Package ‘AnalyzeFMRI’

November 10, 2019

Version 1.1-21
Date 2019-11-10
Title Functions for Analysis of fMRI Datasets Stored in the ANALYZE or NIFTI Format
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Depends R (>= 3.6.0), R.matlab, fastICA, tcltk, tkrplot
Description Functions for I/O, visualisation and analysis of functional Magnetic Resonance Imaging (fMRI) datasets stored in the ANALYZE or NIFTI format. Note that the latest version of XQuartz seems to be necessary under MacOS.
License GPL (>= 2)
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NeedsCompilation yes
Repository CRAN
Date/Publication 2019-11-10 06:30:13 UTC

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analyze2nifti

Create a NIFTI file from an Analyze file

Description

Create a NIFTI file from an Analyze file.

Usage

```r
analyze2nifti(file.in,path.in=".",path.out=".",file.out=NULL,is.nii=TRUE,
qform.code=2,sform.code=2,data.type=rawToChar(raw(10)),db.name=rawToChar(raw(18)),
dim.info=rawToChar(raw(1)),dim=NULL,TR=0,slice.code=rawToChar(raw(1)),
xyzt.units=rawToChar(raw(1)),descrip=NULL,aux.file=rawToChar(raw(24)),
intent.name=rawToChar(raw(16)))
```
Arguments

file.in  character, filename of the Analyze file to be read
path.in  character, Directory path from where to take the .hdr,.img,.mat files
path.out character, Directory path where to write the .hdr/.img or .nii file
file.out character, filename of the NIFTI file to write (without extension). If NULL, same as file.in
is.nii  logical, if TRUE a NIFTI .nii file will be created, if FALSE a .hdr/.img NIFTI file will be created
qform.code value in 0,...,4
sform.code value in 0,...,4
data.type  char[10]. UNUSED in NIFTI-1 but could be filled with what you want
db.name  char[18]. UNUSED in NIFTI-1 but could be filled with what you want
dim.info MRI slice ordering: This field encode which spatial dimension (1=x, 2=y or 3=z) corresponds to which acquisition dimension for MRI data. In fact, it contains three informations: freq.dim, phase.dim and slice.dim, all squished into the single byte field dim.info (2 bits each, since the values for each field are limited to the range 0..3). The R function fps2diminfo can be used to encode these values from the dim.info byte.
dim  vector (of length 8) of image dimensions. dim[1] specifies the number of dimensions. In NIFTI-1 files, dim[2], dim[3], dim[4] are for space, dim[5] is for time. The 5th dimension (dim[6]) of the dataset, if present (i.e., dim[1]=5 and dim[6]> 1), contains multiple values (for example a vector) to be stored at each spatiotemporal location. Uses of dim[7] and dim[8] are not specified in NIFTI-1 format.
TR  Time Repetition to be stored in pixdim[5]
slice.code Slice timing order. If this is nonzero, AND if slice.dim is nonzero, AND if slice.duration is positive, indicates the timing pattern of the slice acquisition. The following codes are defined: 0 (NIFTI SLICE UNKNOWN), 1 (NIFTI SLICE SEQ INC), 2 (NIFTI SLICE SEQ DEC), 3 (NIFTI SLICE ALT INC), 4 (NIFTI SLICE ALT DEC)
xyzt.units  Units of pixdim[2:5]. Bits 1..3 of xyt.units specify the (same) space unit of pixdim[2:4]. Bits 4..6 of xyt.units specify the time unit of pixdim[5]. See ‘xyzt-units.txt’ in the niftidoc directory of the source package. The R function st2xyzt can be used to encode these values from the xyt.units byte.
descrip  char[80]. This field may contain any text you like
aux.file  char[24]. This field is used to store an auxiliary filename.
intent.name char[16]. name or meaning of data. If no data name is implied or needed, intent.name[1] should be set to 0.

Value

Nothing is returned. The NIFTI file is created in the specified path.out directory (default is current directory).
centering

Examples

```r
## Not run:
analyze2nifti(path.in = system.file(package = "AnalyzeFMRI"), file.in = "example",
               file.out = "nifti-tmp", is.nii = TRUE)

## End(Not run)
```

Description

This function center the data in the two dimensions, the first dimension being indicated by `col.first` argument

Usage

```r
centering(X, col.first = TRUE)
```

Arguments

- `X`: a matrix of size `tm x vm` which contains the functional images
- `col.first`: Logical. Center the columns or the rows first

Value

- `Xcentred`: the double centered matrix

See Also

`reduction`

Examples

```r
# TODO!!
# Xcentred <- centering(X.masked, col.first = TRUE)$Xcentred
```
cluster.threshold  

Cluster threshold an array.

Description

Calculate contiguous clusters of locations in a 3D array that are above some threshold and with some minimum size.

Usage

cluster.threshold(x, nmat = NULL, level.thr = 0.5, size.thr)

Arguments

- **x**: A 3D array
- **nmat**: A matrix with 3 columns specifying the neighbourhood system. Default is 6 nearest neighbours in 3D.
- **level.thr**: The level at which to threshold the array values. Default is 0.5 and is designed to cluster 0-1 arrays.
- **size.thr**: The cluster size threshold.

Value

Returns an array of the same size as x with a 1 at all locations which have a value above level.thr and are in a cluster of similar locations with size greater than size.thr.

Author(s)

J. L. Marchini

Examples

```r
x <- array(0, dim = c(64, 64, 21))
x[10:20, 10:20, 1:5] <- 1
x[30:40, 30:40, 6:7] <- 1
x[50, 50, 8:9] <- 1

a <- cluster.threshold(x, size.thr = 400)
sum(x) ## should be 849
sum(a) ## should be 605
```
cov.est

Estimates the covariance between neighbouring voxels

Description

Estimates the covariance between neighbouring voxels using a specified neighbourhood system.

Usage

cov.est(mat, mask, nmat)

Arguments

mat 3D array of voxel values.
mask Array with same dimension as mat that is 1/0 for voxels to be included/excluded.
nmat Neighbourhood matrix.

Value

The estimated covariance

Author(s)

J. L. Marchini

Examples

ksize <- 9
d <- c(64, 64, 21)
FWHM <- 9
sigma <- diag(FWHM^2, 3) / (8 * log(2))
voxdim <- c(2, 2, 4)

filtermat <- GaussSmoothKernel(voxdim, ksize, sigma)

mask <- array(1, dim = d)
num.vox <- sum(mask)

mat <- Sim.3D.GRF(d = d, voxdim = voxdim, sigma = sigma,
  ksize = ksize, mask = mask, type = "field")$mat

nmat <- expand.grid(-1:1, -1:1, seq(-1:1))
nmat4 <- nmat[c(11, 13, 15, 17), ]

cov <- cov.est(mat, mask, nmat4)
Description

Extract freq.dim, phase.dim and slice.dim fields from the one byte dim.info field of a NIFTI header file.

Usage

diminfo2fps(dim.info)

Arguments

dim.info dim.info field of a NIFTI header file

Value

A list containing freq.dim, phase.dim and slice.dim fields.

These are provided to store some extra information that is sometimes important when storing the image data from an FMRI time series experiment. (After processing such data into statistical images, these fields are not likely to be useful.) These fields encode which spatial dimension (1, 2, or 3) corresponds to which acquisition dimension for MRI data.

Examples:
Rectangular scan multi-slice EPI:
freq_dim = 1 phase_dim = 2 slice_dim = 3 (or some permutation)
Spiral scan multi-slice EPI:
freq_dim = phase_dim = 0 slice_dim = 3 since the concepts of frequency- and phase-encoding directions don’t apply to spiral scan.

The fields freq.dim, phase.dim, slice.dim are all squished into the single byte field dim.info (2 bits each, since the values for each field are limited to the range 0..3). This unpleasantness is due to lack of space in the 348 byte allowance.

See Also

fps2diminfo

Examples

dim.info <- f.read.header(system.file("example-nifti.hdr", package="AnalyzeFMRI"))$dim.info
diminfo2fps(dim.info)
Expected Euler Characteristic for a 3D Random Field

Description

Calculates the Expected Euler Characteristic for a 3D Random Field thresholded a level u.

Usage

EC.3D(u, sigma, voxdim = c(1, 1, 1), num.vox, type = c("Normal", "t"), df = NULL)

Arguments

- **u**: The threshold for the field.
- **sigma**: The spatial covariance matrix of the field.
- **voxdim**: The dimensions of the cuboid 'voxels' upon which the discretized field is observed.
- **num.vox**: The number of voxels that make up the field.
- **type**: The marginal distribution of the Random Field (only Normal and t at present).
- **df**: The degrees of freedom of the t field.

Details

The Euler Characteristic $\chi_u$ (Adler, 1981) is a topological measure that essentially counts the number of isolated regions of the random field above the threshold $u$ minus the number of 'holes'. As $u$ increases the holes disappear and $\chi_u$ counts the number of local maxima. So when $u$ becomes close to the maximum of the random field $Z_{max}$ we have that

$$P(\text{reject } H_0 | H_0 \text{ true}) = P(Z_{max}) = P(\chi_u > 0) \approx E(\chi_u)$$

where $H_0$ is the null hypothesis that there is no significant positive activation/signal present in the field. Thus the Type I error of the test can be controlled through knowledge of the Expected Euler characteristic.

Value

The value of the expected Euler Characteristic.

Author(s)

J. L. Marchini

References

See Also

Threshold.RF

Examples

EC.3D(4.6, sigma = diag(1, 3), voxdim = c(1, 1, 1), num.vox = 10000)

EC.3D(4.6, sigma = diag(1, 3), voxdim = c(1, 1, 1), num.vox = 10000, type = "t", df = 100)

Description

This function computes the eigenvalues of a centered and reduced data matrix

Usage

eigenvalues(X, draw=FALSE)

Arguments

X a matrix of size tm x vm which contains the functionnal images centered and reduced
draw Logical. Should we plot the eigenvalues

Value

A list containing

- eigenvalues vector of the eigenvalues

Examples

# TODO!!
# valpcr <- eigenvalues(Xcr,draw=T)$eigenvalues
**f.analyze.file.summary**

*prints summary of .img file contents*

**Description**

Prints a summary of the contents of an ANALYZE .img file using the associated .hdr header file.

**Usage**

```r
f.analyze.file.summary(file)
```

**Arguments**

- `file` The location of .img file to be read

**Value**

A print out containing information about the .img file. This includes File name, Data Dimension, X dimension, Y dimension, Z dimension, Time dimension, Voxel dimensions, Data type

**See Also**

- `f.read.analyze.header`, `f.read.analyze.slice`, `f.read.analyze.slice.at.all.timepoints`
- `f.read.analyze.ts`, `f.write.analyze`, `f.read.analyze.volume`, `f.spectral.summary`, `f.write.array.to.img.2bytes`
- `f.write.array.to.img.float`, `f.write.list.to.hdr`, `f.basic.hdr.list.create`

**Examples**

```r
f.analyze.file.summary(system.file("example.img", package="AnalyzeFMRI"))
```

---

**f.analyzeFMRI.gui**

*starts AnalyzeFMRI GUI*

**Description**

Starts an R/tk interfaced GUI that allows the user to explore an fMRI dataset stored in an ANALYZE format file using the functions of the AnalyzeFMRI package.

**Usage**

```r
f.analyzeFMRI.gui()
```

**Value**

No value is returned
f.basic.hdr.list.create

creates basic .hdr list in ANALYZE format

Description

Creates a basic list that can be used to write a .hdr file

Usage

f.basic.hdr.list.create(X, file.hdr)

Arguments

X
Array that is to be converted to a .img file

file.hdr
Name of the .hdr file that will be created

Value

Returns a list of all the fields needed to create a .hdr file (see the functions code for details).

See Also

f.write.list.to.hdr, f.analyze.file.summary

Examples

```r
## Not run:
a <- array(rnorm(20 * 30 * 40 * 3), dim = c(20, 30, 40, 3))
file <- "temp.hdr"
f.basic.hdr.list.create(a, file)
## End(Not run)
```

f.basic.hdr.nifti.list.create

creates basic .hdr list in NIFTI format

Description

Creates a basic list that can be used to write a .hdr file or the header part of a .nii file

Usage

f.basic.hdr.nifti.list.create(dim.mat, file)
**f.complete.hdr.nifti.list.create**

**Arguments**

- *dim.mat* vector of the dimensions of the image array associated with the header file to be written
- *file* Name of the .hdr file that will be contained in the file field of the header

**Value**

Returns a list of all the fields needed to create a .hdr file (see the function code for details).

**See Also**

`f.write.list.to.hdr.nifti`, `f.nifti.file.summary`

**Examples**

```
## Not run:
dim.mat <- c(20, 30, 40, 3)
file <- "temp.hdr"
f.basic.hdr.nifti.list.create(dim.mat, file)

## End(Not run)
```

---

**f.complete.hdr.nifti.list.create**

*creates complete .hdr list in NIFTI format*

**Description**

Creates a complete list that can be used to write a .hdr file or the header part of a .nii file

**Usage**

```r
```
Arguments

file
The .hdr filename. If file extension is ".nii", this will create a header file for a ".nii" NIFTI file, else for a .hdr/.img NIFTI pair.

dim.info
MRI slice ordering: This field encode which spatial dimension (1=x, 2=y, or 3=z) corresponds to which acquisition dimension for MRI data. In fact, it contains three informations: freq.dim, phase.dim and slice.dim, all squished into the single byte field dim.info (2 bits each, since the values for each field are limited to the range 0..3). The R function fps2diminfo can be used to encode these values into the dim.info character byte.

dim
vector (of length 8) of image dimensions. dim[1] specifies the number of dimensions. In NIFTI-1 files, dim[2], dim[3], dim[4] are for space, dim[5] is for time. The 5th dimension (dim[6]) of the dataset, if present (i.e., dim[1]=5 and dim[6] > 1), contains multiple values (for example a vector) to be stored at each spatio-temporal location. Uses of dim[7] and dim[8] are not specified in NIFTI-1 format.

intent.p1
1st intent parameter: first auxiliary parameter for a possible statistical distribution specified in intent.code

intent.p2
2nd intent parameter: second auxiliary parameter for a possible statistical distribution specified in intent.code

intent.p3
3rd intent parameter: third auxiliary parameter for a possible statistical distribution specified in intent.code

intent.code
NIFTI INTENT code: if 0, this is a raw dataset; if in range 2...24, this indicates that the numbers in the dataset should be interpreted as being drawn from a given distribution. Most such distributions have auxiliary parameters (given with intent.p?); if in range 1001...1011, this is an other meaning. See file ‘intent-code.txt’ in the niftidoc directory of the source package. If the dataset DOES NOT have a 5th dimension (dim[1]=4), then the auxiliary parameters are the same for each voxel, and are given in header fields intent.p1, intent.p2, and intent.p3. If the dataset DOES have a 5th dimension (dim[1]=5), then the auxiliary parameters are different for each voxel.

datatype
integer indicator of data storage type for each voxel. This could be 2 (unsigned char), 4 (signed short), 8 (signed int), 16 (32 bit float), 32 (64 bit complex = two 32 bit floats), 64 (64 bit float = double), 128 (3 8 bit bytes), 256 (signed char), 512 (unsigned short), 768 (unsigned int), 1024 (signed long long), 1280 (unsigned long long), 1536 (128 bit float = long double), 1792 (128 bit complex = 2 64 bit floats), 2048 (256 bit complex = 2 128 bit floats).

bitpix
the number of bits per voxel. This field MUST correspond with the datatype field. The total number of bytes in the image data is dim[2] * ... * dim[dim[1]+1] * bitpix / 8

slice.start
Indicates the start of the slice acquisition pattern, when slice.code is nonzero. These values are present to allow for the possible addition of "padded" slices at either end of the volume, which don’t fit into the slice timing pattern. If there are no padding slices, then slice.start=0 and slice.end=dim[slice.dim+1]-1 are the correct values. For these values to be meaningful, slice.start must be non-negative and slice.end must be greater than slice.start.
pixdim vector (of length 8). Grid spacings. When reading a NIFTI-1 header, pixdim[1] stores qfac (which is either -1 or 1). If pixdim[1]=0 (which should not occur), we take qfac=1. pixdim[2], pixdim[3] and pixdim[4] give the voxel width along dimension x, y and z respectively. pixdim[5] gives the time step (=Time Repetition=TR). The units of pixdim can be specified with the xyzt.units field.

scl.slope Data scaling: If the scl.slope field is nonzero, then each voxel value in the dataset should be scaled as \( y = \text{scl.slope} \times x + \text{scl.inter} \), where \( x \) = voxel value stored and \( y \) = "true" voxel value

scl.inter Data scaling: offset. Idem above.
	slice.end Indicates the end of the slice acquisition pattern, when slice.code is nonzero. These values are present to allow for the possible addition of "padded" slices at either end of the volume, which don’t fit into the slice timing pattern. If there are no padding slices, then slice.start=0 and slice.end=dim[slice.dim+1]-1 are the correct values. For these values to be meaningful, slice.start must be non-negative and slice.end must be greater than slice.start.

slice.code Slice timing order. If this is nonzero, AND if slice.dim is nonzero, AND if slice.duration is positive, indicates the timing pattern of the slice acquisition. The following codes are defined: 0 (NIFTI SLICE UNKNOWN), 1 (NIFTI SLICE SEQ INC), 2 (NIFTI SLICE SEQ DEC), 3 (NIFTI SLICE ALT INC), 4 (NIFTI SLICE ALT DEC)

xyzt.units Units of pixdim[2:5]. Bits 1..3 of xyzt.units specify the (same) space unit of pixdim[2:4]. Bits 4..6 of xyzt.units specify the time unit of pixdim[5]. See ‘xyzt-units.txt’ in the niftidoc directory of the source package. The R function st2xyzt can be used to encode these values into the xyzt.units byte.

cal.max Maximum display intensity (white) corresponds to dataset value cal.max. Dataset values above cal.max should display as white. cal.min and cal.max only make sense when applied to scalar-valued datasets (i.e., dim[1] < 5 or dim[6] = 1).

cal.min Minimum display intensity (black) corresponds to dataset value cal.min. Dataset values below cal.min should display as black.

slice.duration Time for 1 slice. If this is positive, AND if slice.dim is nonzero, indicates the amount of time used to acquire 1 slice.

toffset Time axis shift: The toffset field can be used to indicate a nonzero start point for the time axis. That is, time point \( m \) is at \( t = \text{toffset} + m \times \text{pixdim[5]} \) for \( m=1, ..., \text{dim[5]}-1 \).

descrip char[80]. This field may contain any text you like

aux.file char[24]. This field is used to store an auxiliary filename.

qform.code NIFTI code (in 0, ..., 4). 0: Arbitrary coordinates; 1: Scanner-based anatomical coordinates; 2: Coordinates aligned to another file’s, or to anatomical "truth" (coregistration); 3: Coordinates aligned to Talairach-Tournoux Atlas; 4: MNI 152 normalized coordinates

sform.code NIFTI code (in 0, ..., 4) with the same meaning as qform codes. The basic idea behind having two coordinate systems is to allow the image to store information about (1) the scanner coordinate system used in the acquisition of the volume
(in the qform) and (2) the relationship to a standard coordinate system - e.g. MNI coordinates (in the sform). The qform allows orientation information to be kept for alignment purposes without losing volumetric information, since the qform only stores a rigid-body transformation (rotation and translation) which preserves volume. On the other hand, the sform stores a general affine transformation (shear, scale, rotation and translation) which can map the image coordinates into a standard coordinate system, like Talairach or MNI, without the need to resample the image. By having both coordinate systems, it is possible to keep the original data (without resampling), along with information on how it was acquired (qform) and how it relates to other images via a standard space (sform). This ability is advantageous for many analysis pipelines, and has previously required storing additional files along with the image files. By using NIFTI-1 this extra information can be kept in the image files themselves. Note: the qform and sform also store information on whether the coordinate system is left-handed or right-handed and so when both are set they must be consistent, otherwise the handedness of the coordinate system (often used to distinguish left-right order) is unknown and the results of applying operations to such an image are unspecified.

**quatern.b**  
Quaternion b param. These b,c,d quaternion parameters encode a rotation matrix used when qform.code > 0 to obtain a rigid transformation that maps voxel indices \((i, j, k)\) to spatial coordinates \((x, y, z)\), typically anatomical coordinates assigned by the scanner. This transformation (Method 2 in the ‘nifti1.h’ documentation) is generated using also the voxel dimensions (pixdim[1:4]) and a 3D shift, i.e. a translation, (qoffset.*)

**quatern.c**  
Quaternion c param

**quatern.d**  
Quaternion d param

**qoffset.x**  
Quaternion x shift. If the (0020,0032) DICOM attribute is extracted into \((px, py, pz)\), then qoffset.x = −px, qoffset.y = −py and qoffset.z = pz is a reasonable setting when qform.code=NIFTI XFORM SCANNER ANAT.

**qoffset.y**  
Quaternion y shift

**qoffset.z**  
Quaternion z shift

**srow.x**  
vector of length 4. 1st row affine transform. These srow.* parameters contain an affine (non-rigid) transformation (Method 3 in the ‘nifti1.h’ documentation) that maps voxel indices \((i, j, k)\) to spatial coordinates \((x, y, z)\).

**srow.y**  
vector of length 4. 2nd row affine transform

**srow.z**  
vector of length 4. 3rd row affine transform

**intent.name**  
char[16]. name or meaning of data. If no data name is implied or needed, intent.name[1] should be set to 0.

**Value**

Returns a list of all the fields needed to create a .hdr file (see the function code for details).

**See Also**

f.basic.hdr.nifti.list.create, f.write.list.to.hdr.nifti, f.nifti.file.summary
Examples

```r
## Not run:
dim.mat <- c(20,30,40,3)
dim <- c(length(dim.mat), dim.mat, rep(0, 7 - length(dim.mat)))
filename <- "temp.hdr"
f.complete.hdr.nifti.list.create(file=filename, dim=dim)
## End(Not run)
```

---

**f.ica.fmri**

Applies Spatial ICA (Independent Component Analysis) to fMRI datasets

**Description**

Decomposes an fMRI dataset into a specified number of Spatially Independent Components maps and associated time-courses using the FastICA algorithm

**Usage**

```r
f.ica.fmri(file.name, n.comp, norm.col=TRUE, fun="logcosh", maxit=1000,
alg.type="parallel", alpha=1, tol=1e-04, mask.file.name=NULL, slices=NULL)
```

**Arguments**

- **file.name** path to fMRI dataset (ANALYZE format .img file)
- **n.comp** number of components to extract
- **norm.col** a logical value indicating whether each voxel time series should be standardised to have zero mean and unit variance before the ICA algorithm is applied (default=TRUE recommended in practice)
- **fun** the functional form of the G function used in the approximation to negentropy (see details)
- **maxit** maximum number of iterations to perform
- **alg.type** if alg.type="deflation" the components are extracted one at a time (the default). if alg.type="parallel" the components are extracted simultaneously.
- **alpha** constant in range [1,2] used in approximation to negentropy when fun="logcosh"
- **tol** a positive scalar giving the tolerance at which the un-mixing matrix is considered to have converged.
- **mask.file.name** Optional path to file containing a 0/1 mask for the dataset
- **slices** Optional vector of slices to be included
Details

The fMRI dataset is rearranged into a 2-dimensional data matrix \( X \), where the column vectors are voxel time-series. A mask is used to specify which voxels are included. If this is not supplied by the user then a mask is constructed automatically using a 10\% intensity threshold.

The data matrix is considered to be a linear combination of non-Gaussian (independent) components i.e. \( X = AS \) where rows of \( S \) contain the independent components and \( A \) is a linear mixing matrix. In short ICA attempts to 'un-mix' the data by estimating an un-mixing matrix \( U \) where \( UX = S \).

Under this generative model the measured 'signals' in \( X \) will tend to be 'more Gaussian' than the source components (in \( S \)) due to the Central Limit Theorem. Thus, in order to extract the independent components/sources we search for an un-mixing matrix \( U \) that maximizes the non-gaussianity of the sources.

In FastICA, non-gaussianity is measured using approximations to negentropy \( (J) \) which are more robust than kurtosis based measures and fast to compute.

The approximation takes the form
\[
J(y) = \left( EG(y) - EG(v) \right)^2 \quad \text{where } v \text{ is a N}(0,1) \text{ r.v}
\]

The following choices of \( G \) are included as options 
\[
G(u) = \frac{1}{\alpha} \log \cosh(\alpha u) \quad \text{and} \quad G(u) = -\exp(-u^2/2)
\]

The FastICA algorithm is used to 'un-mix' the data and recover estimates of the mixing matrix \( A \) and the source matrix \( S \). Rows of the source matrix \( S \) represent spatially independent components of the dataset (these are arranged spatially in the output). Columns of \( A \) contain the associated time-courses of the independent components.

Pre-processing involves removing the mean of each row of the data matrix and (optionally) standardizing the columns of the data matrix to have zero mean and unit variance.

All computations are done using C code. This avoids reading the entire dataset into R and thus saves memory space.

Value

A list containing the following components

\[
A \quad \text{estimated mixing matrix}
\]

\[
S \quad \text{estimated source matrix that has been rearranged spatially i.e. } S \text{ is a 4-D array and } S[\ldots,i] \text{ contains the 3-D map of the } i\text{th component}
\]

\[
\text{file} \quad \text{the name of the data file}
\]

\[
\text{mask} \quad \text{the name of the mask file}
\]

Author(s)

J L Marchini <marchini@stats.ox.ac.uk> and C Heaton <chrisheaton99@yahoo.com>

References


f.ica.fmri.gui

See Also

f.ica.fmri.gui, f.plot.ica.fmri

---

f.ica.fmri.gui  tcltk GUI to apply ICA to fMRI datasets

Description

The GUI provides a quick and easy to use interface for applying spatial ICA to fMRI datasets. Computations are done in C for speed and low memory usage.

Usage

f.ica.fmri.gui()

Details

The user is required to enter the location of the fMRI dataset (stored in the ANALYZE format) and (optionally) a mask for the dataset. If no mask is supplied then an option to create mask is available. There is option to normalize the columns of the data matrix and to exclude the top and bottom slices (which are sometimes affected by the registration procedures).

Once completed, the user has the option of saving the results to an R object or viewing the estimated components. The slices of each component map are plotted sequentially in a grid followed by the components associated time-course and that time-courses periodogram/power spectrum.

Value

User named R object (optional)

Once completed, the user has the option of saving the results to an R object named by the user.

Author(s)

J L Marchini <marchini@stats.ox.ac.uk> and C Heaton <chrisheaton99@yahoo.com>

See Also

f.ica.fmri, f.plot.ica.fmri
Applies Spatial or Temporal ICA (Independent Component Analysis) to fMRI NIFTI datasets

Description
Decomposes an fMRI dataset into a specified number of Spatially or Temporally Independent Components maps and associated time-courses using the FastICA algorithm.

Usage
f.icast.fmri(foncfile, maskfile, is.spatial, n.comp.compute=TRUE, n.comp=0, hp.filter=TRUE)

Arguments
- foncfile: path and filename to fMRI dataset (NIFTI format .img or .nii file)
- maskfile: path and filename to fMRI maskfile (0 and 1 values to determine if you are inside or outside the brain) dataset (NIFTI format .img or .nii file)
- is.spatial: Logical. Should we perform a spatial or temporal ICA.
- n.comp.compute: Logical. Should we estimate the number of components to extract. If FALSE, n.comp value (>0) should be provided.
- n.comp: number of components to extract
- hp.filter: Logical. Should we perform high-pass filtering on the data.

Details
TODO!!! The fMRI dataset is rearranged into a 2-dimensional data matrix X, where the column vectors are voxel time-series. A mask is used to specify which voxels are included. If this is not supplied by the user then a mask is constructed automatically using a 10% intensity threshold.

The data matrix is considered to be a linear combination of non-Gaussian (independent) components i.e. \( X = AS \) where rows of S contain the independent components and A is a linear mixing matrix. In short ICA attempts to ‘un-mix’ the data by estimating an un-mixing matrix U where \( UX = S \).

Under this generative model the measured ‘signals’ in X will tend to be ‘more Gaussian’ than the source components (in S) due to the Central Limit Theorem. Thus, in order to extract the independent components/sources we search for an un-mixing matrix U that maximizes the non-gaussianity of the sources.

In FastICA, non-gaussianity is measured using approximations to negentropy (J) which are more robust than kurtosis based measures and fast to compute.

The approximation takes the form
\[
J(y) = [EG(y) - EG(v)]^2
\]
where \( v \) is a N(0,1) r.v.

The following choices of G are included as options \( G(u) = \frac{1}{\alpha} \log \cosh(\alpha u) \) and \( G(u) = -\exp(-\frac{u^2}{2}) \).

The FastICA algorithm is used to ‘un-mix’ the data and recover estimates of the mixing matrix A and the source matrix S. Rows of the source matrix S represent spatially independent components.
of the dataset (these are arranged spatially in the output). Columns of A contain the associated
time-courses of the independent components.

Pre-processing involves removing the mean of each row of the data matrix and (optionally) stan-
dardizing the columns of the data matrix to have zero mean and unit variance.

All computations are done using C code. This avoids reading the entire dataset into R and thus
saves memory space.

Value

Nothing for the moment ... TODO!! The spatial and temporal components are written on disk

Author(s)

P Lafaye de Micheaux <plafaye@club.fr>

References

Neural Networks, 13(4-5):411-430

of Engineering Science, University of Oxford.

See Also

f.icast.fmri.gui

---

f.icast.fmri.gui  tcltk GUI to apply Spatial or Temporal ICA to fMRI NIFTI datasets

Description

The GUI provides a quick and easy to use interface for applying spatial or temporal ICA to fMRI
NIFTI datasets. Computations WILL BE (NOT YET IMPLEMENTED) done in C for speed and
low memory usage.

Usage

f.icast.fmri.gui()

Details

The user is required to enter the location of the fMRI dataset (stored in the NIFTI format) and
(optionally) a mask for the dataset. If no mask is supplied then an option to create mask is available.
TODO!!

Once completed, the user has the option of saving the results to an R object or viewing the estimated
components. The slices of each component map are plotted sequentially in a grid followed by the
components associated time-course and that time-courses periodogram/power spectrum.TODO!!
f.nifti.file.summary

Value
User named R object (optional)
   Once completed, the user has the option of saving the results to an R object
   named by the user.TODO!!

Author(s)
P Lafaye de Micheaux <plafaye@club.fr>

See Also
   f.icast.fmri,f.ica.fmri.gui

f.nifti.file.summary  prints summary of .img file contents

Description
Prints a summary of the contents of a NIFTI .img file using the associated .hdr header file.

Usage
f.nifti.file.summary(file)

Arguments
  file  The location of .img file to be read

Value
A print out containing information about the .img file. This includes File name, Data Dimension, X
dimension, Y dimension, Z dimension, Time dimension, Voxel dimensions, Data type

See Also
   f.read.nifti.header,f.read.nifti.slice,f.read.nifti.slice.at.all.timepoints,f.read.nifti.ts,
f.write.nifti,f.read.nifti.volume,f.spectral.summary.nifti,f.write.array.to.img.2bytes,
f.write.array.to.img.float,f.write.list.to.hdr.nifti,f.basic.hdr.nifti.list.create

Examples
   f.nifti.file.summary(system.file("example-nifti.img", package="AnalyzeFMRI"))
f.plot.ica.fmri

Plots a specified component from the output of f.ica.fmri

Description

Plots a specified component from the output of f.ica.fmri

Usage

f.plot.ica.fmri(obj.ica, comp, cols)

Arguments

obj.ica: R object returned by the function f.ica.fmri
comp: number of the component to plot
cols: optional vector of colours to use for plotting

Details

The slices of the specified component map are plotted sequentially in a grid followed by the components associated time-course and that time-courses periodogram/power spectrum

Author(s)

J L Marchini <marchini@stats.ox.ac.uk> and C Heaton <chrisheaton99@yahoo.com>

See Also

f.ica.fmri,f.ica.fmri.gui

f.plot.ica.fmri.jpg

Plot the components of the output of f.ica.fmri to a series of jpeg files

Description

This function allows the compact graphical storage of the output of a spatial ICA decomposition of an fMRI dataset. each component is plotted to a jpeg.

Usage

f.plot.ica.fmri.jpg(ica.obj, file="./ica", cols=heat.colors(100), width=700, height=700)
f.plot.volume.gui

Arguments

- ica.obj: Object that is the output of f.ica.fmri
- file: The component i will be plotted in file file.comp.i.jpeg
- cols: Optional colour vector for plotting the components
- width: Width of jpeg images
- height: Height of jpeg images

Author(s)

J L Marchini

See Also

f.ica.fmri, jpeg

Description

tcltk GUI to display FMRI or MRI images. This GUI is very useful, for example, for investigating
the results of an ICA performed with f.ica.fmri(). But it can also be used to display an MRI or
an FMRI image

Usage

f.plot.volume.gui(array.fonc=NULL, hdr.fonc=NULL)

Arguments

- array.fonc: An optional array containing the MRI values
- hdr.fonc: If array.fonc is not NULL, one must provide a list 'hdr.fonc' with a 'pixdim'
  field containing a vector of length 4 with the pixel dimensions

Details

One has the possibility to enter either a filename (with its path) or directly an R object in the file
field.

Value

Nothing

Author(s)

P Lafaye de Micheaux <plafaye@club.fr>
**f.read.analyze.header**

**See Also**

*f.icast.fmri.gui*

**Examples**

```r
# TODO!!
```

---

**Description**

Reads the ANALYZE image format .hdr header file into a list.

**Usage**

```r
f.read.analyze.header(file)
```

**Arguments**

- `file`  
  The .hdr file to be read

**Value**

A list containing the information in the fields of the .hdr file.

- `file.name`  
  name of the .img file
- `swap`  
  TRUE or FALSE variable indicating whether files are big or little endian
- `sizeof.hdr`  
  This field implies that Analyze format was originally intended to be extensible, but in practice this did not happen, and instead the file size (and hence the value of this field) is 348. Software commonly tests the value in this field to detect whether the byte ordering is Big-Endian or Little-Endian.
- `data.type`  
  character vector indicating data storage type for each voxel
- `db.name`  
  database name
- `extents`  
  Should be 16384, the image file is created as contiguous with a minimum extent size
- `session.error`  
  Must be ‘r’ to indicate that all images and volumes are the same size
vox.units 3 characters to specify the spatial units of measure for a voxel (mm., um., cm.)
cal.units 7 characters to specify the name of the calibration unit i.e. pixel, voxel
unused1 ??
datatype integer indicator of data storage type for this image: 0 (None or Unknown), 1 (Binary), 2 (Unsigned-char), 4 (Signed-short), 8 (Signed-int), 16 (float), 32 (Complex), 64 (Double), 128 (RGB), 255 (All)
bitpix number of bits per pixel: 1 (packed binary, slices begin on byte boundaries), 8 (unsigned char, gray scale), 16 (signed short), 32 (signed integers or float), or 24 (RGB, 8 bits per channel)
dim.un0 unused
pixdim Parallel vector to dim, giving real world measurements in mm, and ms. pixdim[1]: ?? pixdim[2]: voxel width in mm. pixdim[3]: voxel height in mm. pixdim[4]: slice thickness (interslice distance) in mm. pixdim[5]: timeslice in ms. pixdim[6]: ?? pixdim[7]: ?? pixdim[8]: ??
vox.offset byte offset in the .img file at which voxels start. This value can be negative to specify that the absolute value is applied for every image voxel in the file
funused1 specify the range of calibration values. SPM extends the Analyze format by using a scaling factor for the image from the header
funused2 SPM2 image intensity zero intercept
funused3 ??
cal.max Max display intensity, calibration value, values of 0.0 for both fields imply that no calibration max and min values are used
cal.min Min display intensity, calibration value
compressed ??
verified ??
glmax The maximum pixel values for the entire database
glmin The minimum pixel values for the entire database
....... DATA HISTORY .........
descrip any text you like
aux.file auxiliary filename
orient planar slice orientation for this dataset: 0 transverse unflipped; 1 coronal unflipped; 2 sagittal unflipped; 3 transverse flipped; 4 coronal flipped; 5 sagittal flipped
f.read.analyze.slice

originator  image central voxel coordinates. SPM uses this Analyze header field in an unorthodox way. originator[1]: SPM99 X near Anterior Commissure, originator[2]: SPM99 Y near Anterior Commissure, originator[3]: SPM99 Z near Anterior Commissure, originator[4]: ??, originator[5]: ??

generated ??
scannum ??
patient.id ??
exp.date ??
exp.time ??
hist.un0 ??
views ??
vols.added ??
start.field ??
field.skip ??
onax ??
omin ??
smax ??
smin ??

See Also

f.analyze.file.summary

Examples

f.read.analyze.header(system.file("example.hdr", package="AnalyzeFMRI"))

f.read.analyze.slice  read one slice from a .img file

Description

Reads in a specific slice from an ANALYZE .img image format file into an array.

Usage

f.read.analyze.slice(file, slice, tpt)

Arguments

file  The .img file to be read from
slice  The number of the slice (assumed to be the 3rd dimension)
tpt  The number of the scan that the slice is to be taken from
Details

The entire dataset is assumed to be 4D and a slice is extracted that is referenced by specifying the last two dimensions of the dataset i.e. slice and tpt.

Value

An array containing the slice

See Also

f.read.analyze.slice.at.all.timepoints, f.read.analyze.ts, f.read.analyze.volume

Examples

```r
a<-f.read.analyze.slice(system.file("example.img", package="AnalyzeFMRI"),10,1)
dim(a)
```

f.read.analyze.slice.at.all.timepoints

*reads a slice at all time points from a .img file*

Description

Reads in a slice of a .img file at all time points into an array

Usage

f.read.analyze.slice.at.all.timepoints(file, slice)

Arguments

- **file** file The location of the .img file
- **slice** slice The number of the slice to be read in

Value

An array containing the slice at all time points

See Also

f.read.analyze.slice, f.read.analyze.ts, f.read.analyze.volume

Examples

```r
a<-f.read.analyze.slice.at.all.timepoints(system.file("example.img", package="AnalyzeFMRI"),10)
dim(a)
```
f.read.analyze.tpt  

Read in a volume at one time point

Description
Given a 4D ANALYZE .img/.hdr image pair this function can read in the 3D volume of measurements at a specific time point.

Usage
f.read.analyze.tpt(file, tpt)

Arguments
- **file**: The .img file.
- **tpt**: The time point to read in.

Details
Given a 4D ANALYZE .img/.hdr image pair this function can read in the 3D volume of measurements at a specific time point.

Value
A 3D array containing the volume.

See Also
f.read.analyze.slice, f.read.analyze.slice.at.all.timepoints, f.write.analyze,

Examples
f.read.analyze.tpt(system.file("example.img", package="AnalyzeFMRI"), 1)

f.read.analyze.ts  

read in one voxel time series

Description
Given a 4D ANALYZE .img/.hdr image pair this function can read in the time series from a specified position in 3D into a vector.

Usage
f.read.analyze.ts(file, x, y, z)
Arguments

- **file**: The .img file
- **x**: The x-coordinate
- **y**: The y-coordinate
- **z**: The z-coordinate

Details

Given a 4D ANALYZE .img/.hdr image pair this function can read in the time series from a specified position in 3D into a vector.

Value

A vector containing the time series

See Also

- `f.read.analyze.slice`
- `f.read.analyze.slice.at.all.timepoints`
- `f.write.analyze`

Examples

```r
f.read.analyze.ts(system.file("example.img", package="AnalyzeFMRI"),30,30,10)
```

---

Description

Reads the ANALYZE image format .img file into an array.

Usage

```r
f.read.analyze.volume(file)
```

Arguments

- **file**: The location of the .img file to be read

Value

An array with the appropriate dimensions containing the image volume. A print out of the file information is also given. The function assumes that the corresponding .hdr file is in the same directory as the .img file.

See Also

- `f.read.analyze.slice`
- `f.read.analyze.slice.at.all.timepoints`
- `f.read.analyze.ts`
Examples

```r
a <- f.read.analyze.volume(system.file("example.img", package="AnalyzeFMRI"))
dim(a)
```

Description

Reads the ANALYZE or NIFTI image format .hdr (or .nii) header file into a list. The format type is determined by first reading the magic field.

Usage

```r
f.read.header(file)
```

Arguments

- `file` The .hdr file to be read

Value

A list containing the information in the fields of the .hdr (.nii) file. See `f.read.analyze.header` of `f.read.nifti.header` to have the list of values.

See Also

`f.read.analyze.header` `f.read.nifti.header`

Examples

```r
f.read.header(system.file("example.hdr", package="AnalyzeFMRI"))
f.read.header(system.file("example-nifti.hdr", package="AnalyzeFMRI"))
```

Description

Reads the NIFTI image format .hdr (or .nii) header file into a list.

Usage

```r
f.read.nifti.header(file)
```
Arguments

file
The .hdr (or .nii) file to be read

Value

A list containing the information in the fields of the .hdr (.nii) file.

file.name
path name of the .img file

swap
1 or 0 variable indicating whether files are big (=native) or little (=swapped) endian

sizeof.hdr
MUST be 348

data.type
char[10]. UNUSED

db.name
char[18]. UNUSED

extents
UNUSED

session.error
UNUSED

regular
UNUSED, but filled with 'r' as SPM does

dim.info
MRI slice ordering: This field encode which spatial dimension (1=x, 2=y, or 3=z) corresponds to which acquisition dimension for MRI data. In fact, it contains three informations: freq.dim, phase.dim and slice.dim, all squished into the single byte field dim.info (2 bits each, since the values for each field are limited to the range 0..3). The R function diminfo2fps can be used to extract these values from the dim.info byte.

dim
vector (of length 8) of image dimensions. dim[1] specifies the number of dimensions. In NIFTI-1 files, dim[2], dim[3], dim[4] are for space, dim[5] is for time. The 5th dimension (dim[6]) of the dataset, if present (i.e., dim[1]=5 and dim[6] > 1), contains multiple values (for example a vector) to be stored at each spatiotemporal location. Uses of dim[7] and dim[8] are not specified in NIFTI-1 format.

intent.p1
1st intent parameter: first auxiliary parameter for a possible statistical distribution specified in intent.code

intent.p2
2nd intent parameter: second auxiliary parameter for a possible statistical distribution specified in intent.code

intent.p3
3rd intent parameter: third auxiliary parameter for a possible statistical distribution specified in intent.code

intent.code
NIFTI INTENT code: if 0, this is a raw dataset; if in range 2..24, this indicates that the numbers in the dataset should be interpreted as being drawn from a given distribution. Most such distributions have auxiliary parameters (given with intent.p?); if in range 1001..1011, this is an other meaning. See file intent-code.txt in the niftidoc directory of the source package. If the dataset DOES NOT have a 5th dimension (dim[1]=4), then the auxiliary parameters are the same for each voxel, and are given in header fields intent.p1, intent.p2, and intent.p3. If the dataset DOES have a 5th dimension (dim[1]=5), then the auxiliary parameters are different for each voxel.
datatype
    integer indicator of data storage type for each voxel. This could be 0 (unknown), 2 (unsigned char = 1 byte), 4 (signed short = 2 bytes), 8 (signed int = 4 bytes), 16 (32 bit float = 4 bytes), 32 (64 bit complex = two 32 bit floats = 8 bytes), 64 (64 bits float = double = 8 bytes), 128 (RGB triple = three 8 bits bytes = 3 bytes), 256 (signed char = 1 byte), 512 (unsigned short = 2 bytes), 768 (unsigned int = 4 bytes), 1024 (signed long long = 8 bytes), 1280 (unsigned long long = 8 bytes), 1536 (128 bit float = long double = 16 bytes), 1792 (128 bit complex = 2 64 bit floats = 16 bytes), 2048 (256 bit complex = 2 128 bit floats = 32 bytes).

bitpix
    the number of bits per voxel. This field MUST correspond with the datatype field. The total number of bytes in the image data is $\text{dim}[2]*...*\text{dim}[	ext{dim}[1]+1] * \text{bitpix}/8$

slice.start
    Indicates the start of the slice acquisition pattern, when slice.code is nonzero. These values are present to allow for the possible addition of "padded" slices at either end of the volume, which don’t fit into the slice timing pattern. If there are no padding slices, then slice.start=0 and slice.end=dim[slice.dim+1]-1 are the correct values. For these values to be meaningful, slice.start must be non-negative and slice.end must be greater than slice.start.

pixdim
    vector (of length 8). Grid spacings. When reading a NIFTI-1 header, pixdim[1] stores qfac (which is either -1 or 1). If pixdim[1]=0 (which should not occur), we take qfac=1. pixdim[2], pixdim[3] and pixdim[4] give the voxel width along dimension x, y and z respectively. pixdim[5] gives the time step (=Time Repetition=TR). The units of pixdim can be specified with the xyzt.units field.

vox.offset
    Offset into .nii file. Should be 352 for a .nii file, 0 for a nifti .hdr/.img pair.

scl.slope
    Data scaling: If the scl.slope field is nonzero, then each voxel value in the dataset should be scaled as $y = \text{scl.slope} \times x + \text{scl.inter}$, where $x = \text{voxel value stored}$ and $y = "true" \text{ voxel value}$

scl.inter
    Data scaling: offset. Idem above.

slice.end
    Indicates the end of the slice acquisition pattern, when slice.code is nonzero. These values are present to allow for the possible addition of "padded" slices at either end of the volume, which don’t fit into the slice timing pattern. If there are no padding slices, then slice.start=0 and slice.end=dim[slice.dim+1]-1 are the correct values. For these values to be meaningful, slice.start must be non-negative and slice.end must be greater than slice.start.

slice.code
    Slice timing order. If this is nonzero, AND if slice.dim is nonzero, AND if slice.duration is positive, indicates the timing pattern of the slice acquisition. The following codes are defined: 0 (unknown), 1 (sequential increasing), 2 (sequential decreasing), 3 (alternating increasing), 4 (alternating decreasing), 5 (alternating increasing #2), 6 (alternating decreasing #2)

xyzt.units
    Units of pixdim[2:5]. Bits 1..3 of xyzt.units specify the (same) space unit of pixdim[2:4]. Bits 4..6 of xyzt.units specify the time unit of pixdim[5]. See xyzt.units.txt in the niftidoc directory of the source package. The R function xyzt2st can be used to extract these values from the xyzt.units byte.

cal.max
    Maximum display intensity (white) corresponds to dataset value cal.max. Dataset values above cal.max should display as white. cal.min and cal.max only make sense when applied to scalar-valued datasets (i.e., dim[1] < 5 or dim[6] = 1).
Minimum display intensity (black) corresponds to dataset value cal.min. Dataset values below cal.min should display as black.

Time for 1 slice. If this is positive, AND if slice.dim is nonzero, indicates the amount of time used to acquire 1 slice.

Time axis shift: The toffset field can be used to indicate a nonzero start point for the time axis. That is, time point m is at t=toffset+m*pixdim[5] for m=1, ..., dim[5]-1.

UNUSED

UNUSED

char[80]. This field may contain any text you like

char[24]. This field is used to store an auxiliary filename.

NIFTI code (in 0, ..., 4). 0: Arbitrary coordinates; 1: Scanner-based anatomical coordinates; 2: Coordinates aligned to another file’s, or to anatomical "truth" (coregistration); 3: Coordinates aligned to Talairach-Tournoux Atlas; 4: MNI 152 normalized coordinates

NIFTI code (in 0, ..., 4) with the same meaning as qform codes. The basic idea behind having two coordinate systems is to allow the image to store information about (1) the scanner coordinate system used in the acquisition of the volume (in the qform) and (2) the relationship to a standard coordinate system - e.g. MNI coordinates (in the sform). The qform allows orientation information to be kept for alignment purposes without losing volumetric information, since the qform only stores a rigid-body transformation (rotation and translation) which preserves volume. On the other hand, the sform stores a general affine transformation (shear, scale, rotation and translation) which can map the image coordinates into a standard coordinate system, like Talairach or MNI, without the need to resample the image. By having both coordinate systems, it is possible to keep the original data (without resampling), along with information on how it was acquired (qform) and how it relates to other images via a standard space (sform). This ability is advantageous for many analysis pipelines, and has previously required storing additional files along with the image files. By using NIFTI-1 this extra information can be kept in the image files themselves. Note: the qform and sform also store information on whether the coordinate system is left-handed or right-handed and so when both are set they must be consistent, otherwise the handedness of the coordinate system (often used to distinguish left-right order) is unknown and the results of applying operations to such an image are unspecified.

These b,c,d quaternion parameters encode a rotation matrix used when qform.code > 0 to obtain a rigid transformation that maps voxel indices (i,j,k) to spatial coordinates (x,y,z), typically anatomical coordinates assigned by the scanner. This transformation ("Method 2" in the nifti1.h documentation) is generated using also the voxel dimensions (pixdim[1:4]) and a 3D shift, i.e. a translation, (qoffset.*)
**qoffset.x**  Quaternion x shift. If the (0020,0032) DICOM attribute is extracted into \((px,py,pz)\), then \(qoffset.x = -px\) \(qoffset.y = -py\) \(qoffset.z = pz\) is a reasonable setting when \(qform.code=\text{NIFTI XFORM SCANNER ANAT.}\)

**qoffset.y**  Quaternion y shift

**qoffset.z**  Quaternion z shift

**srow.x**  vector of length 4. 1st row affine transform. These srow.* parameters contain an affine (non-rigid) transformation ("Method 3" in the nifti1.h documentation) that maps voxel indices \((i,j,k)\) to spatial coordinates \((x,y,z)\).

**srow.y**  vector of length 4. 2nd row affine transform

**srow.z**  vector of length 4. 3rd row affine transform

**intent.name**  char[16]. ‘name’ or meaning of data. If no data name is implied or needed, intent.name[1] should be set to 0.

**magic**  MUST be "nix" or "n+x", where x in 0...9

**extension**  By default, all 4 bytes of this array should be set to zero. In a .nii file, these 4 bytes will always be present, since the earliest start point for the image data is byte #352. In a separate .hdr file, these bytes may or may not be present. If not present (i.e., if the length of the .hdr file is 348 bytes), then a NIFTI-1 compliant program should use the default value of extension=0,0,0,0. The first byte (extension[0]) is the only value of this array that is specified at present. The other 3 bytes are reserved for future use.

If extension[0] is nonzero, it indicates that extended header information is present in the bytes following the extension array. In a .nii file, this extended header data is before the image data (and vox_offset must be set correctly to allow for this). In a .hdr file, this extended data follows extension and proceeds (potentially) to the end of the file.

**Examples**

```r
f.read.nifti.header(system.file("example-nifti.hdr", package="AnalyzeFMRI"))
```

**f.read.nifti.slice**  
*read one slice from a .img or .nii file in NIFTI format*

**Description**

Reads in a specific slice from a NIFTI .img or .nii image format file into an array.

**Usage**

```r
f.read.nifti.slice(file, slice, tpt)
```

**Arguments**

- **file**  The .img file to be read from
- **slice**  The number of the slice (assumed to be the 3rd dimension)
- **tpt**  The number of the scan that the slice is to be taken from
f.read.nifti.slice.at.all.timepoints

Details
The entire dataset is assumed to be 4D and a slice is extracted that is referenced by specifying the last two dimensions of the dataset i.e. slice and tpt.

Value
An array containing the slice

See Also
f.read.nifti.slice.at.all.timepoints, f.read.nifti.ts, f.read.nifti.volume

Examples
a<-f.read.nifti.slice.at.all.timepoints(system.file("example-nifti.img", package="AnalyzeFMRI"),10,1)
dim(a)

f.read.nifti.slice.at.all.timepoints
reads a slice at all time points from a NIFTI .img or .nii file

Description
Reads in a slice of a .img or .nii file at all time points into an array

Usage
f.read.nifti.slice.at.all.timepoints(file, slice)

Arguments
file file The location of the .img file
slice slice The number of the slice to be read in

Value
An array containing the slice at all time points

See Also
f.read.nifti.slice, f.read.nifti.ts, f.read.nifti.volume

Examples
a<-f.read.nifti.slice.at.all.timepoints(system.file("example-nifti.img", package="AnalyzeFMRI"),10)
dim(a)
f.read.nifti.tpt  Read in a volume at one time point

Description

Given a 4D NIFTI .img/.hdr image pair or a .nii file this function can read in the 3D volume of measurements at a specific time point.

Usage

f.read.nifti.tpt(file, tpt)

Arguments

file  The .img file.
tpt   The time point to read in.

Details

Given a 4D NIFTI .img/.hdr image pair or a .nii file this function can read in the 3D volume of measurements at a specific time point.

Value

A 3D array containing the volume.

See Also

f.read.nifti.slice, f.read.nifti.slice.at.all.timepoints, f.write.nifti,

Examples

f.read.nifti.tpt(system.file("example-nifti.img", package="AnalyzeFMRI"),1)

f.read.nifti.ts  read in one voxel time series

Description

Given a 4D NIFTI .img/.hdr image pair or a .nii file this function can read in the time series from a specified position in 3D into a vector.

Usage

f.read.nifti.ts(file, x, y, z)
**f.read.nifti.volume**

**Arguments**

- **file**  The .img file
- **x**  The x-coordinate
- **y**  The y-coordinate
- **z**  The z-coordinate

**Details**

Given a 4D NIFTI .img/.hdr image pair or a .nii file this function can read in the time series from a specified position in 3D into a vector.

**Value**

A vector containing the time series

**See Also**

- `f.read.nifti.slice`, `f.read.nifti.slice.at.all.timepoints`, `f.write.nifti`

**Examples**

```r
f.read.nifti.ts(system.file("example-nifti.img", package="AnalyzeFMRI"),30,30,10)
```

---

**Description**

Reads the NIFTI image file into an array.

**Usage**

```r
f.read.nifti.volume(file)
```

**Arguments**

- **file**  The location of the image file to be read

**Value**

An array with the appropriate dimensions containing the image volume. A print out of the file information is also given. The function assumes that the corresponding .hdr file is in the same directory as the .img file (but if a .nii file is provided).

**See Also**

- `f.read.nifti.slice`, `f.read.nifti.slice.at.all.timepoints`, `f.read.nifti.ts`
Examples

```r
a <- f.read.nifti.volume(system.file("example-nifti.img", package="AnalyzeFMRI"))
dim(a)
```

---

**f.read.volume**  
**read whole image file**

**Description**

Reads the ANALYZE or NIFTI image format image file into an array. Autodetects format type.

**Usage**

```r
f.read.volume(file)
```

**Arguments**

- `file`  
The location of the image file to be read

**Value**

An array with the appropriate dimensions containing the image volume. A print out of the file information is also given. The function assumes that the corresponding .hdr file is in the same directory as the .img file. (but if it is a .nii file)

**See Also**

- `f.read.nifti.slice`, `f.read.nifti.slice.at.all.timepoints`, `f.read.nifti.ts`

**Examples**

```r
a <- f.read.volume(system.file("example-nifti.img", package="AnalyzeFMRI"))
dim(a)
```

---

**f.spectral.summary**  
**plots graphical summary of spectral properties of an fMRI dataset**

**Description**

For an analyze .img file the periodogram of the time series are divided by a flat spectral estimate using the median periodogram ordinate. The resulting values are then combined within each Fourier frequency and quantiles are plotted against frequency. This provides a fast look at a fMRI dataset to identify any artifacts that reside at single frequencies.

**Usage**

```r
f.spectral.summary(file, mask.file, ret.flag=FALSE)
```
Arguments

file file The location of .img file
mask.file mask.file Optional location of a .img file containing a mask. If not given then one is created.
ret.flag ret.flag flag specifying whether to return the array of quantiles at each frequency

Value

If ret.flag = TRUE the an array of quantiles at each frequency is returned

See Also

f.analyze.file.summary

Description

For a NIFTI .img file the periodogram of the time series are divided by a flat spectral estimate using the median periodogram ordinate. The resulting values are then combined within each Fourier frequency and quantiles are plotted against frequency. This provides a fast look at a fMRI dataset to identify any artifacts that reside at single frequencies.

Usage

f.spectral.summary.nifti(file, mask.file, ret.flag=FALSE)

Arguments

file file The location of .img file
mask.file mask.file Optional location of a .img file containing a mask. If not given then one is created.
ret.flag ret.flag flag specifying whether to return the array of quantiles at each frequency

Value

If ret.flag = TRUE the an array of quantiles at each frequency is returned

See Also

f.nifti.file.summary
f.write.analyze writes an array to a .img/.hdr pair in ANALYZE format

Description

Creates a .img and .hdr pair of files from a given array

Usage

f.write.analyze(mat, file, size, pixdim, vox.units, cal.units, originator)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>mat</td>
<td>An array</td>
</tr>
<tr>
<td>file</td>
<td>The name of the file to be written, without .img or .hdr suffix</td>
</tr>
<tr>
<td>size</td>
<td>Specify the format of the .img file. Either &quot;float&quot; (for 4 byte floats) or &quot;int&quot; (2 byte integers) or &quot;char&quot; (1 byte integers).</td>
</tr>
<tr>
<td>pixdim</td>
<td>A vector of length 3 specifying the voxel dimensions in mm</td>
</tr>
<tr>
<td>vox.units</td>
<td>String specifying the spatial units of measure for a voxel</td>
</tr>
<tr>
<td>cal.units</td>
<td>String specifying the name of calibration unit</td>
</tr>
<tr>
<td>originator</td>
<td>vector of length 5, only the three first values are used. Put the last two equal to zero</td>
</tr>
</tbody>
</table>

Value

Nothing is returned

See Also

f.write.array.to.img.8bit, f.write.array.to.img.2bytes, f.write.array.to.img.float

Examples

```r
## Not run:
a<-array(rnorm(20*30*40*3),dim=c(20,30,40,3))
file<="temp"
f.write.analyze(a, file, size="float")
f.analyze.file.summary("temp.img")
## End(Not run)
```
f.write.array.to.img.2bytes

Write array of 2 byte integers

Description
Writes an array to a .img file of 2 byte integers

Usage
f.write.array.to.img.2bytes(mat,file)

Arguments
mat  An array
file  The name of the file to be written, preferably with .img suffix

Value
Nothing is returned

See Also
f.write.analyze  f.write.array.to.img.float

f.write.array.to.img.8bit

Write array of 1 byte integers

Description
Writes an array to a .img file of 1 byte integers

Usage
f.write.array.to.img.8bit(mat,file)

Arguments
mat  An array
file  The name of the file to be written, preferably with .img suffix

Value
Nothing is returned
f.write.array.to.img.float

write array of 4 byte floats

Description

Writes an array to a .img file of 4 byte floats

Usage

f.write.array.to.img.float(mat, file)

Arguments

mat  An array
file  The name of the file to be written, preferably with .img suffix

Value

Nothing is returned

See Also

f.write.analyze, f.write.array.to.img.float, f.write.array.to.img.2bytes

f.write.list.to.hdr

writes a .hdr file in ANALYZE format

Description

Writes a list of attributes to a .hdr file

Usage

f.write.list.to.hdr(L, file)

Arguments

L  A list of all the fields included in a .hdr file
file  The name of the file to write, preferably with .hdr suffix
Value

Nothing is returned

See Also

f.basic.hdr.list.create

Examples

## Not run:
a<-array(rnorm(20*30*40*3),dim=c(20,30,40,3))
file<="temp.hdr"
b<-f.basic.hdr.list.create(a, file)
f.write.list.to.hdr(b,file)
## End(Not run)

f.write.list.to.hdr.nifti

writes a .hdr file in NITI format

Description

Writes a list of attributes to a .hdr file

Usage

f.write.list.to.hdr.nifti(L,file)

Arguments

L A list of the all the fields included in a .hdr file
file The name of the file to write, preferably with .hdr suffix

Value

Nothing is returned

See Also

f.basic.hdr.nifti.list.create

Examples

## Not run:
a<-array(rnorm(20*30*40*3),dim=c(20,30,40,3))
file<="temp.hdr"
b<-f.basic.hdr.nifti.list.create(dim(a), file)
f.write.list.to.hdr.nifti(b,file)
## End(Not run)
f.write.nifti

writes an array to a .img/.hdr pair in NIFTI format or to a .nii file

Description

Creates a .img/.hdr pair of files or a .nii file from a given array

Usage

f.write.nifti(mat,file,size,L,nii)

Arguments

mat  An array
file  The name of the file to be written, without .img or .hdr suffix
size Specify the format of the .img file. Either "float" (for 4 byte floats) or "int" (2 byte integers) or "char" (1 byte integers).
L    if NULL, the list is created by the function, else it should be provided. This list contains the header part of a NIFTI image.
nii  should we write only one .nii file or a .hdr/.img pair of files

Value

Nothing is returned

See Also

f.write.array.to.img.8bit, f.write.array.to.img.2bytes, f.write.array.to.img.float
f.write.nii.array.to.img.8bit, f.write.nii.array.to.img.2bytes, f.write.nii.array.to.img.float

Examples

## Not run:
```r
a<-array(rnorm(20*30*40*3),dim=c(20,30,40,3))
file<-'temp'
f.write.nifti(a,file,size="float",nii=TRUE)
```

## End(Not run)
f.write.nii.array.to.img.2bytes

write array of 2 byte integers and add at the begining of the file the NIFTI header part

Description

Writes an array to a .img file of 2 byte integers and add at the begining of the file the NIFTI header part

Usage

f.write.nii.array.to.img.2bytes(mat,L,file)

Arguments

mat  An array
L    A list containing the header information
file The name of the file to be written, preferably with .img suffix

Value

Nothing is returned

See Also

f.writeFile f.write.nii.array.to.img.float

f.write.nii.array.to.img.8bit

write array of 1 byte integers and add at the begining of the file the NIFTI header part

Description

Writes an array to a .img file of 1 byte integers and add at the begining of the file the NIFTI header part

Usage

f.write.nii.array.to.img.8bit(mat,L,file)
f.write.nii.array.to.img.float

Arguments

mat   An array
L     A list containing the header information
file  The name of the file to be written, preferably with .img suffix

Value

Nothing is returned

See Also

f.write.nii,f.write.nii.array.to.img.float,f.write.nii.array.to.img.2bytes

f.write.nii.array.to.img.float

write array of 4 byte floats and add at the begining of the file the NIFTI header part

Description

Writes an array to a .img file of 4 byte floats and add at the begining of the file the NIFTI header part

Usage

f.write.nii.array.to.img.float(mat,L,file)

Arguments

mat   An array
L     A list containing the header information
file  The name of the file to be written, preferably with .img suffix

Value

Nothing is returned

See Also

f.write.nii,f.write.nii.array.to.img.2bytes,f.write.nii.array.to.img.8bit
fourDto2D

Description
This function transforms a 4D image array into a 2D image matrix by unrolling space. This is useful to perform a subsequent ICA.

Usage
fourDto2D(volume.4d, tm)

Arguments
- volume.4d: a 4D array to be transformed
- tm: number of time dimensions

Value
x.2d: matrix of size tm x vm which contains the tm images

See Also
threeDto4D twoDto4D

Examples
# TODO!!

fps2diminfo

Description
Encode freq.dim, phase.dim and slice.dim fields into the one byte dim.info field of a NIFTI header file.

Usage
fps2diminfo(freq.dim,phase.dim,slice.dim)

Arguments
- freq.dim: freq.dim field of a NIFTI file
- phase.dim: phase.dim field of a NIFTI file
- slice.dim: slice.dim field of a NIFTI file
Value

A list containing dim.info field. See Value Section of the help file of function diminfo2fps().

See Also

diminfo2fps

Examples

dim.info <- f.read.header(system.file("example-nifti.hdr", package="AnalyzeFMRI"))$dim.info
mylist <- diminfo2fps(dim.info)
fps2diminfo(mylist$freq.dim,mylist$phase.dim,mylist$slice.dim)

GaussSmoothArray

Spatially smooth an array with Gaussian kernel.

Description

Applies a stationary Gaussian spatial smoothing kernel to a 3D or 4D array.

Usage

GaussSmoothArray(x, voxdim=c(1, 1, 1), ksize=5, sigma=diag(3, 3),
              mask=NULL, var.norm=FALSE)

Arguments

x              The array to be smoothed.
voxdim         The dimensions of the volume elements (voxel) that make up the array.
ksize          The dimensions (in number of voxels) of the 3D discrete smoothing kernel used to smooth the array.
sigma          The covariance matrix of the 3D Gaussian smoothing kernel. This matrix doesn’t have to be non-singular; zero on the diagonal of sigma indicate no smoothing in that direction.
mask           A 3D 0-1 mask that delimits where the smoothing occurs.
var.norm       Logical flag indicating whether to normalize the variance of the smoothed array.

Value

The smoothed array is returned.

Author(s)

J. L. Mrchini
GaussSmoothKernel

Calculates a discrete Gaussian smoothing kernel.

Description

Calculates a simple, discrete Gaussian smoothing kernel of a specific size given the covariance matrix of the Gaussian.

Usage

GaussSmoothKernel(voxdim=c(1, 1, 1), ksize=5, sigma=diag(3, 3))

Arguments

- `voxdim`: Dimensions of each voxel.
- `ksize`: Dimensions of the discrete kernel size.
- `sigma`: The covariance matrix of the Gaussian kernel.

Value

An array of dimension (ksize,ksize,ksize) containing the smoothing kernel.

Author(s)

J. L. Marchini

Examples

```r
a <- GaussSmoothKernel(voxdim=c(1,1,1), ksize=5, sigma=diag(1,3))
```
Description

This function performs a spatial ICA

Usage

ICAspat(X,n.comp,alg.typ="parallel",centering=TRUE,hp.filter=TRUE)

Arguments

- **X**: a matrix of size tm x vm which contains the functionnal images
- **n.comp**: number of maximally independent components to extract
- **alg.typ**: if 'alg.typ == "parallel"' the components are extracted simultaneously (the default). if 'alg.typ == "deflation"' the components are extracted one at a time.
- **centering**: Logical. Should we center the data first. Centering will be performed by firstly removing the column mean.
- **hp.filter**: Logical. Should we perform high-pass filtering on the data

Value

A list containing

- **time.series**: estimated mixing matrix of size tm x n.comp
- **spatial.components**: estimated source matrix of size n.comp x vm

See Also

ICAtemp

Examples

# TODO!!
ICAtemp

Description

This function performs a temporal ICA

Usage

ICAtemp(X,n.comp,alg.typ="parallel",centering=TRUE,hp.filter=TRUE)

Arguments

X           a matrix of size vm x tm which contains the functionnal images
n.comp  number of maximally independent components to extract
alg.typ  if 'alg.typ == "parallel"' the components are extracted simultaneously (the de-
            fault). if 'alg.typ == "deflation"' the components are extracted one at a time.
centering Logical. Should we center the data first. Centering will be performed by firstly
            removing the column mean.
hp.filter Logical. Should we perform high-pass filtering on the data

Value

A list containing

time.series estimated source matrix of size n.comp x tm
spatial.components estimated mixing matrix of size vm x n.comp

See Also

ICAtemp

Examples

# TODO!!
Description

This function maps from data coordinates (e.g. column i, row j, slice k), into some real world (x,y,z) positions in space. These positions could relate to Talairach-Tournoux (T&T) space, MNI space, or patient-based scanner coordinates.

Usage

ijk2xyz(ijk=c(1,1,1),method=2,L)

Arguments

ijk matrix. Each column of ijk should contain a voxel index coordinates (i,j,k) to be mapped to its (x,y,z) real coordinates in some other space

method 1 (qform.code=sform.code=0), 2 (qform.code>0, rigid transformation) or 3 (sform.code>0, affine transformation).

L header list of a NIFTI file

Details

The NIfTI format allows storage on disk to be in either a left- or right-handed coordinate system. However, the format includes an implicit spatial transformation into a RIGHT-HANDED coordinate system. This transform maps from data coordinates (e.g. column i, row j, slice k), into some real world (x, y, z) positions in space. These positions could relate to Talairach-Tournoux (T&T) space, MNI space, or patient-based scanner coordinates. For T&T, and MNI coordinates, x increases from left to right, y increases from posterior to anterior, and z increases in the inferior to superior direction. Directions in the scanner coordinate system are similar. MRI data is usually exported as DICOM format, which encodes the positions and orientations of the slices. When data are converted from DICOM to NIfTI-1 format, the relevant information can be determined from the Pixel Spacing, Image Orientation (Patient) and Image Position (Patient) fields of the DICOM files. NIfTI-1 also allows the space of one image to be mapped to that of another (via a rigid or affine transform). This is to enable on-the-fly resampling of registered images. This would allow intra-subject images, collected with lots of different orientations or resolutions, to be treated as if they are all in register.

Neurological and radiological conventions only relate to visualization of axial images. They are unrelated to how the data are stored on disk, or even how the real-world coordinates are represented. It is more appropriate to consider whether the real-world coordinate system is left- or right-handed (see below). Talairach and Tournoux use a right-handed system, whereas the storage convention of ANALYZE files is usually considered as left-handed. These coordinate systems are mirror images of each other (if you are a psychologist, try explaining why mirror images appear to be left-right flipped, rather than flipped up-down, or back-front). Transforming between left- and right-handed coordinate systems involves flipping, and can not be done by rotations alone.

x=thumb, y=index finger (forefinger), z=left (resp. right) hand’s middle finger for left-handed persons (resp. right-handed persons).
Volume orientation is given by a transformation that maps voxel indices \((i,j,k)\) to spatial coordinates \((x,y,z)\), typically anatomical coordinates assigned by the scanner. This transformation (Method 2 in the ‘nifti1.h’ documentation) is generated using the voxel dimensions, a quaternion encoding a rotation matrix, and a 3D shift, all stored in the NIfTI-1 header; details can be found in the ‘nifti1.h’ comments. The NIfTI-1 header also provides for a general affine transformation, separate from that described by Method 2. This transformation (Method 3) also maps voxel indices \((i,j,k)\) to \((x,y,z)\), which in this case are typically coordinates in a standard space such as the Talairach space. The elements of this transformation matrix are stored in the NIfTI-1 header. For example, the Method 2 transformation can be constructed from the attributes from a set of DICOM files; the Method 3 transform can be computed offline and inserted into the header later. The exact “meaning” of the coordinates given by the Method 2 and Method 3 transformations is recorded in header fields qform.code and sform.code, respectively. Code values can indicate if the \((x,y,z)\) axes are

- Anatomical coordinates from the scanner (e.g., the DICOM header)
- Aligned to some anatomical "truth" or standard
- Aligned and warped to Talairach-Tournoux coordinates
- Aligned and warped to MNI-152 coordinates

It is possible that neither transformation is specified (i.e., qform.code=sform.code=0), in which case we are left with the voxel size in pixdim[], and no orientation is given or assumed. This use (Method 1) is discouraged.

The basic idea behind having two coordinate systems is to allow the image to store information about (1) the scanner coordinate system used in the acquisition of the volume (in the qform) and (2) the relationship to a standard coordinate system - e.g. MNI coordinates (in the sform). The qform allows orientation information to be kept for alignment purposes without losing volumetric information, since the qform only stores a rigid-body transformation which preserves volume. On the other hand, the sform stores a general affine transformation which can map the image coordinates into a standard coordinate system, like Talairach or MNI, without the need to resample the image. By having both coordinate systems, it is possible to keep the original data (without resampling), along with information on how it was acquired (qform) and how it relates to other images via a standard space (sform). This ability is advantageous for many analysis pipelines, and has previously required storing additional files along with the image files. By using NIfTI-1 this extra information can be kept in the image files themselves.

Note: the qform and sform also store information on whether the coordinate system is left-handed or right-handed (see Q15) and so when both are set they must be consistent, otherwise the handedness of the coordinate system (often used to distinguish left-right order) is unknown and the results of applying operations to such an image are unspecified.

There are 3 different methods by which continuous coordinates can be attached to voxels. The discussion below emphasizes 3D volumes, and the continuous coordinates are referred to as \((x,y,z)\). The voxel index coordinates (i.e., the array indexes) are referred to as \((i,j,k)\), with valid ranges:

- \(i = 0,\ldots,\text{dim}[1]-1\)
- \(j = 0,\ldots,\text{dim}[2]-1\) (if \(\text{dim}[0] \geq 2\))
\[ k = 0, \ldots, \text{dim}[3]-1 \text{ (if dim}[0] \geq 3) \]

The \((x, y, z)\) coordinates refer to the CENTER of a voxel. In methods 2 and 3, the \((x, y, z)\) axes refer to a subject-based coordinate system, with 
\[ +x = \text{Right} \quad +y = \text{Anterior} \quad +z = \text{Superior}. \]

This is a right-handed coordinate system. However, the exact direction these axes point with respect to the subject depends on \text{qform.code} (Method 2) and \text{sform.code} (Method 3).

N.B.: The \(i\) index varies most rapidly, \(j\) index next, \(k\) index slowest. Thus, voxel \((i, j, k)\) is stored starting at location 
\[ (i + j \times \text{dim}[1] + k \times \text{dim}[1] \times \text{dim}[2]) \times (\text{bitpix}/8) \]
into the dataset array.

N.B.: The \(i\) index varies most rapidly, \(j\) index next, \(k\) index slowest. Thus, voxel \((i, j, k)\) is stored starting at location 
\[ (i + j \times \text{dim}[1] + k \times \text{dim}[1] \times \text{dim}[2]) \times (\text{bitpix}/8) \]
into the dataset array.

N.B.: The ANALYZE 7.5 coordinate system is 
\[ +x = \text{Left} \quad +y = \text{Anterior} \quad +z = \text{Superior} \]

which is a left-handed coordinate system. This backwardness is too difficult to tolerate, so this NIFTI-1 standard specifies the coordinate order which is most common in functional neuroimaging.

N.B.: The 3 methods below all give the locations of the voxel centers in the \((x, y, z)\) coordinate system. In many cases, programs will wish to display image data on some other grid. In such a case, the program will need to convert its desired \((x, y, z)\) values into \((i, j, k)\) values in order to extract (or interpolate) the image data. This operation would be done with the inverse transformation to those described below.

N.B.: \text{Method 2} uses a factor \text{qfac} which is either -1 or 1; \text{qfac} is stored in the otherwise unused \text{pixdim}[0]. If \text{pixdim}[0]=0.0 (which should not occur), we take \text{qfac}=1. Of course, \text{pixdim}[0] is only used when reading a NIFTI-1 header, not when reading an ANALYZE 7.5 header.

N.B.: The units of \((x, y, z)\) can be specified using the \text{xyzt.units} field.

METHOD 1 (the "old" way, used only when \text{qform.code} = 0):

The coordinate mapping from \((i, j, k)\) to \((x, y, z)\) is the ANALYZE 7.5 way. This is a simple scaling relationship:
\[ x = \text{pixdim}[1] \times i \]
\[ y = \text{pixdim}[2] \times j \]
\[ z = \text{pixdim}[3] \times k \]

No particular spatial orientation is attached to these \((x, y, z)\) coordinates. (NIFTI-1 does not have the ANALYZE 7.5 orient field, which is not general and is often not set properly.) This method is not recommended, and is present mainly for compatibility with ANALYZE 7.5 files.

METHOD 2 (used when \text{qform.code} > 0, which should be the "normal" case):

The \((x, y, z)\) coordinates are given by the \text{pixdim[]} scales, a rotation matrix, and a shift. This method is intended to represent "scanner-anatomical" coordinates, which are often embedded in the image header (e.g., DICOM fields (0020,0032), (0020,0037), (0028,0030), and (0018,0050)), and represent the nominal orientation and location of the data. This method can also be used to represent "aligned" coordinates, which would typically result from some post-acquisition alignment of the volume to a standard orientation (e.g., the same subject on another day, or a rigid rotation to true anatomical orientation from the tilted position of the subject in the scanner). The formula for \((x, y, z)\) in terms of header parameters and \((i, j, k)\) is:
\[
\begin{bmatrix}
    x & [R_{11} R_{12} R_{13}] & \text{pixdim}[1] * i & [\text{qoffset}.x] \\
    y & [R_{21} R_{22} R_{23}] & \text{pixdim}[2] * j & [\text{qoffset}.y] \\
    z & [R_{31} R_{32} R_{33}] & \text{qfac} \times \text{pixdim}[3] * k & [\text{qoffset}.z]
\end{bmatrix}
\]

The \text{qoffset}.* shifts are in the NIFTI-1 header. Note that the center of the \((i, j, k) = (0, 0, 0)\) voxel (first value in the dataset array) is just \((x, y, z) = (\text{qoffset}.x, \text{qoffset}.y, \text{qoffset}.z)\).

The rotation matrix \(R\) is calculated from the quaternion.* parameters. This calculation is described below.

The scaling factor \(\text{qfac}\) is either 1 or -1. The rotation matrix \(R\) defined by the quaternion parameters is "proper" (has determinant 1). This may not fit the needs of the data; for example, if the image grid is
- \(i\) increases from Left-to-Right
- \(j\) increases from Anterior-to-Posterior
- \(k\) increases from Inferior-to-Superior

Then \((i, j, k)\) is a left-handed triple. In this example, if \(\text{qfac}=1\), the \(R\) matrix would have to be
\[
\begin{bmatrix}
    1 & 0 & 0 \\
    0 & -1 & 0 \\
    0 & 0 & 1
\end{bmatrix}
\]
which is "improper" (determinant = -1).

If we set \(\text{qfac}=-1\), then the \(R\) matrix would be
\[
\begin{bmatrix}
    1 & 0 & 0 \\
    0 & -1 & 0 \\
    0 & 0 & -1
\end{bmatrix}
\]
This \(R\) matrix is represented by quaternion \([a, b, c, d] = [0, 1, 0, 0]\) (which encodes a 180 degree rotation about the \(x\)-axis).

- **METHOD 3** (used when \(\text{sform}.\text{code} > 0\)):

The \((x, y, z)\) coordinates are given by a general affine transformation of the \((i, j, k)\) indexes:

\[
\begin{align*}
    z &= \text{srow}.z[0] * i + \text{srow}.z[1] * j + \text{srow}.z[2] * k + \text{srow}.z[3]
\end{align*}
\]

The \text{srow}.* vectors are in the NIFTI-1 header. Note that no use is made of \text{pixdim}[\_] in this method.

- **WHY 3 METHODS?**

Method 1 is provided only for backwards compatibility. The intention is that Method 2 (\(\text{qform}.*\text{code} > 0\)) represents the nominal voxel locations as reported by the scanner, or as rotated to some fiducial orientation and location. Method 3, if present (\(\text{sform}.*\text{code} > 0\)), is to be used to give the location of the voxels in some standard space. The \(\text{sform}.*\text{code}\) indicates which standard space is present. Both methods 2 and 3 can be present, and be useful in different contexts (method 2 for displaying the data on its original grid; method 3 for displaying it on a standard grid).

In this scheme, a dataset would originally be set up so that the Method 2 coordinates represent what the scanner reported. Later, a registration to some standard space can be computed and inserted in the header. Image display software can use either transform, depending on its purposes and needs.
In Method 2, the origin of coordinates would generally be whatever the scanner origin is; for example, in MRI, (0,0,0) is the center of the gradient coil.
In Method 3, the origin of coordinates would depend on the value of sform_code; for example, for the Talairach coordinate system, (0,0,0) corresponds to the Anterior Commissure.

• QUATERNION REPRESENTATION OF ROTATION MATRIX (METHOD 2)

The orientation of the \((x, y, z)\) axes relative to the \((i, j, k)\) axes in 3D space is specified using a unit quaternion \([a, b, c, d]\), where \(a^2 + b^2 + c^2 + d^2 = 1\). The \((b, c, d)\) values are all that is needed, since we require that \(a = \sqrt{1 - (b^2 + c^2 + d^2)}\) be nonnegative. The \((b, c, d)\) values are stored in the \((\text{quatern.b}, \text{quatern.c}, \text{quatern.d})\) fields. The quaternion representation is chosen for its compactness in representing rotations. The (proper) 3x3 rotation matrix that corresponds to \([a, b, c, d]\) is

\[
R = \begin{bmatrix}
  a^2 + b^2 - c^2 - d^2 & 2bc - 2ad & 2bd + 2ac \\
  2bc + 2ad & a^2 + c^2 - b^2 - d^2 & 2cd - 2ab \\
  2bd - 2ac & 2cd + 2ab & a^2 + d^2 - c^2 - b^2
\end{bmatrix}
\]

If \((p, q, r)\) is a unit 3-vector, then rotation of angle \(h\) about that direction is represented by the quaternion

\[
[a, b, c, d] = [\cos(h/2), p \cdot \sin(h/2), q \cdot \sin(h/2), r \cdot \sin(h/2)].
\]

Requiring \(a > 0\) is equivalent to requiring \(-\pi < h < \pi\). (Note that \([-a, -b, -c, -d]\) represents the same rotation as \([a, b, c, d]\); there are 2 quaternions that can be used to represent a given rotation matrix \(R\).) To rotate a 3-vector \((x, y, z)\) using quaternions, we compute the quaternion product

\[
[0, x', y', z'] = [a, b, c, d] \cdot [0, x, y, z] \cdot [a, -b, -c, -d]
\]

which is equivalent to the matrix-vector multiply

\[
\begin{bmatrix}
  x' \\
  y' \\
  z'
\end{bmatrix} = R \begin{bmatrix}
  x \\
  y \\
  z
\end{bmatrix} \text{(equivalence depends on } a^*a + b^*b + c^*c + d^*d = \text{1)}
\]

Multiplication of 2 quaternions is defined by the following:

\[
[a, b, c, d] = a \cdot 1 + b \cdot I + c \cdot J + d \cdot K
\]

where

\[
I \cdot I = J \cdot J = K \cdot K = -1 \text{ (I, J, K are square roots of -1)}
\]

\[
I \cdot J = K, J \cdot K = I, K \cdot I = J
\]

\[
J \cdot I = -K, K \cdot J = -I, I \cdot K = -J \text{ (not commutative!)}
\]

For example

\[
[a, b, 0, 0] \cdot [0, 0, 0, 1] = [0, 0, -b, a]
\]

since this expands to
\[(a + b \cdot I) \cdot (K) = (a \cdot K + b \cdot I \cdot K) = (a \cdot K - b \cdot J)\].

The above formula shows how to go from quaternion \((b, c, d)\) to rotation matrix and direction cosines. Conversely, given \(R\), we can compute the fields for the NIFTI-1 header by

\[
a = 0.5 \cdot \sqrt{1 + R_{11} + R_{22} + R_{33}} \quad \text{(not stored)}
\]
\[
b = 0.25 \cdot (R_{32} - R_{23}) / a \Rightarrow \text{quatern} \cdot b
\]
\[
c = 0.25 \cdot (R_{13} - R_{31}) / a \Rightarrow \text{quatern} \cdot c
\]
\[
d = 0.25 \cdot (R_{21} - R_{12}) / a \Rightarrow \text{quatern} \cdot d
\]

If \(a=0\) (a 180 degree rotation), alternative formulas are needed. See the `nifti1.io.c` function `mat44.to.quatern()` for an implementation of the various cases in converting \(R\) to \([a, b, c, d]\).

Note that \(R\)-transpose (= \(R\)-inverse) would lead to the quaternion \([a, -b, -c, -d]\).

The choice to specify the `qoffset.x` (etc.) values in the final coordinate system is partly to make it easy to convert DICOM images to this format. The DICOM attribute "Image Position (Patient)" (0020,0032) stores the \((X_d, Y_d, Z_d)\) coordinates of the center of the first voxel. Here, \((X_d, Y_d, Z_d)\) refer to DICOM coordinates, and \(X_d = -x, Y_d = -y, Z_d = z\), where \((x, y, z)\) refers to the NIFTI coordinate system discussed above. (i.e., DICOM +\(X_d\) is Left, +\(Y_d\) is Posterior, +\(Z_d\) is Superior, whereas +\(x\) is Right, +\(y\) is Anterior , +\(z\) is Superior.)

Thus, if the (0020,0032) DICOM attribute is extracted into \((px, py, pz)\), then \(\text{qoffset.x} = -px \text{ qoffset.y} = -py \text{ qoffset.z} = pz\) is a reasonable setting when `qform.code=NIFTI.XFORM.SCANNER.ANAT`.

That is, DICOM’s coordinate system is 180 degrees rotated about the \(z\)-axis from the neuroscience/NIFTI coordinate system. To transform between DICOM and NIFTI, you just have to negate the \(x\)- and \(y\)-coordinates.

The DICOM attribute (0020,0037) "Image Orientation (Patient)" gives the orientation of the \(x\)- and \(y\)-axes of the image data in terms of 2 3-vectors. The first vector is a unit vector along the \(x\)-axis, and the second is along the \(y\)-axis. If the (0020,0037) attribute is extracted into the value \((xa, xb, xc, ya, yb, yc)\), then the first two columns of the \(R\) matrix would be

\[
\begin{bmatrix}
-xa & -ya \\
-xb & -yb \\
xc & yc
\end{bmatrix}
\]

The negations are because DICOM’s \(x\)- and \(y\)-axes are reversed relative to NIFTI’s. The third column of the \(R\) matrix gives the direction of displacement (relative to the subject) along the slice-wise direction. This orientation is not encoded in the DICOM standard in a simple way; DICOM is mostly concerned with 2D images. The third column of \(R\) will be either the cross-product of the first 2 columns or its negative. It is possible to infer the sign of the 3rd column by examining the coordinates in DICOM attribute (0020,0032) "Image Position (Patient)" for successive slices. However, this method occasionally fails for reasons that I (RW Cox) do not understand.

Value

A list containing the matrix \(xyz\) of the positions of the points specified in \(ijk\).

See Also

`xyz2ijk`, `Q2R`, `R2Q`
magicfield

Examples

L <- f.read.header(system.file("example-nifti.hdr", package="AnalyzeFMRI"))
ijk <- matrix(c(1,1,1,2,3,7),byrow=FALSE,nrow=3)
ijk2xyz(ijk=ijk,method=2,L)

magicfield

*Get magicfield from the header of an image file*

Description

Determine the type of a file: NIFTI .nii format, NIFTI .hdr/.img pair format, ANALYZE format.

Usage

magicfield(file)

Arguments

file character, filename of an image (or header) file

Value

A list containing the magic and dim fields.

Examples

magicfield(system.file("example-nifti.hdr", package="AnalyzeFMRI"))

mat34.to.TRSZ

*Affine 4x4 (or 3x4) matrix to Translation, Rotation, Shear and Scale*

Description

Extract in that order Translation, Rotation, Shear and Scale from a 4x4 (or 3x4) affine matrix from a NIFTI header list (srow.x, srow.y, srow.z).

Usage

mat34.to.TRSZ(M)

Arguments

M the affine matrix
Details
Decomposes M using the convention: M = translation * scale * skew * rotation. Be careful that rotation can be improper.

Value
A list containing Translation, Scale, Shear and Rotation. Rotation decomposition is also provided (rotation = RotZ*RotY*RotX*Ref where Ref is a Reflexion if the rotation is improper or is Identity if the rotation is proper).

See Also
R2Q Q2R mat34.to.TZSR

Examples
L <- f.read.nifti.header(system.file("example-nifti.hdr", package="AnalyzeFMRI"))
M <- rbind(L$srow.x,L$srow.y,L$srow.z)
mat34.to.TRSZ(M)
model.2.cov.func

Description
Calculates covariance from Hartvig Model 2

Usage
model.2.cov.func(g, par)

Arguments
- g: The value of gamma
- par: A vector of parameters from the N2G model

Value
The calculated covariance

Author(s)
J. L. Marchini

References
**model.2.est.gamma**  
*Estimate gamma for Model 2 of Hartvig and Jensen (2000)*

**Description**
Estimate gamma for Model 2 of Hartvig and Jensen (2000)

**Usage**
```r
model.2.est.gamma(cov, par)
```

**Arguments**
- `cov`  
  An estimate of the spatial covariance  

- `par`  
  N2G model parameter estimates

**Value**
The estimate of gamma

**Author(s)**
J. L. Marchini

**References**

---

**N2G**  
*Fits the N2G model*

**Description**
Fits the N2G model (1 Normal and 2 Gamma’s mixture model) to a dataset using Maximum Likelihood.

**Usage**
```r
N2G(data, par.start = c(4, 2, 4, 2, 0.9, 0.05))
```

**Arguments**
- `data`  
  The dataset.

- `par.start`  
  The starting values for the optimization to maximize the likelihood. The parameters of the model are ordered in the vector par.start in the following way (refer to the model below)  
  ```
c(a, b, c, d, p1, p2)
```
Details

The mixture model considered is a mixture of a standard normal distribution and two Gamma functions. This model is denoted N2G.

\[ x \sim p_1 \ast N(0, 1) + p_2 \ast \text{Gamma(a, b)} + (1 - p_1 - p_2) \ast \text{-Gamma(c, d)} \]

Value

A list with components

- **par**: The fitted parameter values.
- **lims**: The upper and lower thresholds for the Normal component of the fitted model

Author(s)

J. L. Marchini

See Also


Examples

```r
par <- c(3, 2, 3, 2, .3, .4)
data <- c(rnorm(10000), rgamma(2000, 10, 1), -rgamma(1400, 10, 1))hist(data, n = 100, freq = FALSE)

q <- N2G.Fit(data, par, maxit = 10000, method = "BFGS")
p <- seq(-50, 50, .1)
lines(p, N2G.Density(p, q), col = 2)
```

N2G.Class.Probability  Posterior Probabilities for N2G model

Description

Calculates the Posterior Probability of data points being in each class given the parameters of the N2G model.

Usage

```
N2G.Class.Probability(data, par)
```

Arguments

- **data**: The dataset (usually a vector)
- **par**: The parameters of the model
Value

Returns the Posterior Probability of data points being in each class given the parameters of the N2G model.

Author(s)

J. L. Marchini

See Also

N2G.Likelihood.Ratio, N2G.Spatial.Mixture, N2G.Density, N2G.Likelihood, N2G.Transform, N2G.Fit, N2G.Inverse, N2G.Region

---

N2G.Density

Calculates the density function for the N2G model

Description

Calculates the density function for the N2G model

Usage

N2G.Density(data, par)

Arguments

data The dataset (usually a vector)
par The parameters of the model.

Details

Calculates the density function for the N2G model

Value

Returns the density at each point of the datasets

Author(s)

J. L. Marchini

See Also

N2G.Fit

Optimization function for N2G model

Description

Function that carries out the likelihood optimization for the N2G model.

Usage

N2G.Fit(data, par.start, maxit, method)

Arguments

data The dataset (usually a vector)
par.start Starting values for the parameters
maxit Maximum number of iterations
method Optimization method (passed to optim)

Details

Numerical optimization of the N2G model likelihood.

Value

Returns the optimized model parameters.

Author(s)

J. L. Marchini

See Also

N2G.Inverse

*Transform parameters of N2G model back to their real domains*

**Description**

Transform parameters of N2G model back to their real domains

**Usage**

\[
\text{N2G.Inverse}(\text{par})
\]

**Arguments**

- **par**: Parameter vector

**Details**

Transform parameters of N2G model back to their real domains

**Value**

Returns the transformed parameters.

**Author(s)**

J. L. Marchini

**See Also**


N2G.Likelihood

*Calculates the (negative) Likelihood of the N2G model*

**Description**

Calculates the (negative) Likelihood of the N2G model

**Usage**

\[
\text{N2G.Likelihood}(\text{inv.par}, \text{data})
\]

**Arguments**

- **inv.par**: A vector of transformed parameters for the N2G model
- **data**: The dataset (usually a vector)
Details

Calculates the (negative) Likelihood of the N2G model

Value

Returns (negative) Likelihood at each point of the dataset.

Author(s)

J. L. Marchini

See Also

N2G.Class.Probability, N2G.Likelihood.Ratio, N2G.Spatial.Mixture, N2G.Density, N2G.Transform, N2G.Fit, N2G.Inverse, N2G.Region

---

N2G.Likelihood.Ratio  N2G Likelihood Ratio’s

Description

Calculates the ratio of the likelihood that data came from the positive Gamma distribution (activation) to the likelihood that data came from the other two distributions (Normal and negative Gamma)

Usage

N2G.Likelihood.Ratio(data, par)

Arguments

data  The dataset (usually a vector)
par  The parameter vector for the N2G model

Value

Returns the vector of likelihood ratio’s

Author(s)

J. L. Marchini

See Also

N2G.Class.Probability, N2G.Spatial.Mixture, N2G.Density, N2G.Likelihood, N2G.Transform, N2G.Fit, N2G.Inverse, N2G.Region
N2G.Region

N2G Normal component interval

Description

Calculates the interval within which observations are classified as belonging to the Normal component of an N2G model.

Usage

N2G.Region(par1)

Arguments

par1
The parameters of the N2G model.

Value

A vector containing the upper and lower boundaries of the interval.

Author(s)

J. L. Marchini

See Also


N2G.Spatial.Mixture

fMRI Spatial Mixture Modelling

Description

Fits the spatial mixture model of Hartvig and Jensen (2000)

Usage

N2G.Spatial.Mixture(data, par.start = c(4, 2, 4, 2, 0.9, 0.05), ksize, ktype = c("2D", "3D"), mask = NULL)
Arguments

data The dataset (usually a vector)
par.start Starting values for N2G model
ksize Kernel size (see paper)
ktype Format of kernel "2D" or "3D"
mask Mask for dataset.

Value

p.map = a1, par = fit$par, lims = fit$lims

Returns a list with following components

p.map Posterior Probability Map of activation
par Fitted parameters of the underlying N2G model
lims Normal component interval for fitted model

Author(s)

J. L. Marchini

References

Hartvig and Jensen (2000) Spatial Mixture Modelling of fMRI Data

See Also

N2G.Class.Probability, N2G.Likelihood.Ratio, N2G.Density, N2G.Likelihood, N2G.Transform,
N2G.Fit, N2G, N2G.Inverse, N2G.Region

Examples

```r
## simulate image
d <- c(100, 100, 1)
y <- array(0, dim = d)
m <- y
m[, , ] <- 1
z.init <- 2 * m
z.init[20:40, 20:40, 1] <- 1
z.init[50:70, 50:70, 1] <- 3
y[z.init == 1] <- -rgamma(sum(z.init == 1), 4, 1)
y[z.init == 2] <- rnorm(sum(z.init == 2))
y[z.init == 3] <- rgamma(sum(z.init == 3), 4, 1)

mask <- 1 * (y < 1000)

## fit spatial mixture model
ans <- N2G.Spatial.Mixture(y, par.start = c(4, 2, 4, 2, 0.9, 0.05),
```
N2G.Transform

Transform parameters of N2G model so as to lie on the real line.

Description
Transform parameters of N2G model so as to lie on the real line.

Usage
N2G.Transform(par)

Arguments
par Parameter vector for N2G model.

Details
Transformation required for optimization.

Value
Returns the transformed parameters.

Author(s)
J. L. Marchini

See Also
nifti.quaternion.to.mat44

Quaternions (etc.) to affine 4x4 matrix

Description

Generate a 4x4 affine matrix from a NIFIT header list.

Usage

nifti.quaternion.to.mat44(L)

Arguments

L  a NIFTI header list

Value

The 4x4 affine matrix.

See Also

R2Q Q2R

Examples

L <- f.read.nifti.header(system.file("example-nifti.hdr", package="AnalyzeFMRI"))
nifti.quaternion.to.mat44(L)

NonLinearSmoothArray  Non-linear spatial smoothing of 3D and 4D arrays.

Description

Smoothes the values in an array spatially using a weighting kernel that doesn’t smooth across boundaries.

Usage

NonLinearSmoothArray(x, voxdim=c(1, 1, 1), radius=2, sm=3, mask=NULL)
NonLinearSmoothArray

Arguments

x           The array to be smoothed.
voxdim      The voxel dimensions of the array.
radius      The radius of the spatial smoothing
sm          The standard deviation of the Gaussian smoothing kernel.
mask        Optional mask for smoothing.

Details

For a 3D array the smoothed values are obtained through a weighted sum of the surrounding voxel values within the specified radius. The weights are calculated using a Gaussian kernel function applied to the differences between the voxel and its surrounding voxels. In this way the smoothing is anisotropic.

For a 4D array the first 3 dimensions represent space and the fourth represents time. Therefore, each spatial location contains a time series of values. These time series are smoothed spatially in an anisotropic fashion. The sum of squared differences between each pair of time series are used to define the smoothing weights.

Value

The smoothed array is returned.

Author(s)

J. L. Marchini

See Also

GaussSmoothArray

Examples

#3D array
d<-rep(10,3)
a<-array(3,dim=d)
a[5:10,5,5]<7
a<-a+array(rnorm(n=1000,sd=1),dim=d)
h<-NonLinearSmoothArray(a,voxdim=c(1,1,1),radius=2,sm=3)

par(mfrow=c(2,2))
image(a[,,],zlim=c(-1,12));title("Before smoothing")
image(h[,,],zlim=c(-1,12));title("After smoothing")
persp(a[,,],zlim=c(-1,12))
persp(h[,,],zlim=c(-1,12))

#4D array
d<-c(10,10,10,20)
```r
a<-array(1,dim=d)
a[,6:10]<-2
a<-a+array(rnorm(20000,sd=.1),dim=d)

h<-NonLinearSmoothArray(a,voxdim=c(1,1,1),radius=2,sm=3)
par(mfrow=c(2,2),mar=c(0,0,0,0))
for(i in 1:10){
  for(j in 10:1){
    plot(a[1,i,j,],type="l",ylim=c(0,3),axes=FALSE);box()
    lines(h[1,i,j,],col=2)
  }
}
```

---

### orientation

**Orientation storage**

**Description**

To determine if data is stored in Radiological or Neurological order.

**Usage**

```r
orientation(L)
```

**Arguments**

- `L` a NIFTI header list

**Value**

-1 for Radiological and 1 for Neurological.

**Examples**

```r
L <- f.read.nifti.header(system.file("example-nifti.hdr", package="AnalyzeFMRI"))
orientation(L)
```
Q2R  

Quaternion to rotation

Description
Generate a (proper) rotation matrix from a quaternion.

Usage
Q2R(Q,qfac)

Arguments

Q  quaternion vector
qfac  qfac nifti field. It is pixdim[1]

Value
The rotation.

See Also
R2Q

Examples
L <- f.read.nifti.header(system.file("example-nifti.hdr", package="AnalyzeFMRI"))
Q <- c(L$quatern.b,L$quatern.c,L$quatern.d)
Q2R(Q,L$pixdim[1])

R2Q  

Rotation to quaternion

Description
Convert from (proper) rotation matrix to quaternion form.

Usage
R2Q(R,qfac=NULL)

Arguments

R  Rotation matrix
qfac  qfac nifti field. It is pixdim[1]. If NULL, R is transformed to have determinant 1
reduction

Value
The quaternion.

See Also
Q2R

Examples
L <- f.read.nifti.header(system.file("example-nifti.hdr", package="AnalyzeFMRI"))
Q <- c(L$quatern.b,L$quatern.c,L$quatern.d)
R <- Q2R(Q,L$pixdim[1])
Q
R2Q(R)

Description
This function reduces the data in the row or col dimension.

Usage
reduction(X,row.red=TRUE)

Arguments
X a matrix of size tm x vm which contains the functionnal images
row.red Logical. Reduces the columns or the rows

Value
Xred the reduced matrix

See Also
centering

Examples
# TODO!!
# Xcr <- reduction(Xcentred,row.red=TRUE)$Xred
Sim.3D.GammaRF

Simulate Gamma distributed Random Field

Description

Simulates a Gamma distributed random field by simulating a Gaussian Random Field and transforming it to be Gamma distributed.

Usage

Sim.3D.GammaRF(d, voxdim, sigma, ksize, mask, shape, rate)

Arguments

d A vector specifying the dimensions of a 3D or 4D array.
voxdim The dimensions of each voxel.
sigma The 3D covariance matrix of the field.
ksize The size (in voxels) of the kernel with which to filter the independent field.
mask A 3D mask for the field.
shape The shape parameter of the Gamma distribution.
rate The rate parameter of the Gamma distribution.

Value

A 3D array containing the simulated field

Author(s)

J. L. Marchini

Examples

d <- c(64, 64, 21)
FWHM <- 9
sigma <- diag(FWHM^2, 3) / (8 * log(2))
voxdim <- c(2, 2, 4)
m <- array(1, dim = d)

a <- Sim.3D.GammaRF(d = d, voxdim = voxdim, sigma = sigma,
                     ksize = 9, mask = m, shape = 6, rate = 1)
Simulate a GRF

Description

Simulates a Gaussian Random Field with specified dimensions and covariance structure.

Usage

Sim.3D.GRF(d, voxdim, sigma, ksize, mask = NULL, type = c("field", "max"))

Arguments

d             A vector specifying the dimensions of a 3D or 4D array.
voxdim        The dimensions of each voxel.
sigma         The 3D covariance matrix of the field.
ksize         The size (in voxels) of the kernel with which to filter the independent field.
mask          A 3D mask for the field.
type          If type == "field" then the simulated field together with the maximum of the field
               is returned. If type == "max" then the maximum of the field is returned.

Details

The function works by simulating a Gaussian r.v at each voxel location and then smoothing the field
with a discrete filter to obtain a field with the desired covariance structure.

Value

mat            Contains the simulated field if type == "field", else NULL
max            The maximum value of the simulated field.

Author(s)

J. L. Marchini

See Also

GaussSmoothArray, GaussSmoothKernel
Examples

```r
d <- c(64, 64, 21)
FWMH <- 9
sigma <- diag(FWMH^2, 3) / (8 * log(2))
voxdim <- c(2, 2, 4)
msk <- array(1, dim = d)

field <- Sim.3D.GRF(d = d, voxdim = voxdim, sigma = sigma, ksize = 9, mask = msk, type = "max")
```

SmoothEst

Estimate the variance-covariance matrix of a Gaussian random field

Description

Estimate the variance-covariance matrix of a Gaussian random field

Usage

`SmoothEst(mat, mask, voxdim, method = "Forman")`

Arguments

- `mat`: 3D array that is the Gaussian Random Field.
- `mask`: 3D mask array.
- `voxdim`: Vector of length 3 containing the voxel dimensions.
- `method`: The estimator to use. `method = "Forman"` (the default) uses the estimator proposed in [1]. `method = "Friston"` uses the estimator proposed in [2, 3], but this can be biased when the amount of smoothing is small compared to the size of each voxel (see [1] for more details and example below)

Details

Calculates the variance-covariance matrix using the variance covariance matrix of partial derivatives.

Value

A (3x3) diagonal matrix.

Author(s)

J. L. Marchini
References


Examples

# example that illustrates the bias of the Friston method when smoothing is small compared to voxel size
# NB. The presence of bias becomes clearer if the simulations below are run about 100 times and the results averaged

ksize <- 13
d <- c(64, 64, 64)
voxdim <- c(1, 1, 1)
FWHM <- 2 ## using a small value of FWHM (=2) compared to voxel size (=1)
sigma <- diag(FWHM^2, 3) / (8 * log(2))
mask <- array(1, dim = d)
num.vox <- sum(mask)

grf <- Sim.3D.GRF(d = d, voxdim = voxdim, sigma = sigma,
                  ksize = ksize, mask = mask, type = "field")$mat

SmoothEst(grf, mask, voxdim, method = "Friston")

# the Forman estimator is better (on average) than the Friston estimator

# example that illustrates the bias of the Friston method when smoothing is large compared to voxel size

ksize <- 13
d <- c(64, 64, 64)
voxdim <- c(1, 1, 1)
FWHM <- 5 ## using a large value of FWHM (=5) compared to voxel size (=1)
sigma <- diag(FWHM^2, 3) / (8 * log(2))
mask <- array(1, dim = d)
num.vox <- sum(mask)

grf <- Sim.3D.GRF(d = d, voxdim = voxdim, sigma = sigma,
st2xyzt

ksize = ksize, mask = mask, type = "field")$mat

SmoothEst(grf, mask, voxdim, method = "Friston")
SmoothEst(grf, mask, voxdim, method = "Forman")
sigma

st2xyzt  st2xyzt

Description

Encode and assemble a space code with a time code dimension into the combined one byte xyzt.units field of a NIFTI header file.

Usage

st2xyzt(space, time)

Arguments

space  space field of a NIFTI file

time   time field of a NIFTI file

Value

A list containing xyzt.units field.

Bits 0..2 of xyzt.units specify the units of pixdim[2..4] (e.g., spatial units are values 0,1,2,...,7).
Bits 3..5 of xyzt.units specify the units of pixdim[5] (e.g., temporal units are multiples of 8: 0,8,16,24,32,40,48,56).

This compression of 2 distinct concepts into 1 byte is due to the limited space available in the 348 byte ANALYZE 7.5 header.

Some NIFTI codes: 0 (unspecified units), 1 (meters), 2 (millimeters), 3 (micrometers), 8 (seconds), 16 (milliseconds), 24 (microseconds), 32 (Hertz), 40 (ppm, part per million) and 48 (radians per second).

See Also

xyzt2st

Examples

xyzt.units <- f.read.header(system.file("example-nifti.hdr", package="AnalyzeFMRI"))$xyzt.units
mylist <- xyzt2st(xyzt.units)
st2xyzt(mylist$space,mylist$time)
Description

To read tm functionnal images files in ANALYZE or NIFTI format, and concatenate them to obtain one 4D image file in Analyze (hdr/img pair) or Nifti format (hdr/img pair or single nii) which is written on disk. Note that this function outputs the files in the format sent in. If desired, one can use the function analyze2nifti to create NIFTI files from ANALYZE files.

Usage

threeDto4D(outputfile,path.in=NULL,prefix=NULL,regexp=NULL,times=NULL,
list.of.in.files=NULL,path.out=NULL,is.nii.pair=FALSE,hdr.number=1)

Arguments

- **outputfile**: character. Name of the outputfile without extension
- **path.in**: character with the path to the directory containing the image files
- **prefix**: character. common prefix to each file
- **regexp**: character. Regular expression to get all the files
- **times**: vector. numbers of the image files to retrieve
- **list.of.in.files**: names of img files to concatenate (with full path)
- **path.out**: where to write the output hdr/img pair files. Will be taken as path.in if not provided.
- **is.nii.pair**: logical. Should we write a signle nii NIFTI file or a hdr/img NIFTI pair file
- **hdr.number**: Number of the original 3D Analyze or NIFTI image file from which to take the header that should serve as the final header of the newly 4D created image file

Value

None.

See Also

twoDto4D fourDto2D

Examples

# path.fonc <- "/network/home/lafayep/Stage/Data/map284/functional/
# MondrianApril2007/preprocessing/1801/smoothed/"
# threeDto4D("essai",path.in=path.fonc,prefix="su1801_",regexp="?????.img",times=1:120)
Threshold.Bonferroni  
Calculates Bonferroni Threshold

Description

Calculate the Bonferroni threshold for n iid tests that results in an overall p-value of p.val. The tests can be distributed as Normal, t or F.

Usage

Threshold.Bonferroni(p.val, n, type = c("Normal", "t", "F"), df1 = NULL, df2 = NULL)

Arguments

- **p.val**: The required overall p-value.
- **n**: The number of tests.
- **type**: The distribution of the tests. One of "Normal", "t" or "F"
- **df1**: The degrees of freedom of the t-distribution or the first degrees of freedom parameter for the F distribution.
- **df2**: The second degrees of freedom parameter for the F distribution.

Value

Returns the Bonferroni threshold.

Examples

Threshold.Bonferroni(0.05, 1000)
Threshold.Bonferroni(0.05, 1000, type = c("t"), df1 = 20)
Threshold.Bonferroni(0.05, 1000, type = c("F"), df1 = 3, df2 = 100)

Threshold.FDR  
False Discovery Rate (FDR) Threshold

Description

Calculates the False Discovery Rate (FDR) threshold for a given vector of statistic values.

Usage

Threshold.FDR(x, q, cV.type = 2, type = c("Normal", "t", "F"), df1 = NULL, df2 = NULL)
Threshold.RF

Arguments

x  A vector of test statistic values.
q  The desired False Discovery Rate threshold.
cV.type  A flag that specifies the assumptions about the joint distribution of p-values. Choose cV.type = 2 for fMRI data (see Genovese et al (2001)).
type  The distribution of the statistic values. Either "Normal", "t" or "F".
df1  The degrees of freedom of the t-distribution or the first degrees of freedom parameter for the F distribution.
df2  The second degrees of freedom parameter for the F distribution.

Value

Returns the FDR threshold.

Author(s)

J. L. Marchini

References

Genovese et al. (2001) Thresholding of Statistical Maps in Functional NeuroImaging Using the False Discovery Rate.

Examples

x <- c(rnorm(1000), rnorm(100, mean = 3))
Threshold.RF(x = x, q = 0.20, cV.type = 2)

Threshold.RF  Random Field Theory Thresholds.

Description

Calculates the Random Field theory threshold to give that results in a specified p-value.

Usage

Threshold.RF(p.val, sigma, voxdim = c(1, 1, 1), num.vox, type = c("Normal", "t"), df = NULL)

Arguments

p.val  The required p-value.
sigma  The 3D covariance matrix of the random field.
voxdim  The dimesnions of a voxel.
num.vox  The number of voxels that constitute the random field.
type  The type of random field, "Normal" or "t".
df  The degrees of the t distributed field.
Details
Calculates the threshold that produces an expected Euler characteristic equal to the required p-value.

Value
Returns the Random Field threshold.

Author(s)
J. L. Marchini

See Also
EC.3D

Examples
```r
a <- Threshold.RF(p.val = 0.05, sigma = diag(1, 3), voxel = c(1, 1, 1), num.vox = 10000)
EC.3D(a, sigma = diag(1, 3), voxel = c(1, 1, 1), num.vox = 10000)
```

---

twoDto4D
twoDto4D

description
This function transforms a 2D matrix of size tm x vm containing images in each row into a 4D array image.

Usage
twoDto4D(x.2d, dim)

Arguments
- `x.2d`: a 2D matrix to be transformed
- `dim`: vector of length 4 containing the dimensions of the array. dim[1:3] are the space dimensions. dim[4] is the time dimension

Value
- `volume.4d`: a 4D array image

See Also
threeDto4D fourDto2D
xyz2ijk

Examples

# TODO !!

xyz2ijk  xyz2ijk

Description

This function maps from some real world (x,y,z) positions in space into data coordinates (e.g. column i, row j, slice k). These original positions could relate to Talairach-Tournoux (T&T) space, MNI space, or patient-based scanner coordinates.

Usage

xyz2ijk(xyz=c(1,1,1),method=2,L)

Arguments

xyz matrix. Each column of xyz should contain a voxel real world index coordinates (x,y,z) to be mapped to its (i,j,k) voxel index coordinates in the dataset

method 1 (qform.code=sform.code=0), 2 (qform.code>0, rigid transformation) or 3 (sform.code>0, affine transformation).

L header list of a NIFTI file

Details

See help page of function ijk2xyz().

Value

A list containing the matrix xyz of the positions of the points specified in ijk.

See Also

ijk2xyz Q2R R2Q

Examples

L <- f.read.header(system.file("example-nifti.hdr", package="AnalyzeFMRI"))
xyz <- matrix(c(1,1,1,2,3,7),byrow=FALSE,nrow=3)
xyz2ijk(xyz=xyz,method=2,L)
Description

Extract space and time dimension codes from the one byte xyzt.units field of a NIFTI header file.

Usage

xyzt2st(xyzt.units)

Arguments

xyzt.units xyzt.units field of a NIFTI header file

Value

A list containing space and time fields.

See also the Value Section of the help file of function st2xyzt().

See Also

st2xyzt

Examples

xyzt.units <- f.read.header(system.file("example-nifti.hdr", package="AnalyzeFMRI"))$xyzt.units
xyzt2st(xyzt.units)
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