Package 'easyFMRI'

September 17, 2010

Type Package

Title Functions of fMRI analysis

Version 1.0

Date 2010-09-17

Author Wonsang You

Maintainer Wonsang You <you@ifn-magdeburg.de>

Description Functions for ROI segmentation in EPI sequence.

License GPL (>=2)

LazyLoad yes

Depends oro.nifti, AnalyzeFMRI

R topics documented:

---

easyFMRI-package   *Functions for FMRI Analysis*

Description

Functions for ROI segmentation in EPI sequences

Details

1

Package:	easyFMRI
Type:	Package
Version:	1.0
Date:	2010-09-17
License:	GPL (>=2)
LazyLoad:	yes

Author(s)

Wonsang You

Maintainer: Wonsang You <you@ifn-magdeburg.de>

References

Wonsang You (2010) ROI Data Extraction from FMRI BOLD Signals of the Human Brain, Technical Reports of the Leibniz Institute for Neurobiology, TR 10016.

Examples

```
ROIdata<-orthoROIs()
```

---

meanROIs	*The average time series of each ROI*

Description

Computing the average time series of each ROI in the given EPI sequence

Usage

```
meanROIs(EPIfname, nROIs = 31, ROIdir = "", prefix = "roi_",
      outfname = "meanROIs", writefile = TRUE)
```

Arguments

EPIfname   the file name of a EPI sequence (The file format should be ANALYZE such as
                hdr and img. For example, if the original file is "foo.img", the input value
                should be "foo".)

nROIs   the number of ROIs. Default is 31.

ROIdir   the directory of ROI definition files. These files should contain the individual
                zipped NIFTI files (nii.gz) corresponding to ROIs. Default is current working
                directory.

prefix	the common prefix of ROI definition files. Default is `roi_`. Then, the files should be titled as `roi_1.nii.gz`, `roi_2.nii.gz`, and so forth.
outfname	the outout text file name. Default is `meanROIs`.
writefile	Enable to write the output text file. Default is `TRUE`.

Details

This function computes the average time series of each ROI in the given EPI sequence. The ROI definition files should be given a priori.

Value

A matrix of averaged time series for ROIs. Row indicates a time point, and column does an ROI.

Author(s)

Wonsang You

References

Wonsang You (2010) ROI Data Extraction from FMRI BOLD Signals of the Human Brain, Technical Reports of the Leibniz Institute for Neurobiology, TR 10016.

See Also

tsROI

Examples

```
mts<-meanROIs("foo")
```

---

orthoROIs	*Orthogonalization of ROIs*

Description

Orthogonalizes ROIs in the EPI sequence. In other words, it eliminates all overlapped parts among ROIs, and then creates new ROIs which are spatially independent each other.

Usage

```
orthoROIs(nROIs = 31, ThRes = 5, ROIdir = "",
      targetdir = "newROIs", mode = "minimal", prefix = "roi_",
      newprefix = "roi_", writefile = TRUE, gzipped = TRUE,
      verbose = TRUE)
```

Arguments

nROIs	the number of ROIs
ThRes	the resolution of threshold. It is applied only when you choose the mode as thresholding. For example, if `ThRes=5`, the precision becomes `1e-5`. Default is `5`.
ROIdir	the directory of ROI definition files. These files should contain the individual zipped NIFTI files (nii.gz) corresponding to ROIs. Default is current working directory.
targetdir	the directory of output ROI definition files. Default is `newROIs`.
mode	the mode of orthogonalization. `thres` denotes thresholding, and `minimal` denotes minimal overlapping elimination. Default is `minimal`.
prefix	the common prefix of ROI definition files. Default is `roi_`. Then, the files should be titled as `roi_1.nii.gz`, `roi_2.nii.gz`, and so forth.
newprefix	the common prefix of output ROI definition files. Default is `roi_`.
writefile	Enable to write the output text file. Default is `TRUE`.
gzipped	Enable out NIFTI file to be zipped. Default is `TRUE`.
verbose	Allows message notification duringexecution of the function.

Details

ROIs is normally defined from the anatomical high-resolution image of the brain. To define the ROIs in the EPI sequence, the Brain Voyager can be exploited, however it can cause seriosu distortion such as spatial and temporal blurring. To avoid temporal blurring, we can match each ROI into the EPI space through rotation, translation, and resampling. In this case, overlaps among ROIs can be generated. This function resizes all ROIs by eliminating all overlapped parts.

Value

ROIData	A list of matrices of ROI data. Each matrix is three-dimensional, and indicates a segmented ROI region at the 3D volume of FMRI data. The number of matrices is the same as the number of ROIs.
thr	A vector of thresholds of ROIs. Notice that each ROI can have different threshold. The length of this vector is the same as the number of ROIs.
nOverlapROIpairs	
	An integer which indicates the number of overlapped ROI pairs.
nOverlapVoxels	
	An integer which indicates the number of overalpped voxels.
nNewOverlapROIpairs	
	An integer which indicates the number of overlapped ROI pairs after orthogonalization. In general, it is expected to be zero.
nNewOverlapVoxels	
	An integer which indicates the number of overalpped voxels after orthogonalization. In general, it is expected to be zero.

Author(s)

Wonsang You

References

Wonsang You (2010) ROI Data Extraction from FMRI BOLD Signals of the Human Brain, Technical Reports of the Leibniz Institute for Neurobiology, TR 10016.

Examples

```
dat<-orthoROIs()
```

---

tsROI   *Extraction of ROI Time Series*

Description

Extracts a set of time series which belong to a predefined ROI in the given EPI sequence.

Usage

```
tsROI(ROIidx, EPIfname, ROIdir = "", prefix = "roi_",
        outfname = "tsROI", writefile = TRUE)
```

Arguments

ROIidx	the index of ROI
EPIfname	the file name of a EPI sequence (The file format should be ANALYZE such as hdr and img. For example, if the original file is "foo.img", the input value should be "foo".)
ROIdir	the directory of ROI definition files. These files should contain the individual zipped NIFTI files (nii.gz) corresponding to ROIs. Default is current working directory.
prefix	the common prefix of ROI definition files. Default is roi_. Then, the files should be titled as roi_1.nii.gz, roi_2.nii.gz, and so forth.
outfname	the outout text file name. Default is tsROI.
writefile	Enable to write the output text file. Default is TRUE.

Details

This function extracts a set of time series of a predefined ROI in the given EPI sequence. The ROI definition file should be given a priori.

Value

A matrix of time series in a ROI. Row indicates a time point, and column does a voxel in the ROI.

Author(s)

Wonsang You

References

Wonsang You (2010) ROI Data Extraction from FMRI BOLD Signals of the Human Brain, Technical Reports of the Leibniz Institute for Neurobiology, TR 10016.

See Also

[meanROIs](#)

Examples

```
mts<-meanROIs(10,"foo")
```

Index