Package ‘dpmixsim’

February 19, 2015

Version 0.0-8
Date 2012-07-24
Title Dirichlet Process Mixture model simulation for clustering and image segmentation
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Depends R (>= 2.10.0), oro.nifti, cluster
Description The package implements a Dirichlet Process Mixture (DPM) model for clustering and image segmentation. The DPM model is a Bayesian nonparametric methodology that relies on MCMC simulations for exploring mixture models with an unknown number of components. The code implements conjugate models with normal structure (conjugate normal-normal DP mixture model). The package’s applications are oriented towards the classification of magnetic resonance images according to tissue type or region of interest.
License GPL (>= 2)
Repository CRAN
Date/Publication 2012-07-25 06:29:31
NeedsCompilation yes

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dpmixsim

Dirichlet Process mixture model for clustering and image segmentation

Description
dpmixsim implements a Dirichlet Process mixture (DPM) model. The DPM model is a Bayesian nonparametric methodology that relies on MCMC simulations for exploring mixture models with an unknown number of components. The function implements conjugate models with normal structure (conjugate normal-normal DP mixture model).

Usage
dpmixsim(x, M=1, a=1, b=1, upalpha=1, a0=2, b0=2, maxiter=4000, rec=3000, fsave=NA, kmax=30, nclinit=NA, minvar=0.001)

Arguments

- x: scaled input data as vector in range {0,1}
- M: Dirichlet Process precision hyperparameter
- a: Gamma prior hyperparameter
- b: Gamma prior hyperparameter
- upalpha: is a logical variable for simulations with {automatic, fixed} calibration of the precision hyperparameter M (default = 'true')
- a0: Gamma prior hyperparameter for M (default 2)
- b0: Gamma prior hyperparameter for M (default 2)
- maxiter: maximum number of MCMC iteration steps
- rec: record the last 'rec' iteration steps
- fsave: filename for saving the MCMC simulation (def: ‘NULL’ do not save)
- kmax: maximum number of clusters in the simulation, (default 30)
- nclinit: number of initial clusters to use at the beginning of the simulation. If not specified (NA) the number of initial clusters is equal to the length of x (one element per cluster); (default: NA)
- minvar: minimum value admissible for a cluster variance (default=0.001). Decreasing ‘minvar’ may improve resolution (distribution fitness), but increases the maximum number of admissible clusters (‘kmax’). In this case, you may have to increase (‘kmax’) as well.
Details

Consider \( n \) observations \( x_1, \ldots, x_n \) which we regard as exchangeable. We model the distribution from which the \( x_i \) are drawn as a mixture of distributions. Dirichlet process mixture models are based on Dirichlet process priors for the primary parameters \( \theta_i \). DP mixture models assume that the prior distribution function \( G \) itself is uncertain, drawn from a Dirichlet process \( G \sim DP(\mathcal{M}G_0) \), with base prior \( G_0 \) and precision parameter \( \mathcal{M} \). This specification may be expressed by the hierarchical model:

\[
x_i \sim N(.|\theta_i, \sigma^2) \\
\theta_i \sim G \\
G \sim DP(\mathcal{M}N(0,1)) \\
\sigma^{-2} \sim Gamma(a,b)
\]

Value

simulation output as a list of draws containing:

- \text{Krec} \quad \text{cluster indicator variables}
- \text{Wrec} \quad \text{cluster weights}
- \text{Phirec} \quad \text{theta cluster parameters}
- \text{Varrec} \quad \text{sigma cluster parameters}

Author(s)

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References


See Also

readsliceimg, postdataset, postdpmixciz, postimgclgrp, postimgcomps, postkcluster, premask, readsliceimg

Examples

```r
## not run:  
## Example 1: simple test using `galaxy' data  
data("galaxy")  
x0 <- galaxy$speed  
x <- prescale(x0)  
maxiter <- 4000; rec <- 3000; ngrid <- 100  
res <- dpmixsim(x, M=1, a=1, b=0.1, upalpha=1, maxiter=maxiter, rec=rec,  
nclinit=4)  
z <- postdpmixciz(x=x, res=res, rec=rec, ngrid=ngrid, plot=T)
```
### Example 2:
demo(testMaronWand)

### Example 3: MRI segmentation

## Testing note: this example should reproduce the equivalent segmented images used in the author’s references

```r
slicedata <- readsliceimg(ftime="t1_pn3_rf0", swap=FALSE)
image(slicedata$niislice, col=gray((0:255)/256), main="original image")
x0 <- premask(slicedata, subsamp=TRUE)
x <- prescale(x0)
rec <- 3000
res <- dpmixsim(x, M=1, a=1, b=1, upalpha=1, maxiter=4000,
                 rec=rec, nclinit=8, minvar=0.002)
## post-simulation
ngrid <- 200
z <- postdpmixciz(x, res=res, rec=rec, ngrid=ngrid, plot=TRUE)
x0 <- premask(slicedata, subsamp=FALSE) # use full-sized image after estimation
x <- prescale(x0)
cx <- postdataseg(x, z, ngrid=ngrid)
cat("*** view grouped segmentations:")
postimgclgrp(slicedata$mask, cx, palcolor=FALSE)
cat("*** display all clusters:")
postimgcomps(slicedata$mask, cx)
cat("*** re-cluster with 4 clusters:")
postkcluster(slicedata$mask, cx, clk=4)
```

## End(Not run)

---

galaxy  

### Galaxy velocities

#### Description

This data set considers physical information on velocities (km/second) for 82 galaxies reported by Roeder (1990). These are drawn from six well-separated conic sections of the Corona Borealis region.

#### Usage

data(galaxy)

#### Format

A data frame with 82 observations on the following variable.

| speed | a numeric vector giving the speed of galaxies ((km/second)) |
Source

References

Examples
data(galaxy)
## maybe str(galaxy) ; plot(galaxy) ...

postdataseg  

Description
postdataseg performs data segmentation based on labelled cluster estimates.

Usage
postdataseg(x, z, ngrid, dbg=FALSE)

Arguments
x  full-sized scaled image data prepared by premask
z  cluster labels produced by postdpmixciz
ngrid  dimension of the grid used in estimation
dbg  logical variable to show debugging output (default = ‘FALSE’)

Details
Once the distributions of the indicator variables $z_i$ are calculated we can separate the components of the mixture. Individual components are selected according to the most probable $z_i$ value in a given region of the distributional space, leading to a partition of this space into regions. Intensity threshold values are associated with the partition of the distributional space to drive the image segmentation. In brief, the partition of the distributional space induced by the $z$ values is used to segment the data space. From a computational point of view, the use of these two separate spaces enables us to optimize the MCMC implementation.

Value
cx  vector of image cluster values
postdpmxiciz

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See Also
dpmixsim, readsliceimg, premask, postdpmxiciz

Examples

## not run:
## see Example 2 in dpmixsim.
## End(Not run)

postdpmxiciz     Summary statistics and cluster estimation

Description
postdpmxiciz computes post-simulation summary statistics, and estimates cluster partition.

Usage
postdpmxiciz(x, res, kmax=30, rec=300, ngrid=200, plot=TRUE)

Arguments
x  data used in the simulation
kmax  maximum number of clusters
res  output of the MCMC simulation
rec  number of recorded iteration steps
ngrid  dimension of the grid used in density estimation
plot  logical variable to omit plots (default = ‘TRUE’)

Value
z  cluster partition estimation

Author(s)
A. Ferreira da Silva, Universidade Nova de Lisboa, Faculdade de Ciencias e Tecnologia, <afs@fct.unl.pt>.
References


See Also
dpmixsim

Examples

```r
## Not run:
## example: MRI brain image segmentation
slicedata <- readsliceimg(fbase="t1_pn3_rf0", swap=FALSE)
image(slicedata$niislice, col=gray((0:255)/256), main="original image")
x0 <- premask(slicedata, subsamp=TRUE)
x <- prescale(x0)
rec <- 3000
res <- dpmixsim(x, M=1, a=1, b=2, upalpha=1, maxiter=4000,
rec=rec, nclinit=8)
## post-simulation
ngrid <- 200
z <- postdpmixciz(x, res=res, rec=rec, ngrid=ngrid, plot=TRUE)
## End(Not run)
```

postimgclgrp  Segment image with the estimated number of components

Description

postimgclgrp displays the segmented image with the estimated number of components

Usage

`postimgclgrp(mask, cx, palcolor=TRUE)`

Arguments

- `mask`  full-sized scaled image data prepared by `premask`
- `cx`  data segmentation prepared by `postdataseg`
- `palcolor`  logical variable for selecting colored/grey image visualization (default = ‘TRUE’)

Details

Display image segmentation with the estimated number of components.
postimgcomps

Description

postimgcomps displays the components of the segmented image with the estimated number of components.

Usage

postimgcomps(mask, cx)

Arguments

- mask: scaled masked full-sized image data prepared by premask
- cx: data segmentation prepared by postdataseteg

Details

Display components based on the estimated number of clusters.

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References


See Also
dpmixsim, readsliceimg, premask, postdpmixciz, postdataset, postimgclgrp

Examples

```r
## not run:
## see Examples in 'dpmixsim'.
## End(Not run)
```

postkcluster  Segmentation with a fixed number of clusters

Description

postkcluster re-clusters the data with a user-specified number of components, and displays the segmented image.

Usage

```r
postkcluster(mask, cx, clk=4, plot=TRUE)
```

Arguments

- **mask**: masked full-sized image data prepared by `premask`
- **cx**: data segmentation prepared by `postdataset`
- **clk**: desired fixed number of components, including the background component, to use in the data segmentation; default `clk=4`: gray matter (GM), white matter (WM), CSF, and background
- **plot**: logical variable; enables suspension of output images (default = `TRUE`)

Details

Partitioning clustering around medoids (PAM) is applied to the classes simulated from `dpmixsim` as a post-processing step. This procedure may be applied to merge clusters, and reduce the number of clusters to the specified value `clk`. `postkcluster` computes a `clara` object using `cluster` (see Struyf et.al.), a list representing a clustering of the data into `clk` clusters.
Author(s)

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References


See Also
dpmixsim, readsliceimg, premask, postdpmixciz, postdataset, postimgcomps

Examples

```r
## Not run:
## see Examples in `dpmixsim`.

## End(Not run)
```

Description

premask applies a pre-defined mask to a MRI slice in order to select regions of interest (ROIs) for processing

Usage

```r
premask(slicedata, subsamp=TRUE)
```

Arguments

- `slicedata`: list as output by `read.sliceimg`
- `subsamp`: logical variable; if `TRUE` a downsampled image by a factor of 2 is used in the MCMC simulation, otherwise the full-sized image is taken. After parameter estimation, the full-sized image should be used for clustering and image segmentation. The use of downsampled images can substantially reduce runtime, with little quality degradation.
Value

\( xv \)  
processed data vector

Author(s)

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See Also

dpmixsim, readsliceimg

Examples

```r
## not run:
slicedata <- readsliceimg(fbase="t1_pn3_rf0", swap=FALSE)
x0 <- premask(slicedata, subsamp=TRUE)
x <- prescale(x0)
print(str(x))

## End(not run)
```

Description

prescale scales data to be in the range \( \{0,1\} \), as a preparation for simulation.

Usage

```
prescale(xv)
```

Arguments

\( xv \)  
unscaled data vector

Value

\( x \)  
scaled data vector

Author(s)

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See Also

dpmixsim, readsliceimg
Examples

```r
## Not run:
data("galaxy")
x0 <- galaxy$speed
x <- prescale(x0)
print(range(x))

## End(Not run)
```

### Description

`readsliceimg` reads MRI and mask data.

### Usage

```r
readsliceimg(fbase="t1_pn3_rf0", swap=FALSE)
```

### Arguments

- `fbase`: Indicates the dataset prefix of the MRI dataset to use. The prefix applies to data files: `{fbase}_slice_009.nii.gz`, and `{fbase}_slice_009_mask.nii.gz`. These data files were obtained from the BrainWeb repository of the McConnell Brain Imaging Center at the Montreal Neurological Institute. BrainWeb anatomical models uses MRI slices of dimension 181x217 pixels. The datasets included in the package for demonstration correspond to a T1 BrainWeb image for slice number 92, with 3% noise and 0% intensity non-uniformity.

- `swap`: logical variable (default = ‘FALSE’) for choosing the right/left data display convention consistent with FSLVIEW

### Details

The FSL tools may be used to prepare the MRI data and the mask required as data input. The package `oro.nifti` is used for reading gzipped NIFTI files.

### Value

A list containing:

- `fbase`: dataset prefix of the dataset used in the analysis
- `niislice`: slice data at all timepoints
- `mask`: slice mask
- `nrow`: number of rows
- `ncol`: number of columns
- `swap`: relative orientation used in the data setup


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References


FSL/FEAT Analysis tool, FMRIB Software Library (FSL) (www.fmrib.ox.ac.uk/fsl)

See Also

dpmixsim

Examples

### Not run:
```r
slicedata <- readsliceimg(fbase="t1_pn3_rf0", swap=FALSE)
print(str(slicedata))
```

### End(Not run)

---

Example of a pre-processed MRI slice from the BrainWeb database

Description

The file 't1_pn3_rf0_slice_0092.nii.gz' is a pre-processed image of slice '92' with '3%' noise extracted from the Brainweb database file 't1_icbm_normal_1mm_pn3_rf0\[1\].mnc.gz'. BrainWeb simulations are based on an anatomical model of normal brain, which can serve as the ground truth for any analysis procedure. BrainWeb datasets and are provided by the McConnell Brain Imaging Center at the Montreal Neurological Institute, [http://www.bic.mni.mcgill.ca/](http://www.bic.mni.mcgill.ca/), (see Collins et. al. 1998).

Format

The file 't1_pn3_rf0_slice_0092.nii.gz' is in gzipped NIFTI format. The R-package oro.nifti is required to read gzipped NIFTI files.

References


**Mask file for MRI slice**

**Description**

The `t1_pn3_rf0_slice_0092_mask.nii.gz` defines the mask for `t1_pn3_rf0_slice_0092.nii.gz`, as used in the examples. The mask used here is an all-brain mask; it just removes non-brain regions, as the result of applying a brain extraction tool to the specified dataset. Other masks may be defined to select regions of interest (ROIs).

**Format**

The file `t1_pn3_rf0_slice_0092_mask.nii.gz` is in gzipped NIFTI format. The R-package `oro.nifti` is required to read gzipped NIFTI files.

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