Package 'neuroSCC'

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Type Package

Title Estimation of SCC's for PET Neuroimaging Data

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Description This package provides functions for the estimation of Simultaneous Confidence Corridors (SCCs) on PET neuroimaging data. It is designed to help with the replication of methods implemented in the Ph.D. Thesis ``Development of statistical methods for neuroimage data analysis towards early diagnostic of neurodegenerative diseases" and it is best applied using the scripts available in the link below. Further information on the methodology for SCCs estimation can be found in: ``Wang Y, Wang G, Wang L, Ogden RT. Simultaneous confidence corridors for mean functions in functional data analysis of imaging data. Biometrics. 2020 Jun;76(2):427-437".

License use_mit_license()

URL https://github.com/iguanamarina/neuroSCC

Encoding UTF-8

LazyData true

RoxygenNote 7.3.1

Suggests roxygen2 (>= 7.1.0),
knitr,
rmarkdown

Roxygen list(markdown = TRUE)

Depends R (>= 2.10)

R topics documented:

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databaseCreator   *Create a database of processed PET image data with the appropiate format*

Description

This function automates the processing of PET images based on a specified file name pattern within a working directory. It reads each file matching the pattern, processes it using `neuroSCC::neuroCleaner`, and compiles the results into a comprehensive data frame.

Usage

```
databaseCreator(pattern)
```

Arguments

pattern   `character`, a regular expression pattern that specifies which files to process.

Details

The function first checks if there are files matching the pattern in the working directory. If no files are found, it throws an error. Otherwise, it processes each file individually, extracts necessary data, and appends it to a growing database. The function leverages `neuroSCC::neuroCleaner` for data processing. Each file's subject number is extracted from its name using regular expressions.

Value

A `data.frame` that aggregates processed data from each image. Each row represents data from one image, including subject numbers and image data.

See Also

[neuroCleaner](#) for the underlying image processing.

Examples

```
# Set the working directory where your PET images are stored
setwd("~/GitHub/PhD-2023-Neuroimage-article-SCC-vs-SPM/PETimg_masked for simulations")

# Define the pattern for file names to process
pattern <- "^masked_swwwC\\d+_tripleNormEsp_w00_rrec_OSEM3D_32_it1.nii"

# Create the database
database_CN <- databaseCreator(pattern)
```

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getDimensions *Get Dimensions from a DICOM File*

Description

This function loads a DICOM image file using the oro.nifti package and extracts its dimensions. It provides the X and Y dimensions as well as the total number of elements ('dim') in the image data.

Usage

```
getDimensions(filename = NULL)
```

Arguments

filename   character, optional; the name of the DICOM file to read. If not provided, the function will search for the first .img file in the current working directory.

Details

If no filename is provided, the function searches the current directory for the first file with a .img extension. It stops with an error message if no such files are found. It is important to ensure that the specified file or files in the directory are in the DICOM format.

Value

A list containing xDim, yDim, and dim, representing the dimensions of the image in the X and Y axes, and the total number of elements in the image, respectively.

See Also

[readNIfTI](#) for the function used to read the DICOM files.

Examples

```
# If 'filename' is not provided, it will get the first image in the current working directory:
dimensions <- getDimensions()

# Providing a specific filename:
dimensions <- getDimensions("003_S_1059.img")
```

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neuroCleaner   *Cleans and loads data from NIFTI files*

Description

This function reads a NIFTI image, transforms it into a dataframe, preserves the cross-section specified by the Z axis, and organizes the data into a structured table that other functions work on subsequently.

Usage

```
neuroCleaner(name, demo = NULL)
```

Arguments

name   character, the name of the NIFTI file to read.

demo   data.frame, a dataframe containing demographic data formatted according to
                the demoCleaner function. If not provided, only image data will be processed.

Details

The function first reads the NIFTI file using the oro.nifti::readNIfTI function from the package. Then, it converts the image data to a dataframe and selects only the cross-section of interest. If the demographic dataframe is provided, it checks if it contains the necessary columns and extracts the data for the specified participant. Finally, it combines these data with the image data and returns the resulting dataframe for that patient. If demo is not provided, it returns only the image data.

Value

A data.frame that combines the NIFTI image data with the demographic data in the appropriate format. Each row represents a pixel, and the columns include demographic data and pixel intensity. If demo is not provided, the dataframe will contain only the image data.

Author(s)

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See Also

demoCleaner and oro.nifti::readNIfTI().

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