Package ‘label.switching’

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Title Relabelling MCMC Outputs of Mixture Models
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Description The Bayesian estimation of mixture models (and more general hidden Markov models) suffers from the label switching phenomenon, making the MCMC output non-identifiable. This package can be used in order to deal with this problem using various relabelling algorithms.
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Description

This package can be used to reorder MCMC outputs of parameters of mixture models (or more general ones, like hidden Markov). The label switching phenomenon is a fundamental problem to MCMC estimation of the parameters of such models. This package contains eight label switching solving algorithms: the default and iterative versions of ECR algorithm (Papastamoulis and Iliopoulos, 2010, 2013, Rodriguez and Walker, 2014, Papastamoulis, 2014), the data-based algorithm (Rodriguez and Walker, 2014), the Kullback-Leibler based algorithm of Stephens (2000), the probabilistic relabelling algorithm of Sperrin et al (2010), the artificial identifiability constraints method and the PRA algorithm (Marin et al, 2005, Marin and Robert, 2007). The user input depends on each method. Each algorithm returns a list of permutations. For comparison purposes, the user can also provide his/hers own set of permutations.

Details

Package: label.switching
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This is NOT a package to simulate MCMC samples from the posterior distribution of mixture models. MCMC output and related information serves as input to the available methods. There are eight functions that can be used to post-process the MCMC output:

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Each function returns an $m \times K$ array of permutations, where $m$ and $K$ denote the MCMC sample size and number of mixture components, respectively. Next, these permutations can be applied to reorder the MCMC sample by applying the function `permute.mcmc`. The useR can call any of the
above functions simultaneously using the main function of the package: `label.switching`.

**Note**

The most common method is to impose an identifiability constraint $\text{aic}$, however this approach has been widely criticized in the literature. The methods `ecr`, `ecr.iterative.1`, `ecr.iterative.2`, `stephens`, `dataBased` are solving the label switching problem using the function `lpAssign` of the package `lpSolve`. This is an integer programming algorithm for the solution of the assignment problem. Hence, these functions are computationally efficient even in cases where the number of components is quite large. On the other hand, methods `pr.a` and `sjw` are not designed in this way, so they are not suggested for large $K$.

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**References**


**See Also**

`label.switching`
Artificial Identifiability Constraints

Description

This function relabels the MCMC output by simply ordering a specific parameter. Let \( m, K \) and \( J \) denote the number of simulated MCMC samples, number of mixture components and different parameter types, respectively.

Usage

\[
aic(mcmc.pars, \text{constraint})
\]

Arguments

- `mcmc.pars`: \( m \times K \times J \) array of simulated MCMC parameters.
- `constraint`: An integer between 1 and \( J \) corresponding to the parameter that will be used to apply the Identifiability Constraint. In this case, the MCMC output is reordered according to the constraint

\[
mcmc.pars[i, 1, \text{constraint}] < \ldots < mcmc.pars[i, K, \text{constraint}],
\]

for all \( i = 1, \ldots, m \). If `constraint` = "ALL", all \( J \) Identifiability Constraints are applied.

Value

- `permutations`: an \( m \times K \) array of permutations.

Author(s)

Panagiotis Papastamoulis

See Also

`permute.mcmc`, `label.switching`

Examples

```r
# load a toy example: MCMC output consists of the random beta model
# applied to a normal mixture of \code(K=2) components. The number of
# observations is equal to \code(n=5). The number of MCMC samples is
# equal to \code(m=300). The 1000 generated MCMC samples are stored
# to array mcmc.pars.
data("mcmc_output")
mcmc.pars<-data_list"mcmc.pars"

# mcmc parameters are stored to array \code(mcmc.pars)
# mcmc.pars[,1]: simulated means of the two components
```
compare.clust

Make all estimated clusters agree with a pivot allocation

Description

Given a pivot allocation vector, a set of simulated allocations and a set of permutations from different relabelling algorithms, this function relabels the permutations so that all methods maximize their similarity with the pivot. This is helpful when comparing different label switching algorithms.

Usage

compare.clust(pivot.clust, perms, z, K)

Arguments

pivot.clust a pivot allocation vector of the \( n \) observations among the \( K \) clusters.
perms a list containing \( f \) permutation arrays, as returned by \texttt{label.switching} function.
z a set of simulated allocation arrays.
K number of mixture components

Value

similarity \((f + 1)K \times (f + 1)\) matrix containing the similarity coefficient of the resulting clusters.
clusters \(f \times n\) array of single best clusterings, relabelled in order to maximize their similarity with \texttt{pivot.clust}.
permutations relabelled permutations.

Author(s)

Panagiotis Papastamoulis

See Also

\texttt{label.switching}
**Description**

This function reorders the MCMC output according the data-based relabelling algorithm of Rodriguez and Walker (2014). The idea is to define a loss function which resembles a k-means type diverging measure of cluster centers. After the cluster centers have been estimated, the algorithm finds the optimal permutations that switch every simulated MCMC sample to them.

**Usage**

dataBased(x, K, z)

**Arguments**

- **x**: n-dimensional data vector/array.
- **K**: the number of mixture components.
- **z**: m × n integer array of the latent allocation vectors generated from an MCMC algorithm.

**Value**

- **permutations**: m × K dimensional array of permutations

**Author(s)**

Panagiotis Papastamoulis

**References**


**See Also**

permute.mcmc.label.switching

**Examples**

```r
# load a toy example: MCMC output consists of the random beta model # applied to a normal mixture of K=2 components. The number of # observations is equal to n=5. The number of MCMC samples is # equal to m=300. The 1000 generated MCMC samples are stored # to array mcmc.pars.
data("mcmc_output")
z<-data_list$"z"
K<-data_list$"K"
```
data_list

x <- data_list$x
mcmc.pars <- data_list$mcmc.pars
# mcmc parameters are stored to array \texttt{mcmc.pars}
# mcmc.pars[,1]: simulated means of the two components
# mcmc.pars[,2]: simulated variances of the two components
# mcmc.pars[,3]: simulated weights of the two components
# apply database relabelling
run <- dataBased(x = x, K = K, z = z)
# apply the permutations returned by typing:
reordered.mcmc <- permute.mcmc(mcmc.pars, run$permutations)
# reordered.mcmc[,1]: reordered means of the two components
# reordered.mcmc[,2]: reordered variances of the components
# reordered.mcmc[,3]: reordered weights

data_list

Simulated MCMC sample and related information

Description

This is a (very) small MCMC sample corresponding to data of 5 observations from a mixture 2 normal distributions. The MCMC sample consists of 300 iterations. It is stored to \texttt{data_list$mcmc.pars}. \texttt{data_list$mcmc.pars[,1]} corresponds to means, \texttt{data_list$mcmc.pars[,2]} corresponds to variances and \texttt{data_list$mcmc.pars[,3]} corresponds to weights.

Usage

data_list

Format

A list containing simulated MCMC sample and all information required for the relabelling algorithms.

ecr

ECR algorithm (default version)

Description

This function applies the standard version of Equivalence Classes Representatives (ECR) algorithm (Papastamoulis and Iliopoulos, 2010). The set of all allocation variables is partitioned into equivalence classes and exactly one representative is chosen from each class. The practical implementation of this idea is to reorder the output so that all simulated allocation vectors (z) are as similar as possible with a pivot allocation vector (zpivnot).

Usage

ecr(zpivot, z, K)
Arguments

zpiv0t  $n$-dimensional integer vector $(z_1, \ldots, z_n)$ with $z_i \in \{1, \ldots, K\}, i = 1, \ldots, n$.

$z$  $m \times n$ integer array of the latent allocation vectors generated from an MCMC algorithm.

$K$  the number of mixture components (at least equal to 2).

Details

zpiv0t should be chosen as an allocation vector that corresponds to a high-posterior density area, or in general as an allocation that is considered as a good allocation of the observations among the $K$ components. The useR has to specify this pivot allocation vector as a good allocation of the observations among the mixture components. Some typical choices are the allocations that correspond to the complete or non-complete MAP/ML estimates.

Value

permutations  $m \times K$ dimensional array of permutations

Author(s)

Panagiotis Papastamoulis

References


See Also

permute.mcmc, label.switching, ecr.iterative.1, ecr.iterative.2

Examples

# load a toy example: MCMC output consists of the random beta model # applied to a normal mixture of K=2 components. The # number of observations is equal to n=5. The number # of MCMC samples is equal to m=300. The 300 # simulated allocations are stored to array z. The # complete MAP estimate corresponds to iteration mapindex. data("mcmc_output")
z<-data_list$"z"
K<-data_list$"K"
mapindex<-data_list$"mapindex"

# mcmc parameters are stored to array mcmc.pars
mcmc.pars<-data_list$"mcmc.pars"
# mcmc.pars[,1]: simulated means of the two components
# mcmc.pars[,2]: simulated variances
# mcmc.pars[,3]: simulated weights
run<-.ecr(zpivot = z[mapindex,], z = z, K = K)
# apply the permutations returned by typing:
reordered.mcmc<-.permute.mcmc(mcmc.pars, run$permutations)
# reordered.mcmc[,1]: reordered means of the two components
# reordered.mcmc[,2]: reordered variances
# reordered.mcmc[,3]: reordered weights

ecr.iterative.1

**ECR algorithm (iterative version 1)**

**Description**
This function applies the first iterative version of Equivalence Classes Representatives (ECR) algorithm (Papastamoulis and Iliopoulos, 2010, Rodriguez and Walker, 2012). The set of all allocation variables is partitioned into equivalence classes and exactly one representative is chosen from each class. The difference with the default version of ECR algorithm is that no pivot is required and the method is iterative, until a fixed pivot has been found.

**Usage**

ecr.iterative.1(z, K, opt_init, threshold, maxiter)

**Arguments**

- **z**  
  $m \times n$ integer array of the latent allocation vectors generated from an MCMC algorithm.

- **K**  
  the number of mixture components (at least equal to 2).

- **opt_init**  
  An (optional) $m \times K$ array of permutations to initialize the algorithm. The identity permutation is used if it is not specified.

- **threshold**  
  An (optional) positive number controlling the convergence criterion. Default value: 1e-6.

- **maxiter**  
  An (optional) integer controlling the max number of iterations. Default value: 100.

**Value**

- **permutations**  
  $m \times K$ dimensional array of permutations

- **iterations**  
  integer denoting the number of iterations until convergence

- **status**  
  returns the exit status

**Author(s)**
Panagiotis Papastamoulis
References


See Also

permute.mcmc, label.switching, ecr, ecr.iterative.2

Examples

# load a toy example: MCMC output consists of the random beta model
# applied to a normal mixture of \( K \) components. The number of
# observations is equal to \( n = 5 \). The number of MCMC samples is
# equal to \( m = 1000 \). The 300 simulated allocations are stored to
# array \( z \).

data("mcmc_output")
# mcmc parameters are stored to array \( \text{mcmc.pars} \)
mcmc.pars<-data_list$"mcmc.pars"
z<-data_list$"z"
K<-data_list$"K"
# mcmc.pars[,1]: simulated means of the two components
# mcmc.pars[,2]: simulated variances
# mcmc.pars[,3]: simulated weights
# the relabelling algorithm will run with the default initialization
# (no opt_init is specified)
run<-ecr.iterative.2(z = z, K = K)
# apply the permutations returned by typing:
reordered.mcmc<-permute.mcmc(mcmc.pars,run$permutations)
# reordered.mcmc[,1]: reordered means of the two components
# reordered.mcmc[,2]: reordered variances
# reordered.mcmc[,3]: reordered weights

describe

ECR algorithm (iterative version 2)

Description

This function applies the second iterative version of Equivalence Classes Representatives (ECR) algorithm (Papastamoulis and Iliopoulos, 2010, Rodriguez and Walker, 2012). The set of all allocation variables is partitioned into equivalence classes and exactly one representative is chosen from each class. In this version the \( m \times n \times K \) of allocation probabilities should be given as input as well.

Usage

ecr.iterative.2(z, K, p, threshold, maxiter)
Arguments

- $z$: $m \times n$ integer array of the latent allocation vectors generated from an MCMC algorithm.
- $K$: the number of mixture components (at least equal to 2).
- $p$: $m \times n \times K$ dimensional array of allocation probabilities of the $n$ observations among the $K$ mixture components, for each iteration $t = 1, \ldots, m$ of the MCMC algorithm.
- threshold: An (optional) positive number controlling the convergence criterion. Default value: $1e^{-6}$.
- maxiter: An (optional) integer controlling the max number of iterations. Default value: 100.

Details

For a given MCMC iteration $t = 1, \ldots, m$, let $w_k^{(t)}$ and $\theta_k^{(t)}$, $k = 1, \ldots, K$ denote the simulated mixture weights and component specific parameters respectively. Then, the $(t, i, k)$ element of $p$ corresponds to the conditional probability that observation $i$ belongs to component $k$ and is proportional to $p_{tik} \propto w_k^{(t)} f(x_i | \theta_k^{(t)}), k = 1, \ldots, K$, where $f(x_i | \theta_k)$ denotes the density of component $k$. This means that:

$$p_{tik} = \frac{w_k^{(t)} f(x_i | \theta_k^{(t)})}{w_1^{(t)} f(x_i | \theta_1^{(t)}) + \ldots + w_K^{(t)} f(x_i | \theta_K^{(t)})}.$$

In case of hidden Markov models, the probabilities $w_k$ should be replaced with the proper left (normalized) eigenvector of the state-transition matrix.

Value

- permutations: $m \times K$ dimensional array of permutations
- iterations: integer denoting the number of iterations until convergence
- status: returns the exit status

Author(s)

Panagiotis Papastamoulis

References


See Also

permute.mcmc, label.switching, ecr, ecr.iterative.1, stephens
Examples

# load a toy example: MCMC output consists of the random beta model
# applied to a normal mixture of \code{k=2} components. The number of
# observations is equal to \code{n=5}. The number of MCMC samples is
# equal to \code{m=1000}. The 300 simulated allocations are stored to
# array \code{z}. The matrix of allocation probabilities is stored to
# array \code{p}.
data("mcmc_output")
z<-data.list$"z"
K<-data.list$"K"
p<-data.list$"p"
# mcmc parameters are stored to array \code{mcmc.pars}
mcmc.pars<-data.list$"mcmc.pars"
# mcmc.pars[,1]: simulated means of the two components
# mcmc.pars[,2]: simulated variances
# mcmc.pars[,3]: simulated weights
# the relabelling algorithm will run with the default initialization
# (no opt_init is specified)
run<ecr.iterative2(z = z, K = 2, p = p)
# apply the permutations returned by typing:
reordered.mcmc<permute.mcmc(mcmc.pars, run$permutations)
# reordered.mcmc[,1]: reordered means of the two mixture components
# reordered.mcmc[,2]: reordered variances of the two components
# reordered.mcmc[,3]: reordered weights of the two components

label.switching

Main calling function

Description

This is the main function of the package. It is used to reorder a simulated MCMC sample of the
parameters of a mixture (or more general a hidden Markov model) according to eight label switching
solving methods: ECR algorithm (default version), ECR algorithm (two iterative versions), PRA
algorithm, Stephens’ algorithm, Artificial Identifiability Constraint (AIC), Data-Based relabelling
and a probabilistic relabelling algorithm (SJW). The input depends on the type of the label switching
method. The output contains a list with the permutation returned by each method, the corresponding
single best clusterings and the CPU time demanded for each method. In what follows: \( m \) denotes
the number of MCMC iterations, \( n \) denotes the sample size of the observed data, \( K \) denotes the
number of mixture components and \( J \) the number of different types of parameters of the model.

Usage

label.switching(method, zpivot, z, K, prapivot, p, complete,
mcmc, sjwinit, data, constraint,
groundtruth, thrECR, thrSTE, thrSJW,
maxECR, maxSTE, maxSJW, userPerm)
Arguments

method any non-empty subset of c("ECR","ECR-ITERATIVE-1","PRA","ECR-ITERATIVE-2","STEPHENS","SJW","AIC","DATA-BASED") indicating the desired label-switching solving method. Also available is the option "USER-PERM" which corresponds to a user-defined set of permutations userPerm.

zpivot $d \times n$-dimensional array of pivot allocation vectors, where $d$ denotes the number of pivots. This is demanded by the ecr method. The method will be applied $d$ times.

z $m \times n$ integer array of the latent allocation vectors generated from an MCMC algorithm.

K the number of mixture components. This is demanded by the ecr, ecr.iterative.1 and ecr.iterative.2 methods.

prapivot $K \times J$ array containing the parameter that will be used as a pivot by the pra method.

p $m \times n \times K$ dimensional array of allocation probabilities of the $n$ observations among the $K$ mixture components, for each iteration $t = 1, \ldots, m$ of the MCMC algorithm. This is demanded by the ecr.iterative.2 and stephens methods.

complete function that returns the complete log-likelihood of the mixture model. Demanded by sjw method.

mcmc $m \times K \times J$ array of simulated MCMC parameters. Needed by sjw and pra methods.

sjwinit An index pointing at the MCMC iteration whose parameters will initialize the sjw algorithm (optional).

data $n$-dimensional data vector/array. Needed by the sjw and dataBased algorithms.

constraint An (optional) integer between 1 and J corresponding to the parameter that will be used to apply the Identifiability Constraint. In this case the mcmc output is reordered according to the constraint \[ \text{mcmc}[i,1,\text{constraint}] < \ldots < \text{mcmc}[i,K,\text{constraint}] \]. If \text{constraint} = "ALL", all $J$ Identifiability Constraints are applied. Default value: 1.

groundTruth Optional integer vector of $n$ allocations, which are considered as the ‘ground truth’ allocations of the $n$ observations among the $K$ mixture components. The output of all methods will be relabelled in a way that the resulting single best clusterings maximize their similarity with the ground truth. This option is very useful in simulation studies or in any other case that the cluster labels are known in order to perform comparisons between methods.

thrECR An (optional) positive number controlling the convergence criterion for ecr.iterative.1 and ecr.iterative.2. Default value: 1e-6.

thrSTE An (optional) positive number controlling the convergence criterion for stephens. Default value: 1e-6.

thrSJW An (optional) positive number controlling the convergence criterion for sjw. Default value: 1e-6.

maxECR An (optional) integer controlling the max number of iterations for ecr.iterative.1 and ecr.iterative.2. Default value: 100.
maxSTE  An (optional) integer controlling the max number of iterations for stephens. Default value: 100.

maxSJW  An (optional) integer controlling the max number of iterations for sjw. Default value: 100.

userPerm  An (optional) list with user-defined permutations. It is required only if "USER-PERM" has been chosen in method. In this case, userPerm[[i]] is an $m \times K$ array of permutations for all $i = 1, \ldots, S$, where $S$ denotes the number of permutation arrays. This is useful in case that the user wants to compare his/hers own relabelling method with the available ones.

Value

permutations  an $m \times K$ array of permutations per method.

clusters  an $n$ dimensional vector of best clustering of the the observations for each method.

timings  CPU time needed for each relabelling method.

similarity  correlation matrix between the label switching solving methods in terms of their matching best-clustering allocations.

Note

If the ground truth is not given, all methods are reordered using the estimated single best clustering of the first provided method. The methods sjw and pra are not suggested for large number of components. Also note that sjw might be quite slow even for small number of components. In this case try adjusting thrsjw or maxSJW to smaller values the default ones.

Author(s)

Panagiotis Papastamoulis

References


See Also

ecr, ecr.iterative.1, ecr.iterative.2, stephens, pra, sjw, dataBased, aic

Examples

# We will apply four methods:
# ECR, ECR-ITERATIVE-1, PRA, AIC, STEPHENS and DATA-BASED.
# default ECR will use two different pivots.

#load a toy example: MCMC output consists of the random beta model
# applied to a normal mixture of \code{K=2} components. The number of
# observations is equal to \code{n=5}. The number of MCMC samples is
# equal to \code{m=300}. simulated allocations are stored to array \code{z}.
data("mcmc_output")
mcmc.pars<-data$"mcmc.pars"
# mcmc parameters are stored to array \texttt{mcmc.pars}
# mcmc.pars[,1]: simulated means of the two components
# mcmc.pars[,2]: simulated variances
# mcmc.pars[,3]: simulated weights
# We will use two pivots for default ECR algorithm:
# the first one corresponds to iteration \texttt{mapindex} (complete MAP)
# the second one corresponds to iteration \texttt{mapindex.non} (observed MAP)
# The array \texttt{c(p)} corresponds to the allocation probabilities
z<-data$"z"
K<-data$"K"
p<-data$p"
x<-data$x"
mapindex<-data$"mapindex"
mapindex.non<-data$"mapindex.non"
# The PRA method will use as pivot the iteration that corresponds to
# the non-complete MAP estimate \texttt{mapindex}.

# Apply the six methods by typing:
ls<-label.switching(method=c("ECR","ECR-ITERATIVE-1","PRA","STEPS","AIC","DATA-BASED"),
zpivot=z[c(mapindex,mapindex.non),],z = z,K = K, data = x,
prapivot = mcmc.pars[mapindex,,],p=p,mcmc = mcmc.pars)

# plot the raw and reordered means of the K=2 normal mixture components for each method
par(mfrow = c(2,4))
# raw MCMC output for the means (with label switching)
matplot(mcmc.pars[,1],type="l",
 xlab="iteration",main="Raw MCMC output",ylab = "means")
# Reordered outputs
matplot(permute.mcmc(mcmc.pars,ls$"ECR-1")$output[,1],type="l",
 xlab="iteration",main="ECR (1st pivot)",ylab = "means")
matplot(permute.mcmc(mcmc.pars,ls$"ECR-2")$output[,1],type="l",
 xlab="iteration",main="ECR (2nd pivot)",ylab = "means")
matplot(permute.mcmc(mcmc.pars,ls$"ECR-ITERATIVE-1")$output[,1],
type="l",xlab="iteration",main="ECR-iterative-1",ylab = "means")
matplot(permute.mcmc(mcmc.pars,ls$"PRA")$output[,1],type="l",
 xlab="iteration",main="PRA",ylab = "means")
matplot(permute.mcmc(mcmc.pars,ls$"STEPS")$output[,1],type="l",
 xlab="iteration",main="STEPS",ylab = "means")
matplot(permute.mcmc(mcmc.pars,ls$"AIC")$output[,1],type="l",
 xlab="iteration",main="AIC",ylab = "means")
matplot(permute.mcmc(mcmc.pars,ls$"DATA-BASED")$output[,1],type="l",
 xlab="iteration",main="DATA-BASED",ylab = "means")

# if the user wants to apply the SJW algorithm as well:
# The SJW method needs to define the complete log-likelihood of the
# model. For the univariate normal mixture, this is done as follows:
complete.normal.loglikelihood<-function(x,z,pars){
  #x: denotes the n data points
#z: denotes an allocation vector (size=n)
#pars: K\times 3 vector of means, variance, weights
# pars[k,1]: corresponds to the mean of component k
# pars[k,2]: corresponds to the variance of component k
# pars[k,3]: corresponds to the weight of component k

g <- dim(pars)[1]
n <- length(x)
logl<- rep(0, n)
    logpi <- log(pars[,3])
mean <- pars[,1]
sigma <- sqrt(pars[,2])
logl<-logpi[z] + dnorm(x,mean = mean[z],sd = sigma[z],log = T)
return(sum(logl))

# and then run (after removing all #):
#ls<--label.switching(method=c(“ECR”,”ECR-ITERATIVE-1”,”ECR-ITERATIVE-2”,
#”PRA”,”STEPHENS”,”SJW”,”AIC”,”DATA-BASED”),
#zpivot=z[c(mapindex,mapindex.non)],z = z,
#K = K,prapivot = mcmc.pars[mapindex,,],p=p,
#complete = complete.normal.loglikelihood,mcmc.pars,
#data = x)

---

lamb

**Fetal lamb dataset**

**Description**

240 body movement measurements of a fetal lamb at consecutive 5 second intervals.

**Usage**

lamb

**Format**

Count data.

**References**

Description

This function applies the permutation returned by any relabelling algorithm to a simulated MCMC output.

Usage

permute.mcmc(mcmc, permutations)

Arguments

mcmc  \( m \times K \times J \) array of simulated MCMC parameters.
permutations  \( m \times K \) dimensional array of permutations.

Value

output  \( m \times K \times J \) array of reordered MCMC parameters.

Author(s)

Panagiotis Papastamoulis

See Also

label.switching, ecr, ecr.iterative.1, ecr.iterative.2, stephens.pra, sjw.aic, dataBased

Examples

# load MCMC simulated data
data("mcmc_output")
mcmc.pars<-data_list$mcmc.pars"z<-data_list"z"
K<-data_list"K"

# apply \code{ecr.iterative.1} algorithm
run<ecr.iterative.1(z = z, K = 2)
# reorder the MCMC output according to this method:
reordered.mcmc<-permute.mcmc(mcmc.pars, run$permutations)
# reordered.mcmc[,1]: reordered means of the two components
# reordered.mcmc[,2]: reordered variances of the components
# reordered.mcmc[,3]: reordered weights of the two components
**Description**

This function reorders the MCMC output using the geometrically-based Pivotal Reordering Algorithm (PRA) (Marin et al, 2005, Marin and Robert, 2007). The method requires as input the generated MCMC sample and a pivot parameter vector. The user should be careful in order the pivot elements have the same parameters with the generated MCMC output. The simulated MCMC sample should be provided by the user as a \( m \times K \times J \) dimensional array, where \( m \) denotes the number of MCMC samples, \( K \) denotes the number of mixture components and \( J \) corresponds to the number of different parameter types of the model. The pivot should correspond to a high-posterior density point.

**Usage**

\[ \text{pra}(\text{mcmc.pars, pivot}) \]

**Arguments**

- `mcmc.pars` \( m \times K \times J \) array of simulated MCMC parameters.
- `pivot` \( K \times J \) array containing the parameter that will be used as a pivot.

**Details**

The positive integer \( J \) denotes the number of different parameter types of the model. For example, in a univariate normal mixture model there are \( J = 3 \) different types: means, variances and weights. In a Poisson mixture there are \( J = 2 \) types: means and weights.

**Value**

- `permutations` \( m \times K \) dimensional array of permutations

**Author(s)**

Panagiotis Papastamoulis

**References**


**See Also**

`permute.mcmc`, `label.switching`
Examples

```r
# load a toy example: MCMC output consists of the random beta model
# applied to a normal mixture of \code{K=2} components. The number of
# observations is equal to \code{n=5}. The number of MCMC samples is
# equal to \code{m=300}. The 1000 generated MCMC samples are stored
# to array mcmc.pars.
data("mcmc_output")
mcmc.pars<-data_list$mcmc.pars
mapindex<-data_list$mapindex

# mcmc parameters are stored to array \code{mcmc.pars}
# mcmc.pars[,,1]: simulated means of the two components
# mcmc.pars[,,2]: simulated variances of the two components
# mcmc.pars[,,3]: simulated weights of the two components
# We will apply PRA using as pivot the complete MAP estimate
# which corresponds to \code{mcmc.pars[mapindex,]}
runc<-pra(mcmc = mcmc.pars, pivot = mcmc.pars[mapindex,])
# apply the permutations returned by typing:
reordered.mcmc<-permute.mcmc(mcmc.pars,run$purations)
# reordered.mcmc[,1]: reordered means of the two components
# reordered.mcmc[,2]: reordered variances of the components
# reordered.mcmc[,3]: reordered weights
```

**sjw**

---

**Probabilistic relabelling algorithm**

---

**Description**

Function to apply the probabilistic relabelling strategy of Sperrin et al (2010). The concept here is to treat the MCMC output as observed data, while the unknown permutations need to be applied to each mcmc data point is treated as unobserved data with associated uncertainty. Then, an EM-type algorithm estimates the weights for each permutation per MCMC data point.

**Usage**

```r
sjw(mcmc.pars, z, complete, x, init, threshold, maxiter)
```

**Arguments**

- `mcmc.pars` \( m \times K \times J \) array of simulated MCMC parameters.
- `z` \( m \times n \) integer array of the latent allocation vectors generated from an MCMC algorithm.
- `complete` function that returns the complete log-likelihood of the mixture model.
- `x` \( n \)-dimensional data vector/array
- `init` An (optional) index pointing at the MCMC iteration whose parameters will initialize the algorithm. If it is less or equal to zero, the overall MCMC mean will be used for initialization.
threshold An (optional) positive number controlling the convergence criterion. Default value: 1e-6.
maxiter An (optional) integer controlling the max number of iterations. Default value: 100.

Details
Let \( x = (x_1, \ldots, x_n) \) denote the observed data and \( w, \theta \) denote the mixture weights and component specific parameters, respectively. Assume that \( K \) is the the number of components. Then,

\[
L(w, \theta | x) = \prod_{i=1}^{n} \sum_{k=1}^{K} w_k f_k(x_i | \theta_k),
\]

\( i = 1, \ldots, n \) is the observed likelihood of the mixture model. Given the latent allocation variables \( z = (z_1, \ldots, z_n) \), the complete likelihood of the model is defined as:

\[
L_c(w, \theta | x, z) = \prod_{i=1}^{n} w_{z_i} f_{z_i}(x_i | \theta_{z_i}).
\]

Then, complete corresponds to the log of \( L_c \) and should take as input the following: a vector of \( n \) allocations, the observed data and the parameters of the model as a \( K \times J \) array where \( J \) corresponds to the different parameter types of the model. See the example for an implementation at a univariate normal mixture.

Value

- permutations \( m \times K \) dimensional array of permutations
- iterations integer denoting the number of iterations until convergence
- status returns the exit status

Note
This algorithm is not suggested for large number of components due to the computational overload: \( K! \) permutation probabilities are computed at each MCMC iteration. Moreover, the user should carefully provide the complete log-likelihood function of the model as input to the algorithm and this makes its use quite complicated.

Author(s)
Panagiotis Papastamoulis

References

See Also
permute.mcmc, label.switching
Examples

# load a toy example: MCMC output consists of the random beta model
# applied to a normal mixture of \code{K=2} components. The number of
# observations is equal to \code{n=5}. The number of MCMC samples is
# equal to \code{m=300}.
data("mcmc_output")
mcmc.pars<-data_list$"mcmc.pars"
z<-data_list$"z"
K<-data_list$"K"
x<-data_list$"x"

# mcmc parameters are stored to array \code{mcmc.pars}
# mcmc.pars[,1]: simulated means of the two components
# mcmc.pars[,2]: simulated variances
# mcmc.pars[,3]: simulated weights
# The number of different parameters for the univariate
# normal mixture is equal to \code{J=3}: means, variances
# and weights. The generated allocations variables are
# stored to \code{z}. The observed data is stored to \code{x}.
# The complete data log-likelihood is defined as follows:
#run the algorithm:
run<-sjw(mcmc = mcmc.pars,z = z,
complete = complete.normal.loglikelihood,x = x, init=0,threshold = 1e-4)

# apply the permutations returned by typing:
reordered.mcmc<-permute.mcmc(mcmc.pars,run$permutations)
# reordered.mcmc[,1]: reordered means of the two components
# reordered.mcmc[,2]: reordered variances
# reordered.mcmc[,3]: reordered weights

stephens  Stephens' algorithm
Description

Stephens (2000) developed a relabelling algorithm that makes the permuted sample points to agree as much as possible on the \( n \times K \) matrix of classification probabilities, using the Kullback-Leibler divergence. The algorithm’s input is the matrix of allocation probabilities for each MCMC iteration.

Usage

```
stephens(p, threshold, maxiter)
```

Arguments

- \( p \): \( m \times n \times K \) dimensional array of allocation probabilities of the \( n \) observations among the \( K \) mixture components, for each iteration \( t = 1, \ldots, m \) of the MCMC algorithm.
- \( \text{threshold} \): An (optional) positive number controlling the convergence criterion. Default value: \( 1e-6 \).
- \( \text{maxiter} \): An (optional) integer controlling the max number of iterations. Default value: 100.

Details

For a given MCMC iteration \( t = 1, \ldots, m \), let \( w_k^{(t)} \) and \( \theta_k^{(t)} \), \( k = 1, \ldots, K \) denote the simulated mixture weights and component specific parameters respectively. Then, the \((t, i, k)\) element of \( p \) corresponds to the conditional probability that observation \( i = 1, \ldots, n \) belongs to component \( k \) and is proportional to:

\[
p_{tik} \propto w_k^{(t)} f(x_i | \theta_k^{(t)}), \quad k = 1, \ldots, K,
\]

where \( f(x_i | \theta_k) \) denotes the density of component \( k \). This means that:

\[
p_{tik} = \frac{w_k^{(t)} f(x_i | \theta_k^{(t)})}{w_1^{(t)} f(x_i | \theta_1^{(t)}) + \ldots + w_K^{(t)} f(x_i | \theta_K^{(t)})}.
\]

In case of hidden Markov models, the probabilities \( w_k \) should be replaced with the proper left (normalized) eigenvector of the state-transition matrix.

Value

- \( \text{permutations} \): \( m \times K \) dimensional array of permutations
- \( \text{iterations} \): integer denoting the number of iterations until convergence
- \( \text{status} \): returns the exit status

Author(s)

Panagiotis Papastamoulis

References

See Also

permute.mcmc.label.switching

Examples

# load a toy example: MCMC output consists of the random beta model
# applied to a normal mixture of \code{K=2} components. The number
# of observations is equal to \code{n=5}. The number of MCMC samples
# is equal to \code{m=300}. The matrix of allocation probabilities
# is stored to matrix \code{p}.
data("mcmc_output")
# mcmc parameters are stored to array \code{mcmc.pars}
mcmc.pars<-data_list$"mcmc.pars"
# mcmc.pars[,1]: simulated means of the two components
# mcmc.pars[,2]: simulated variances
# mcmc.pars[,3]: simulated weights
# the computed allocation matrix is \code{p}
p<-data_list$"p"
run<-stephens(p)
# apply the permutations returned by typing:
reordered.mcmc<-permute.mcmc(mcmc.pars,run$permutations)
# reordered.mcmc[,1]: reordered means of the components
# reordered.mcmc[,2]: reordered variances
# reordered.mcmc[,3]: reordered weights
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