

Package ‘mritc’

April 20, 2012

Title MRI tissue classification.

Version 0.4-0

Author Dai Feng and Luke Tierney

Description Various methods for MRI tissue classification.

Maintainer Dai Feng <dai_feng@merck.com>

Depends R (>= 2.14.0), lattice (>= 0.18-8), misc3d (>= 0.8-1), fmri (>= 1.4-6), AnalyzeFMRI (>= 1.1-14)

Suggests tkrplot (>= 0.0-23)

License GPL

Repository CRAN

Date/Publication 2012-04-20 16:07:46

R topics documented:

mritc-package	2
emnormmix	3
initNormMix	5
makeMRIspatial	6
measureMRI	7
mritc	9
plot.mritc	12
print.mritc	13
readMRI	14
rnormmix	15
summary.mritc	16
writeMRI	16
Index	18

Description

Use various methods to do MRI tissue classification.

Introduction

This package provides tools for MRI tissue classification using normal mixture models and (higher resolution) hidden Markov normal mixture models fitted by various methods.

Magnetic resonance imaging (MRI) is used to identify the major tissues within a subject's brain. Classification is usually based on a single image providing one measurement for each volume element, or voxel, in a discretization of the brain. A simple model for MRI tissue classification views each voxel as homogeneous, belonging entirely to one of the three major tissue types (cerebrospinal fluid (CSF), gray matter (GM), and white matter (WM)); the intensity of voxels are thus normally distributed with means and variances depending on the tissue types of their voxels. The tissue types are not known and need to be identified from the image. The assumption that all tissue types are independent leads to a simple normal mixture model with parameters estimated by the EM algorithm and tissue types assigned using the Bayes classifier.

Since nearby voxels tend to be of the same tissue type, a Markov random field model (a model from the Potts model family is used in this case) can be used to capture the spatial similarity of voxels by assigning homogeneity relationship among tissue types of neighboring voxels. Again, given the tissue types, the intensity of voxels are independently and normally distributed with means and variances depending on their tissue types. Furthermore, the Markov random field model defined on finite space is referred to as the hidden Markov model. Therefore the model combine the normal mixture part and the Potts model part is called the hidden Markov normal mixture model. This model can be fitted by the Iterated Conditional Mode algorithm, the Hidden Markov Random Field EM algorithm, or a Markov chain Monte Carlo approach.

A more realistic model than the one just described would take into account the fact that the volume elements are not homogeneous; while some may contain only one tissue type, others on the interface will contain two or possibly three different tissue types. This phenomenon is called the partial volume (PV) effect. One approach to address the PV effect is to introduce intermediate classes. Usually this is done by introducing two more classes: the combination of the CSF and the GM and the combination of the GM and the WM. Voxels containing WM and CSF are very rare and are ignored. This helps reduce confounding in estimation and a number of studies have used this approach. Among these methods, the Gaussian partial volume hidden Markov random field models fitted by the modified EM algorithm appears to be more competitive in performance. A new approach to this problem is to construct a higher resolution image in which each voxel is divided into eight subvoxels. For each voxel the measured value is the sum of the unobserved measurements for the subvoxels. The subvoxels are in turn assumed to be homogeneous and follow the simpler model described above. This approach could provide more accurate tissue classification and also allow more effective estimation of the proportion of each voxel that belongs to each of the major tissue types.

Usage

The function `readMRI` and `writeMRI` are I/O functions for MRI data. Right now, the "Analyze", "NIFTI", and raw byte (unsigned with 1 byte per element in the byte stream) gzip formats are supported.

For each MR image, there has to be a corresponding array, mask, with values 1 and 0. Voxels with value 1 are inside the brain and 0 are outside. Tissue classification is conducted on voxels inside the brain.

The functions `mritc.em`, `mritc.icm`, `mritc.hmrfem`, and `mritc.bayes` are used to conduct the MRI tissue classification using the normal mixture model fitted by the EM algorithm, the hidden Markov normal mixture model at the voxel level fitted by the Iterated Conditional Mode algorithm, the Hidden Markov Random Field EM algorithm, or the Bayesian method, and the higher resolution model fitted by the Bayesian method. The function `mritc.pvhmrfem` is for classification using Gaussian partial volume hidden Markov random field models fitted by the modified EM algorithm. Different components of the normal mixture model correspond to different tissue types. The number of components is flexible, say using five components model to address the PV effect by `mritc.em`, `mritc.icm`, `mritc.hmrfem`, or `mritc.bayes`.

In order to use the previous functions, the parameters of the normal mixture model and the Potts model have to be specified. Some parameters can be obtained using the functions `initOtsu` and `makeMRIspatial`. There are default values for other parameters.

The function `mritc` integrates all methods together, provides a uniform platform with easier usage, and generates an object of class "mritc", for which generic functions `print.mritc`, `summary.mritc`, and `plot.mritc` are provided.

Computation Issues

To improve the speed, the table lookup method was used in various places, vectorized computation was used to take advantage of conditional independence. Some computations are performed by C code, and the **OpenMP** is used to parallelize key loops in the C code.

emnormmix

Estimate the Parameters of a Normal Mixture Model Using the EM Algorithm

Description

Use the EM Algorithm to estimate the parameters of a normal mixture model.

Usage

```
emnormmix(y, prop, mu, sigma, err, maxit, verbose)
```

Arguments

<code>y</code>	vector of observations.
<code>prop</code>	vector of initial estimate of the proportions of different components of a normal mixture model.
<code>mu</code>	vector of initial estimate of the means of different components of a normal mixture model.
<code>sigma</code>	vector of initial estimate of the standard deviations of different components of a normal mixture model.
<code>err</code>	relative maximum error(s) used to decide when to stop the iteration. It could be a vector of length three corresponding to the relative maximum errors of the means, standard deviations, and proportions of all components of a normal mixture model. When it is a scalar, all have the same relative maximum error.
<code>maxit</code>	maximum number of iterations to perform.
<code>verbose</code>	logical. If TRUE, then indicate the level of output as the algorithm runs after every 10 iterations.

Details

It is tailor-made for the case when observations are from a finite set (MRI data for example). The table lookup method is used to speed up the computation.

Value

<code>prop</code>	a vector of estimated proportions of different components of a normal mixture model.
<code>mu</code>	a vector of estimated means of different components of a normal mixture model.
<code>sigma</code>	a vector of estimated standard deviations of different components of a normal mixture model.

Examples

```
prop <- c(0.3, 0.3, 0.4)
mu <- c(-10, 0, 10)
sigma <- rep(1, 3)
y<- floor(rnormmix(n=100000, prop, mu, sigma)[,1])
initial <- initOtsu(y, 2)
emnormmix(y=y, prop=initial$prop, mu=initial$mu, sigma=initial$sigma,
          err=1e-7, maxit=100, verbose=TRUE)
```

initNormMix	<i>Get the Initial Estimate of the Parameters of a Normal Mixture Model</i>
-------------	---

Description

Obtain initial estimation of proportions, means, and standard deviations of different components (tissue types for MRI) based on threshold values generated by Otsu's method implemented by a fast algorithm, or proportion of different components.

Usage

```
initOtsu(y, m)
initProp(y, prop)
```

Arguments

y	a vector of intensity values of an image.
m	number of classes (tissue types for MRI) minus 1.
prop	the initial estimate of proportion of different components.

Details

The exhaustive search part of the function for Otsu's algorithm is adapted from [combn](#). For [initProp](#), the threshold values are quantiles based on the initial estimate of proportion of different components.

Value

prop	a vector of initial estimate of the proportions of different components (tissue types for MRI).
mu	a vector of initial estimate of the means of different components (tissue types for MRI).
sigma	a vector of initial estimates of the standard deviations of different components (tissue types for MRI).

Note

For [initOtsu](#), it supports any number of m . However, for MRI data, it can be slow if m is bigger than 3 even with the fast algorithm implemented, since the Otsu's algorithm uses an exhaustive search. But it should be fine with m equal to 2, which corresponds to the typical case in MRI classification with three major tissue types CSF, GM, and WM.

References

Nobuyuki Otsu (1979). A threshold selection method from gray-level histograms *IEEE Transactions on Systems, Man and Cybernetics* **vol. 9**, 62-66

Ping-Sung Liao, Tse-Sheng Chen and Pau-Choo Chung (2001) A Fast Algorithm for Multilevel Thresholding *Journal of Information Science and Engineering* **vol. 17**, 713-727

Examples

```

#Example 1
prop <- c(.3, .4, .3)
mu <- c(40, 90, 130)
sigma <- c(4, 8, 4)
y <- floor(rnormmix(n=100000, prop, mu, sigma)[,1])
initOtsu(y, 2)
initProp(y, prop)

#Example 2
T1 <- readMRI(system.file("extdata/t1.rawb.gz", package="mritc"),
              c(91,109,91), format="rawb.gz")
mask <-readMRI(system.file("extdata/mask.rawb.gz", package="mritc"),
              c(91,109,91), format="rawb.gz")
initOtsu(T1[mask==1], 2)
initProp(T1[mask==1], c(0.17, 0.48, 0.35))

```

makeMRIspatial

Obtain Spatial Features of a Mask of an MR Image

Description

Obtain various spatial features of an MR image, which are used in tissue classification.

Usage

```
makeMRIspatial(mask, nnei, sub)
```

Arguments

mask	three dimensional array. The voxels with value 1 are inside the mask; with value 0 are outside. We just focus on voxels inside the mask.
nnei	the number of neighbors. Right now only 6, 18, and 26 neighbors are supported. For a 3D image, besides defining 6 neighbors in the x, y, and z directions, one can add 12 diagonal neighbors in the x-y, x-z, and y-z planes, and another 8 on the 3D diagonals. This leads to a six neighbor structure, an eighteen neighbor structure, and a twenty-six neighbor structure.
sub	logical; if TRUE, a new mask which splits each voxel into eight subvoxels is generated, and then obtain the neighbors and blocks of subvoxels; otherwise obtain the neighbors and blocks at the voxel level.

Value

A list containing the following components:

neighbors	a matrix, each row of which giving the neighbors of a voxel or subvoxel. The number of rows is equal to the number of (sub)voxels within the mask and the number of columns is the number of neighbors of each (sub)voxel. For the (sub)voxels on the boundaries, when one or more of their neighbors are missing, the missing are represented by the total number of (sub)voxels within the mask plus 1.
blocks	the (sub)voxels within each block are mutually independent given the (sub)voxels in other blocks.
sub	logical; the same as the input sub.
subvox	if sub is TRUE, it is a matrix, with each row giving the eight subvoxels of a voxel; otherwise it is equal to NULL.

References

Dai Feng (2008) Bayesian Hidden Markov Normal Mixture Models with Application to MRI Tissue Classification *Ph. D. Dissertation, The University of Iowa*

Examples

```
mask <- array(1, dim=c(2,2,2))
spa <- makeMRIspatial(mask, nnei=6, sub=FALSE)
spa <- makeMRIspatial(mask, nnei=6, sub=TRUE)
```

measureMRI

Compare the Predicted Classification Results with the Truth

Description

Calculate and demonstrate different measures for classification results based on the truth.

Usage

```
measureMRI(intvec, actual, pre)
```

Arguments

intvec	a vector of intensity values. If it is not NULL, the density plots of each component corresponding to the actual and predicted classification results are shown. The default is NULL.
actual	matrix of the true classification result. Each row corresponds to one voxel. Column i represents the probabilities that all voxels are allocated to tissue type i .
pre	matrix of the predicted classification result. Each row corresponds to one voxel. Column i represents the probabilities that all voxels are allocated to tissue type i .

Value

mse	mean square error.
misclass	mis-classification rate.
rseVolume	root square error of volume with respect to reference tissue volume.
DSM	Dice Similary Measure of each tissue type.

$$DSM_{a,b}^t = \frac{2 \times N_{a \cap b}^t}{N_a^t + N_b^t}$$

where N_a^t and N_b^t are the number of voxels classified as tissue type t by method a and b respectively, and $N_{a \cap b}^t$ is the number of voxels classified as tissue type t by both methods a and b . The larger the DSM, the more similar the results from the two methods.

conTable	confusion table. Each column of the table represents the instances in an actual class, while each row represents the instances in a predicted class.
----------	--

Examples

```
#Example 1
prop <- c(.3, .4, .3)
mu <- c(-4, 0, 4)
sigma <- rep(1, 3)
y <- rnormmix(n=1e4, prop, mu, sigma)
intvec <- y[,1]
actual <- y[,2]
pre <- actual
pre[sample(1:1e4, 100, replace=FALSE)] <- sample(1:3, 100, replace=TRUE)
actual <- do.call(cbind, lapply(1:3, function(i) ifelse(actual==i, 1, 0)))
pre <- do.call(cbind, lapply(1:3, function(i) ifelse(pre==i, 1, 0)))
measureMRI(intvec, actual, pre)

#Example 2
T1 <- readMRI(system.file("extdata/t1.rawb.gz", package="mritc"),
              c(91,109,91), format="rawb.gz")
mask <- readMRI(system.file("extdata/mask.rawb.gz", package="mritc"),
               c(91,109,91), format="rawb.gz")
tc.icm <- mritc(T1, mask, method="ICM")

csf <- readMRI(system.file("extdata/csf.rawb.gz", package="mritc"),
              c(91,109,91), format="rawb.gz")
gm <- readMRI(system.file("extdata/gm.rawb.gz", package="mritc"),
             c(91,109,91), format="rawb.gz")
wm <- readMRI(system.file("extdata/wm.rawb.gz", package="mritc"),
             c(91,109,91), format="rawb.gz")
truth <- cbind(csf[mask==1], gm[mask==1], wm[mask==1])
truth <- truth/255
measureMRI(T1[mask==1], truth, tc.icm$prob)
```

Description

Conduct the MRI tissue classification using different methods including: the normal mixture model (NMM) fitted by the Expectation-Maximization (EM) algorithm; the hidden Markov normal mixture model (HMNMM) fitted by the Iterated Conditional Mode (ICM) algorithm, the Hidden Markov Random Field EM (HMRFEM) algorithm, or the Bayesian method (MCMC); the partial volume HMNMM fitted by the modified EM (PVHMRFEM) algorithm ; the higher resolution HMNMM fitted by the Bayesian method (MCMCsub).

Usage

```
mritc.em(y, prop, mu, sigma, err, maxit, verbose)
mritc.icm(y, neighbors, blocks, spatialMat, beta, mu, sigma,
         err, maxit, verbose)
mritc.hmrfem(y, neighbors, blocks, spatialMat, beta, mu, sigma,
            err, maxit, verbose)
mritc.pvhmrfem(y, neighbors, blocks, spatialMat, beta, mu, sigma,
              err, maxit, verbose)
mritc.bayes(y, neighbors, blocks, sub, subvox, spatialMat, beta,
           mu, sigma, niter, verbose)
mritc(intarr, mask, method)
```

Arguments

y	a vector of intensity values of voxels.
prop	a vector of initial estimate of the proportions of different components of a normal mixture model. It can be obtained using the function init0tsu .
mu	a vector of initial estimate of the means of different components of a normal mixture model. It can be obtained using the function init0tsu .
sigma	a vector of initial estimates of the standard deviations of different components of a normal mixture model. It can be obtained using the function init0tsu .
err	relative maximum error(s) used to decide when to stop the iteration. It could be a vector corresponding to the relative maximum errors of the means, standard deviations (for mritc.em , mritc.icm , mritc.hmrfem , and mritc.pvhmrfem), and proportions (for mritc.em) of all components of a normal mixture model. When it is a scalar, all have the same relative maximum error. The default value is 1e-4.
maxit	maximum number of iterations to perform. The default is 200 for mritc.em , 20 for mritc.icm , mritc.hmrfem , and mritc.pvhmrfem .
verbose	logical. If TRUE, then indicate the level of output as the algorithm runs.
neighbors	a matrix of neighbors of voxels. One row per voxel. It can be obtained using the function makeMRIspatial .

sigma a vector of estimated standard deviations of the normal mixture model.
 method the method used for computation.
 mask mask of a brain. Voxels inside it are classified.

Generic functions `print.mritc`, `summary.mritc`, and `plot.mritc` are provided.

For others, only `prob`, `mu`, and `sigma` are generated.

Note

The functions support the various normal mixture models with at most eight components.

References

- Julian Besag (1886) On the statistical analysis of dirty pictures (with discussion) *Journal of the Royal Statistical Society. Series B (Methodological)* **vol. 48** 259-302
- Yongyue Zhang, Michael Brady, and Stephen Smith (2001) Segmentation of brain MR images through a hidden Markov random field model and the expectation-maximization algorithm *IEEE Transactions on Medical Imaging* **vol. 20** 45-57
- Meritxell Bach Cuadra, Leila Cammoun, Torsten Butz, Olivier Cuisenaire, and Jean-Philippe Thiran (2005) Comparison and Validation of Tissue modelization and statistical classification methods in T1-weighted MR brain images *IEEE Transactions on Medical Imaging*, **vol.24** 1548-1565
- Dai Feng (2008) Bayesian Hidden Markov Normal Mixture Models with Application to MRI Tissue Classification *Ph. D. Dissertation, The University of Iowa*
- Dai Feng and Luke Tierney (2011) mritc: A Package for MRI Tissue Classification *Journal of Statistical Software*, **vol. 44, no. 7** 1-20 <http://www.jstatsoft.org/v44/i07/>
- Feng D, Tierney L, and Magnotta V (2011) MRI Tissue Classification Using High Resolution Bayesian Hidden Markov Normal Mixture Models *Journal of the American Statistical Association* Accepted for publication. DOI: 10.1198/jasa.2011.ap09529

Examples

```
#Example 1
T1 <- readMRI(system.file("extdata/t1.rawb.gz", package="mritc"),
              c(91,109,91), format="rawb.gz")
mask <- readMRI(system.file("extdata/mask.rawb.gz", package="mritc"),
                c(91,109,91), format="rawb.gz")
y <- T1[mask==1]
initial <- initOtsu(y, 2)
prop <- initial$prop
mu <- initial$mu
sigma <- initial$sigma
tc.em <- mritc.em(y, prop, mu, sigma, verbose=TRUE)

## Not run:
mrispatial <- makeMRIsatial(mask, nnei=6, sub=FALSE)
tc.icm <- mritc.icm(y, mrispatial$neighbors, mrispatial$blocks,
                  mu=mu, sigma=sigma, verbose=TRUE)
tc.hmrfem <- mritc.hmrfem(y, mrispatial$neighbors, mrispatial$blocks,
```

```

                                mu=mu, sigma=sigma, verbose=TRUE)
tc.pvhmrfem <- mritc.pvhmrfem(y, mrispatial$neighbors, mrispatial$blocks,
                                mu=mu, sigma=sigma, verbose=TRUE)
tc.mcmc <- mritc.bayes(y, mrispatial$neighbors, mrispatial$blocks,
                                mrispatial$sub, mrispatial$subvox,
                                mu=mu, sigma=sigma, verbose=TRUE)
mrispatial <- makeMRIspace(mask, nnei=6, sub=TRUE)
tc.mcmbsub <- mritc.bayes(y, mrispatial$neighbors, mrispatial$blocks,
                                mrispatial$sub, mrispatial$subvox,
                                mu=mu, sigma=sigma, verbose=TRUE)

## End(Not run)
#Example 2
T1 <- readMRI(system.file("extdata/t1.rawb.gz", package="mritc"),
              c(91,109,91), format="rawb.gz")
mask <-readMRI(system.file("extdata/mask.rawb.gz", package="mritc"),
              c(91,109,91), format="rawb.gz")
tc.icm <- mritc(T1, mask, method="ICM")

```

plot.mritc

Plot Method for Class "mritc"

Description

Visualize MRI tissue classification results.

Usage

```
## S3 method for class 'mritc'
plot(x, ...)
```

Arguments

x an object of class "mritc"
... any additional arguments for function [slices3d](#).

Details

Allocate a voxel to the tissue type with the highest probability and then use [slices3d](#) to show the result.

Value

NULL

See Also

[slices3d](#)

Examples

```
T1 <- readMRI(system.file("extdata/t1.rawb.gz", package="mritc"),
               c(91,109,91), format="rawb.gz")
mask <-readMRI(system.file("extdata/mask.rawb.gz", package="mritc"),
               c(91,109,91), format="rawb.gz")
tc.icm <- mritc(T1, mask, method="ICM")
plot(tc.icm)
```

print.mritc	<i>Print Method for Class "mritc"</i>
-------------	---------------------------------------

Description

Print out some information of an object of class "mritc".

Usage

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

Arguments

x	an object of class "mritc".
...	any additional arguments.

Value

The function computes and returns some summary statistics of the object obtained from running the function `mritc`.

Examples

```
T1 <- readMRI(system.file("extdata/t1.rawb.gz", package="mritc"),
               c(91,109,91), format="rawb.gz")
mask <-readMRI(system.file("extdata/mask.rawb.gz", package="mritc"),
               c(91,109,91), format="rawb.gz")
tc.icm <- mritc(T1, mask, method="ICM")
tc.icm
```

readMRI	<i>Read an MR Image into an Array</i>
---------	---------------------------------------

Description

Read an MR image of different formats into an array.

Usage

```
readMRI(file, dim, format)
```

Arguments

file	the name of the image file to be read in.
dim	the dimensions of the image. It is required for the image of type raw.gz, in which dim is a vector of length three specifying dimensions in x, y, and z directions. The default is NULL.
format	the format of the image file. Right now only the "Analyze", "NIfTI", and raw byte (unsigned with 1 byte per element in the byte stream) gzip formats are supported.

Details

The files of "Analyze" format are read in through the functions [f.read.analyze.volume](#). The files of "NIfTI" format are read in through an adapted version of [read.NIFTI](#). Besides the original ".nii" files and the "hdr/img" files, it can read the "nii.gz" files as well.

Value

An array with the appropriate dimensions containing the image volume. For the images of "Analyze" format, the ".hdr" file and its corresponding ".img" file should be in the same directory. For "NIfTI" format, If the extension of the filename is not included, the function searches for the "nii.gz" file, then for the ".nii" file, and finally for the "hdr/img" files in pair.

See Also

[f.read.analyze.volume](#), [read.NIFTI](#)

Examples

```
## Not run:
vol1 <- readMRI("t1.rawb.gz", c(91,109,91), "rawb.gz")

vol2 <- readMRI("t1.nii.gz", format="nifti")

vol3 <- readMRI("t1.nii", format="nifti")

vol4 <- readMRI("t1-nifti.img", format="nifti")
```

```
vol5 <- readMRI("t1-analyze.img", format="analyze")  
  
## End(Not run)
```

rnormmix

Generate Random Samples from a Normal Mixture Model

Description

Generate random samples from a normal mixture model.

Usage

```
rnormmix(n, prop, mu, sigma)
```

Arguments

n	number of observations.
prop	a vector of proportions of different components.
mu	a vector of means of different components.
sigma	a vector of standard deviations of different components

Value

A matrix with each row corresponding to one sample. The first column are sample values from a normal mixture model; the second column are the components from which observations come.

Examples

```
prop <- c(.17, .48, .35)  
mu <- c(-4, 0, 4)  
sigma <- rep(1, 3)  
y <- rnormmix(n=10000, prop, mu, sigma)  
densityplot(~ y[,1], groups = y[,2],  
            plot.points = FALSE, ref = TRUE,  
            xlab="sample values",  
            auto.key = list(columns = 3))
```

summary.mritc	<i>Summary Method for Class "mritc"</i>
---------------	---

Description

Summarize some information of an object of class "mritc".

Usage

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

Arguments

object	an object of class "mritc".
...	any additional arguments.

Value

The function computes and returns some summary statistics of the object obtained from running the function `mritc`.

Examples

```
T1 <- readMRI(system.file("extdata/t1.rawb.gz", package="mritc"),  
              c(91,109,91), format="rawb.gz")  
mask <- readMRI(system.file("extdata/mask.rawb.gz", package="mritc"),  
                c(91,109,91), format="rawb.gz")  
tc.icm <- mritc(T1, mask, method="ICM")  
summary(tc.icm)
```

writeMRI	<i>Write an MR Image</i>
----------	--------------------------

Description

Write an MR image into a file of different formats.

Usage

```
writeMRI(data, file, header, format)
```

Arguments

data	MRI data in a three dimensional array or four dimensional array with the forth dimension equal to 1.
file	the name of the image file to be written out.
header	the header file. For file of the "rawb.gz" format, header is NULL.
format	the format of the image file. Right now only the "Analyze", "NIfTI", and raw byte (unsigned with 1 byte per element in the byte stream) gzip formats are supported.

Details

Header file is needed for the file of "Analyze" or "NIfTI" format. For details of the header files for "Analyze" format, see <http://eeg.sourceforge.net/ANALYZE75.pdf>. For details of the header files for "NIfTI" format and the comparison between the "Analyze" and "NIfTI" formates, see <http://nifti.nimh.nih.gov/>.

Files of "Analyze" format are written out through the function `write.ANALYZE`. An adapted version of `write.NIFTI` is used to write files of "NIfTI" format. Instead of ".nii", the adapted version writes data out into ".nii.gz" files to save space.

Value

Nothing is returned.

See Also

[write.ANALYZE](#), [write.NIFTI](#)

Examples

```
## Not run:
writeMRI(vol, file="vol.rawb.gz", header=NULL, format="rawb.gz")

writeMRI(vol, file="vol", header=niftiheader, format="nifti")

writeMRI(vol, file="vol", header=analyzeheader, format="analyze")

## End(Not run)
```

Index

- *Topic **classif**
 - initNormMix, 5
 - mritc, 9
- *Topic **distribution**
 - rnormmix, 15
- *Topic **methods**
 - plot.mritc, 12
 - print.mritc, 13
 - summary.mritc, 16
- *Topic **package**
 - mritc-package, 2
- *Topic **spatial**
 - makeMRIsatial, 6
- *Topic **utilities**
 - emnormmix, 3
 - measureMRI, 7
 - readMRI, 14
 - writeMRI, 16

combn, 5

emnormmix, 3

f.read.analyze.volume, 14

initNormMix, 5

initOtsu, 3, 5, 9, 10

initOtsu (initNormMix), 5

initProp, 5

initProp (initNormMix), 5

makeMRIsatial, 3, 6, 9, 10

measureMRI, 7

mritc, 3, 9, 10, 13, 16

mritc-package, 2

mritc.bayes, 3, 10

mritc.em, 3, 9, 10

mritc.hmrfem, 3, 9, 10

mritc.icm, 3, 9, 10

mritc.pvhmrfem, 3, 9, 10

plot.mritc, 3, 11, 12

print.mritc, 3, 11, 13

read.NIFTI, 14

readMRI, 3, 14

rnormmix, 15

slices3d, 12

summary.mritc, 3, 11, 16

write.ANALYZE, 17

write.NIFTI, 17

writeMRI, 3, 16