Package 'ARIbrain'

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Title All-Resolution Inference

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Description It performs All-Resolutions Inference (ARI) on functional Magnetic Resonance Image (fMRI) data. As a main feature,
it estimates lower bounds for the proportion of active voxels in a set of clusters as, for example, given by a cluster-wise analysis.
The method is described in Rosenblatt, Finos, Weeda, Solari, Goeman (2018) <doi:10.1016/j.neuroimage.2018.07.060>.

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RoxygenNote 6.0.1

Suggests knitr, rmarkdown

Imports hommel, RNifti, plyr

VignetteBuilder knitr

NeedsCompilation no

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ARIbrain-package *All-Resolutions Inference*

Description

It performs All-Resolutions Inference on fMRI data. As a main feature, it estimates lower bounds for the proportion of active voxels in a set of clusters as, for example, given by a cluster-wise analysis.

Author(s)

all of us

Examples

```
pvalue_name <- system.file("extdata", "pvalue.nii.gz", package="ARIbrain")
cluster_name <- system.file("extdata", "cluster_th_3.2.nii.gz", package="ARIbrain")
zstat_name <- system.file("extdata", "zstat.nii.gz", package="ARIbrain")
mask_name <- system.file("extdata", "mask.nii.gz", package="ARIbrain")

ARI(Pmap = pvalue_name, clusters= cluster_name,
    mask=mask_name, Statmap = zstat_name)
```

ARI *Valid Circular Inference (ARI) for Brain Imaging*

Description

Valid Circular Inference (ARI) for Brain Imaging

Usage

```
ARI(Pmap, clusters, mask = NULL, alpha = 0.05, Statmap = function(ix)
  -qnorm(Pmap[ix]), summary_stat = c("max", "center-of-mass"),
  silent = FALSE)
```

Arguments

Pmap	3D array of p-values or a (character) nifti file name.
clusters	3D array of cluster ids (0 when voxel does not belong to any cluster) or a (character) nifti file name.
mask	3D array of locicals (i.e. TRUE/FALSE in/out of the brain). Alternatively it may be a (character) nifti file name. If mask=NULL, it is assumed that non of the voxels have to be excluded.

alpha	Significance level. alpha=.05 by default.
Statmap	Statistics (usually t-values) on which the summaries are based. Can be either a 3D array, a (character) nifti file name or a function with argument ix used in the function to select the voxels belonging to a given cluster. By default Statmap = function(ix) -qnorm(Pmap[ix]) which convert the p-values in one-sided z-score.
summary_stat	Choose among =c("max", "center-of-mass").
silent	FALSE by default.

Value

A matrix reporting Size, FalseNull, TrueNull, ActiveProp and other statistics for each cluster.

Examples

```
pvalue_name <- system.file("extdata", "pvalue.nii.gz", package="ARIbrain")
cluster_name <- system.file("extdata", "cluster_th_3.2.nii.gz", package="ARIbrain")
zstat_name <- system.file("extdata", "zstat.nii.gz", package="ARIbrain")
mask_name <- system.file("extdata", "mask.nii.gz", package="ARIbrain")

print(mask_name)
print(pvalue_name)
print(cluster_name)
print(zstat_name)

ARI(Pmap = pvalue_name, clusters= cluster_name,
    mask=mask_name, Statmap = zstat_name)
```

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cluster_threshold *cluster_threshold*

Description

Get spatially-connected clusters starting from a 3D map of logical values

Usage

```
cluster_threshold(map, max_dist = sqrt(3))
```

Arguments

map	3D map of logical values. TRUE if the voxel it to be clustered (e.g. it is supra-threshold).
max_dist	maximum distance allowed to in the same cluster. By default: max_dist=sqrt(3) i.e. comprises all the voxels up to the corners souranding the target voxel. A value such as max_dist=sqrt(2) excludes the corners.

Value

a 3D map (same size of `map`) with integer values identifying the cluster and 0 elsewhere.

Examples

```
## Not run:
Tmap = RNifti::readNifti(system.file("extdata", "zstat.nii.gz", package="ARIbrain"))
clstr=cluster_threshold(Tmap>3.2)
table(clstr)

## End(Not run)
```

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