional.
ar_low	Lowest threshold for the acceptance rate of the MALA proposal (optional) .
ar_up	Highest threshold for the acceptance rate of the MALA proposal (optional).
withRandom	Logical. If TRUE (default) then a random permutation is applied to the supplied starting values.

**Details**

See the paper for details.

**Value**

nClusters	sampled values of the number of clusters (non-empty mixture components).
allocations	sampled values of the latent allocation variables.
logLikelihood	Log-likelihood values per MCMC iteration.
mixing_proportions	sampled values of mixing proportions.
coefficients	sampled values of the coefficients of the multinomial logit.
complete_logLikelihood	Complete log-likelihood values per MCMC iteration.
class_probs	Classification probabilities per iteration (optional).
AR	Acceptance rate of the MALA proposal.

**Note**

The output of the MCMC sampler is not identifiable, due to possible label switching. In order to draw meaningful inferences, the output should be post-processed by [dealWithLabelSwitching](#).

**Author(s)**

Panagiotis Papastamoulis

**References**

Papastamoulis, P (2022). Model-based clustering of multinomial count data.

**Examples**

```
# Generate synthetic data

K <- 2
p <- 2
D <- 3
n <- 2
set.seed(116)
simData <- simulate_multinomial_data(K = K, p = p, D = D, n = n, size = 20, prob = 0.025)

# apply mcmc sampler based on random starting values

Kmax = 2
nChains = 2
dirPriorAlphas = c(1, 1 + 5*exp((seq(2, 14, length = nChains - 1)))/100)/(200)
nCores <- 2
mcmc_cycles <- 2
iter_per_cycle = 2
warm_up <- 2

mcmc_random1 <- gibbs_mala_sampler_ppt(y = simData$count_data, X = simData$design_matrix,
```

```

tau = 0.00035, nu2 = 100, K = Kmax, dirPriorAlphas = dirPriorAlphas,
mcmc_cycles = mcmc_cycles, iter_per_cycle = iter_per_cycle,
start_values = 'RANDOM',
nChains = nChains, nCores = nCores, warm_up = warm_up, showGraph = 1000,
checkAR = 1000)

#sampled values for the number of clusters (non-empty mixture components) per chain (columns)
mcmc_random1$nClusters

```

---

log\_dirichlet\_pdf      *Log-density function of the Dirichlet distribution*

---

### Description

Log-density function of the Dirichlet distribution

### Usage

```
log_dirichlet_pdf(alpha, weights)
```

### Arguments

alpha	Parameter vector
weights	Vector of weights.

### Value

Log-density of the  $D(\alpha_1, \dots, \alpha_k)$  evaluated at  $w_1, \dots, w_k$ .

### Author(s)

Panagiotis Papastamoulis

---

mala\_proposal      *Proposal mechanism of the MALA step.*

---

### Description

Only the mala\_proposal\_cpp function is used in the package - which is written as an RCPP function.

### Usage

```
mala_proposal(y, X, b, z, tau, A = FALSE, pr, nu2)
```

**Arguments**

y	count data
X	design matrix
b	coefficients (array
z	allocation vector
tau	prior variance
A	A
pr	mixing proportions
nu2	parameter nu2

**Value**

theta	theta values
b	coefficients
acceptance	log-likelihood.
gradient	log-likelihood.

**Author(s)**

Panagiotis Papastamoulis

---

mixLoglikelihood\_GLM *Log-likelihood of the multinomial logit.*

---

**Description**

Log-likelihood of the multinomial logit.

**Usage**

```
mixLoglikelihood_GLM(y, theta, pi)
```

**Arguments**

y	matrix of counts
theta	a three-dimensional array containing the multinomial probabilities per cluster, for each observation.
pi	a numeric vector of length K (the number of mixture components) containing the mixing proportions.

**Value**

Log-likelihood value.

**Author(s)**

Panagiotis Papastamoulis

---

 mix\_mnm\_logistic      *EM algorithm*


---

**Description**

Estimation of the multinomial logit mixture using the EM algorithm. The algorithm exploits a careful initialization procedure (Papastamoulis et al., 2016) combined with a ridge-stabilized implementation of the Newton-Raphson method (Goldfeld et al., 1966) in the M-step.

**Usage**

```
mix_mnm_logistic(y, X, Kmax = 10, maxIter = 100, emthreshold = 1e-08,
maxNR = 5, nCores, tsplit = 8, msplit = 5, split = TRUE,
shake = TRUE, random = TRUE, criterion = "ICL",
plotting = FALSE, R0 = 0.1, method = 5)
```

**Arguments**

y	matrix of counts
X	design matrix (including constant term).
Kmax	Maximum number of mixture components.
maxIter	Maximum number of iterations.
emthreshold	Minimum loglikelihood difference between successive iterations in order to terminate.
maxNR	maximum number of Newton Raphson iterations
nCores	number of cores for parallel computations.
tsplit	positive integer denoting the number of different runs for each call of the splitting small EM used by split-small EM initialization procedure.
msplit	positive integer denoting the number of different runs for each call of the splitting small EM.
split	Boolean indicating if the split initialization should be enabled in the small-EM scheme.
shake	Boolean indicating if the shake initialization should be enabled in the small-EM scheme.
random	Boolean indicating if random initializations should be enabled in the small-EM scheme.
criterion	set to "ICL" to select the number of clusters according to the ICL criterion.
plotting	Boolean for displaying intermediate graphical output.
R0	controls the step size of the update: smaller values result to larger step sizes. See description in paper.
method	this should be set to 5.

**Value**

estimated\_K      selected value of the number of clusters.  
 all\_runs          detailed output per run.  
 BIC\_values        values of bayesian information criterion.  
 ICL\_BIC\_values   values of ICL-BIC.  
 estimated\_clustering  
                     Single best-clustering of the data, according to the MAP rule.

**Author(s)**

Panagiotis Papastamoulis

**References**

Papastamoulis P (2022). Model-based clustering of multinomial count data. arXiv:2207.13984 [stat.ME]

**Examples**

```

# Generate synthetic data

K <- 2
p <- 2
D <- 3
n <- 2
set.seed(116)
simData <- simulate_multinomial_data(K = K, p = p, D = D, n = n, size = 20, prob = 0.025)

SplitShakeSmalleM <- mix_mnm_logistic(y = simData$count_data,
X = simData$design_matrix, Kmax = 2, maxIter = 1,
emthreshold = 1e-8, maxNR = 1, nCores = 2, tsplit = 1,
msplit = 2, split = TRUE, R0 = 0.1, method = 5,
plotting = FALSE)
#selected number of clusters
SplitShakeSmalleM$estimated_K
#estimated single best-clustering, according to MAP rule
SplitShakeSmalleM$estimated_clustering
# detailed output for all parameters of the selected number of clusters
SplitShakeSmalleM$all_runs[[SplitShakeSmalleM$estimated_K]]

```

---

multinomialLogitMix      *Main function*

---

**Description**

The main function of the package.

**Usage**

```
multinomialLogitMix(response, design_matrix, method,
  Kmax = 10, mcmc_parameters = NULL, em_parameters = NULL,
  nCores, splitSmalleM = TRUE)
```

**Arguments**

<code>response</code>	matrix of counts.
<code>design_matrix</code>	design matrix (including constant term).
<code>method</code>	character with two possible values: "EM" or "MCMC" indicating the desired method in order to estimate the model.
<code>Kmax</code>	number of components of the (overfitting) mixture model.
<code>nCores</code>	Total number of CPU cores for parallel processing.
<code>mcmc_parameters</code>	List with the parameter set-up of the MCMC sampler. See details for changing the defaults.
<code>em_parameters</code>	List with the parameter set-up of the EM algorithm. See details for changing the defaults.
<code>splitSmalleM</code>	Boolean value, indicating whether the split-small EM scheme should be used to initialize the method. Default: true (suggested).

**Details**

The details of the parameter setup of the EM algorithm and MCMC sampler. The following specification correspond to the minimal default settings. Larger values of `tsplit` will result to better performance.

```
em_parameters <- list(maxIter = 100, emthreshold = 1e-08, maxNR = 10, tsplit = 16, msplit = 10,
  split = TRUE, R0 = 0.1, plotting = TRUE)
```

```
mcmc_parameters <- list(tau = 0.00035, nu2 = 100, mcmc_cycles = 2600, iter_per_cycle = 20,
  nChains = 8, dirPriorAlphas = c(1, 1 + 5 * exp((seq(2, 14, length = nChains - 1)))/100)/(200),
  warm_up = 48000, checkAR = 500, probsSave = FALSE, showGraph = 100, ar_low = 0.15, ar_up
  = 0.25, burn = 100, thin = 1, withRandom = TRUE)
```

**Value**

<code>EM</code>	List with the results of the EM algorithm.
<code>MCMC_raw</code>	List with the raw output of the MCMC sampler - not identifiable MCMC output.
<code>MCMC_post_processed</code>	Post-processed MCMC, used for the inference.

**Author(s)**

Panagiotis Papastamoulis

## References

Papastamoulis, P. Model based clustering of multinomial count data. *Advances in Data Analysis and Classification* (2023). <https://doi.org/10.1007/s11634-023-00547-5>

## Examples

```
# Generate synthetic data

K <- 2 #number of clusters
p <- 2 #number of covariates (constant incl)
D <- 5 #number of categories
n <- 20 #generated number of observations
set.seed(1)
simData <- simulate_multinomial_data(K = K, p = p, D = D, n = n, size = 20, prob = 0.025)

# EM parameters
em_parameters <- list(maxIter = 100, emthreshold = 1e-08,
  maxNR = 10, tsplit = 16, msplit = 10, split = TRUE,
  R0 = 0.1, plotting = TRUE)

# MCMC parameters - just for illustration
# typically, set `mcmc_cycles` and `warm_up` to a larger values
# such as `mcmc_cycles = 2500` or more
# and `warm_up = 40000` or more.
nChains <- 2 #(set this to a larger value, such as 8 or more)
mcmc_parameters <- list(tau = 0.00035, nu2 = 100, mcmc_cycles = 260,
  iter_per_cycle = 20, nChains = nChains, dirPriorAlphas = c(1,
  1 + 5 * exp((seq(2, 14, length = nChains - 1)))/100)/(200),
  warm_up = 4800, checkAR = 500, probsSave = FALSE,
  showGraph = 100, ar_low = 0.15, ar_up = 0.25, burn = 100,
  thin = 1, withRandom = TRUE)

# run EM with split-small-EM initialization, and then use the output to
# initialize MCMC algorithm for an overfitting mixture with
# Kmax = 5 components (max number of clusters - usually this is
# set to a larger value, e.g. 10 or 20).
# Note:
# 1. the MCMC output is based on the non-empty components
# 2. the EM algorithm clustering corresponds to the selected
# number of clusters according to ICL.
# 3. `nCores` should be adjusted according to your available cores.

mM <- multinomialLogitMix(response = simData$count_data,
  design_matrix = simData$design_matrix, method = "MCMC",
  Kmax = 5, nCores = 2, splitSmallEM = TRUE,
  mcmc_parameters = mcmc_parameters, em_parameters = em_parameters)
# retrieve clustering according to EM
mM$EM$estimated_clustering
# retrieve clustering according to MCMC
mM$MCMC_post_processed$cluster
```

---

`multinomial_logistic_EM`*Part of the EM algorithm for multinomial logit mixture*

---

**Description**

Part of the EM algorithm for multinomial logit mixture

**Usage**

```
multinomial_logistic_EM(y, x, K, w_start, b_start,  
maxIter = 1000, emthreshold = 1e-08, maxNR = 5,  
nCores = NULL, verbose = FALSE, R0, method)
```

**Arguments**

<code>y</code>	<code>y</code>
<code>x</code>	<code>X</code>
<code>K</code>	<code>K</code>
<code>w_start</code>	<code>w</code>
<code>b_start</code>	<code>b</code>
<code>maxIter</code>	<code>max</code>
<code>emthreshold</code>	<code>em</code>
<code>maxNR</code>	<code>maxnr</code>
<code>nCores</code>	<code>nc</code>
<code>verbose</code>	<code>verb</code>
<code>R0</code>	<code>or</code>
<code>method</code>	<code>method</code>

**Value**

value

**Author(s)**

Panagiotis Papastamoulis

---

myDirichlet	<i>Simulate from the Dirichlet distribution</i>
-------------	---

---

**Description**

Generate a random draw from the Dirichlet distribution  $D(\alpha_1, \dots, \alpha_k)$ .

**Usage**

```
myDirichlet(alpha)
```

**Arguments**

alpha	Parameter vector
-------	------------------

**Value**

Simulated vector

**Author(s)**

Panagiotis Papastamoulis

---

newton_raphson_mstep	<i>M-step of the EM algorithm</i>
----------------------	-----------------------------------

---

**Description**

Implements the maximization step of the EM algorithm based on a ridge-stabilized version of the Newton-Raphson algorithm, see Goldfeld et al. (1966).

**Usage**

```
newton_raphson_mstep(y, X, b, w, maxNR = 5, R0 = 0.1, method = 5, verbose = FALSE)
```

**Arguments**

y	count data matrix
X	design matrix (including const).
b	coefficients of the multinomial logit mixture
w	mixing proportions
maxNR	threshold
R0	inital value for the parameter that controls the step-size of the update.
method	set to 5. Always.
verbose	Boolean.

**Value**

b	coefficients
theta	theta values
ll	log-likelihood.

**Author(s)**

Panagiotis Papastamoulis

**References**

Goldfeld, S. M., Quandt, R. E., and Trotter, H. F. (1966). Maximization by quadratic hill-climbing. *Econometrica: Journal of the Econometric Society*, 541-551.

---

shakeEM\_GLM

*Shake-small EM*


---

**Description**

Assume that there are at least two clusters in the fitted model. We randomly select 2 of them and propose to randomly re-allocate the assigned observations within those 2 clusters.

**Usage**

```
shakeEM_GLM(y, x, K, equalModel, tsplit = 10, maxIter = 20,
emthreshold = 1e-08, maxNR = 5, nCores,
split = TRUE, R0, method)
```

**Arguments**

y	y
x	X
K	K
equalModel	eq
tsplit	tsplit
maxIter	maxiter
emthreshold	em
maxNR	max
nCores	nc
split	spl
R0	ro
method	met

**Value**

valu

**Author(s)**

Panagiotis Papastamoulis

---

simulate\_multinomial\_data

*Synthetic data generator*

---

**Description**

This function simulates data from mixture of multinomial logistic regression models.

**Usage**

```
simulate_multinomial_data(K, p, D, n, size = 20, prob = 0.025, betaTrue = NULL)
```

**Arguments**

K	Number of clusters.
p	Number of covariates, including constant.
D	Number of multinomial categories.
n	Number of data points to simulate.
size	Negative Binomial parameter (number of successes). Default: 20.
prob	Negative Binomial parameter (probability of success). Default: 0.025.
betaTrue	An array which contains the true values of the logit coefficients per cluster. Default: randomly generated values.

**Value**

count_data	matrix of data counts.
design_matrix	design matrix.
clustering	Ground-truth partition of the data.

**Author(s)**

Panagiotis Papastamoulis

---

splitEM\_GLM

*Split-small EM scheme.*


---

**Description**

Split two randomly selected clusters based on a model with one component smaller than the current one. This procedure is repeated within a small-EM scheme. The best split is chose to initialize the model.

**Usage**

```
splitEM_GLM(y, x, K, smallerModel, tsplit = 10, maxIter = 20,
emthreshold = 1e-08, maxNR = 5, nCores,
split = TRUE, R0, method)
```

**Arguments**

y	y
x	x
K	k
smallerModel	smla
tsplit	tsp
maxIter	max
emthreshold	thr
maxNR	maxn
nCores	nc
split	spi
R0	ro
method	meth

**Value**

val

**Author(s)**

Panagiotis Papastamoulis

**References**

Papastamoulis, P., Martin-Magniette, M. L., and Maugis-Rabusseau, C. (2016). On the estimation of mixtures of Poisson regression models with large number of components. *Computational Statistics & Data Analysis*, 93, 97-106.

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