

Package ‘neuroSCC’

April 15, 2024

Type Package

Title Estimation of Simultaneous Confidence Corridors for PET Neuroimaging Data

Version 0.2.0

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Description This package provides auxiliary functions for calculating Simultaneous Confidence Corridors (SCCs) on PET neuroimaging data. It includes functions to load neuroimaging and demographic data in the standard format required, and assists in various tasks throughout the process. Overall, this package is designed to help with the replication process of a cornerstone paper from my thesis ``Development of statistical methods for neuroimage data analysis towards early diagnostic of neurodegenerative diseases" and it is best followed using the scripts available at ``<https://github.com/iguanamarina/SCCneuroimage>". Overall, this serves as a support package.

License use_mit_license()

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

Encoding UTF-8

LazyData true

RoxygenNote 7.3.1

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neuroCleaner	<i>Cleans and loads data from NIFTI files</i>
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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)
```

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.

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. Afterward, it checks if the demographic dataframe 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.

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.

Author(s)

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See Also

[demoCleaner](#) and 'oro.nifti::readNIFTI()'.

Examples

```
# Assuming your working directory is set to where the files to load are:
names <- unique(tools::file_path_sans_ext(list.files()))
# Assuming 'demo' is a dataframe generated with \link[neuroSCC]{demoCleaner}:
result <- neuroCleaner(names[1], demo = demo)
head(result)
```

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