

Package ‘LESYMAP’

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Title Leions to Symptom Mapping in R

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Description LESYMAP maps the specific brain areas responsible for cognitive deficits by taking a series of lesion maps and a vector of behavioral scores. Both univariate (t-test, Brunner-Munzel, regression) and multivariate (sparse canonical corelations) tests are available. LESYMAP is built to run both real and simulated lesion-to-symptom mapping analyses.

License Apache License 2.0

Encoding UTF-8

LazyData true

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ANTsR

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<i>.createFolds</i>	<i>createFolds</i>
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Description

Used to create folds for k-fold validation

Usage

```
.createFolds(y, k = 10, list = TRUE, returnTrain = FALSE)
```

Arguments

<code>y</code>	split sample by balancing y
<code>k</code>	number of folds
<code>list</code>	logical whether to return folds in a list
<code>returnTrain</code>	logical whether to return training indices (T) or the test samples (F)

Author(s)

Caret Package

BM	<i>Massive Brunner-Munzel tests</i>
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Description

Takes a binary matrix of voxels and a vector of behavior and runs Brunner-Munzel tests on each voxel. This function is not compiled and is slow.

Usage

```
BM(lesmat, behavior)
```

Arguments

lesmat	matrix of voxels
behavior	vector of behavior

Value

Returned list with:

- statistic statistical values
- dof degrees of freedom

Author(s)

Dorian Pustina

Examples

```
set.seed(123)
lesmat = matrix(rbinom(200,1,0.5), ncol=2)
set.seed(123)
behavior = rnorm(100)
result = BM(lesmat, behavior)
```

BMfast	<i>Fast Brunner-Munzel tests (v1)</i>
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Description

Takes a binary matrix of voxels and a vector of behavior and runs Brunner-Munzel tests on each voxel. This is a fast function, but may produce infinite values for perfectly separated group. Use BMfast2 which avoids this problem.

Usage

```
BMfast(X, y)
```

Arguments

<code>x</code>	binary matrix of voxels (columns) for all subjects (rows)
<code>y</code>	vector of behavioral scores.

Value

List with two vectors: - statistic - BM values - dfbm - degrees of freedom

Author(s)

Dorian Pustina

BMfast2

Fast Brunner-Munzel tests (v2)

Description

Takes a binary matrix of voxels and a vector of behavior and runs Brunner-Munzel tests on each voxel. This is a fast function that corrects for infinite values with a similar approach as the `nparcomp` package.

Usage

```
BMfast2(X, y, computeDOF = TRUE)
```

Arguments

<code>x</code>	binary matrix of voxels (columns) for all subjects (rows)
<code>y</code>	vector of behavioral scores.
<code>computeDOF</code>	(true) chooses whether to compute degrees of freedom. Set to false to save time during permutations.

Value

List with two vectors: - statistic - BM values - dfbm - degrees of freedom

Author(s)

Dorian Pustina

checkAntsInput	<i>checkAntsInput</i>
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Description

Function to check a variable whether is composed of an antsImage, list of antsImages, or simply filenames. If none of the above, an error is returned.

Usage

```
checkAntsInput(input, checkHeaders = F)
```

Arguments

`input` the variable to be checked
`checkHeaders` make sure all images have the same headers

Value

Type of variable (antsImage, antsImageList, antsFiles) or error if variable cannot be established.

Author(s)

Dorian Pustina

Examples

```
## Not run:
files = Sys.glob('/data/jag/nifti/*.nii.gz')
myimagelist = imageFileNames2ImageList(files)
checkAntsInput(myimagelist) # returns 'antsImageList'
checkAntsInput(antsFiles) # returns 'antsFiles'
checkAntsInput(myimagelist[[1]]) # returns 'antsImage'

## End(Not run)
```

checkFilenameHeaders	<i>checkFilenameHeaders</i>
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Description

Function to check that all filenames in a vector point to existing files with the same resolution, orientation, size, and origin.

Usage

```
checkFilenameHeaders(files, showError = T)
```

Arguments

<code>files</code>	character vector of filenames
<code>showError</code>	logical whether to show an error (True) or to return a boolean instead. Returned values are True=pass,False=Fail

Value

logical if the test was successful or not

Author(s)

Dorian Pustina

<code>checkImageList</code>	<i>checkImageList</i>
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Description

Function to check that all `antsImages` in a list have the same orientation, origin, and resolution. The function stops with an error if one of the images has unusual headers. This behavior can be overcome by setting `showError=F`, and using the returned status (True=pass, False=fail) to make decisions outside this function.

Usage

```
checkImageList(imgList, showError = T, binaryCheck = F)
```

Arguments

<code>imgList</code>	list of <code>antsImages</code>
<code>showError</code>	boolean indicating whether to show the exact error and interrupt the function (TRUE, default), or don't show the error and return the check status (FALSE). The returned values when <code>showError=F</code> are T=passed or F=Failed.
<code>binaryCheck</code>	boolean, check if images re binary (0/1 values). Useful when checking masks or lesions. This check slows the output of the function.

Value

True if list has images with same headers, otherwise False.

Author(s)

Dorian Pustina

Examples

```
## Not run:
files = Sys.glob('/data/jag/nifti/*.nii.gz')
myimagelist = imageFileNames2ImageList(files)
checkImageList(myimagelist) # no value returned
checkImageList(lesions, showError=F) # True returned
myimagelist[[4]] = cropIndices(myimagelist[[4]], c(1,1,1), c(20,20,20))
checkImageList(myimagelist) # error on image 4

## End(Not run)
```

checkMask

*checkMask***Description**

Function to check if mask is in the same space as inputs

Usage

```
checkMask(lesions.list, mask)
```

Arguments

`lesions.list` list of antsImages or character vector of filenames
`mask` antsImage of mask to check

Value

Nothing returned, function stops with error if mask is not in same space as images in lesions.list

Author(s)

Dorian Pustina

getLesionLoad

*getLesionLoad***Description**

Computes lesion loads from a series of images. A parcellation image (or simple mask) is required to define the regions from which to compute the lesion load.

Usage

```
getLesionLoad(lesions.list, parcellation, label = NA, mask = NA,
  binaryCheck = F, keepAllLabels = F, minSubjectPerLabel = "10%")
```

Arguments

<code>lesions.list</code>	list of antsImages or filenames. Must be binary (0 and 1 values).
<code>parcellation</code>	ansImage or filename of the parcellated volumes. A parcellation is an image brain regions showned as with integer values (i.e. ,1,2,3,...).
<code>label</code>	(default=NA) you can ask to get output for a specific label in the parcellation volume (i.e., label=122).
<code>mask</code>	(default=NA) if this mask is specified (antsImage or filename) lesioned voxels outside the mask are ignored. This is not a good choice, but in case you need it its there.
<code>binaryCheck</code>	(default=FALSE) check whether lesion maps are binary (0/1). Will output an error if lesion files are not binary.
<code>keepAllLabels</code>	(default=FALSE) by default labels are removed if affected in just few subjects. Setting this to TRUE will keep all labels.
<code>minSubjectPerLabel</code>	minimum number of subjects a parcel must be lesioned to keep and return it.

Value

- `outputMatrix` of lesion loads between 0 and 1. 1 means 100% lesioned. Each column is a single parcel and each row a single subject. Parcel numbers are placed as column names.

Author(s)

Dorian Pustina

Examples

```
lesydata = file.path(find.package('LESYMAP'),'extdata')
filenames = Sys.glob(file.path(lesydata, 'lesions', '*.nii.gz'))
lesions = imageFileNames2ImageList(filenames[1:10])
parcellation = antsImageRead(
  file.path(lesydata,'template', 'Parcellation_403areas.nii.gz'))
lesload = getLesionLoad(lesions, parcellation)
```

getLesionSize

getLesionSize

Description

Compute lesion sizes from a list of antsImages.

Usage

```
getLesionSize(lesions.list)
```

Arguments

`lesions.list` List of antsImages. For proper measurement, images must be binary.

Value

vector of lesion sizes

Author(s)

Dorian Pustina

```
getUniqueLesionPatches
```

Unique Lesion Patches

Description

Compute unique patches of voxels with the same pattern of lesions in all subjects. Useful to understand the number of patterns that will be analyzed in a lesion dataset. A patch is a group of voxels, not necessarily close to each other, which have the same identical lesion pattern.

Usage

```
getUniqueLesionPatches(lesions.list, mask = NA, returnPatchMatrix = F,
  thresholdPercent = 0.1, binaryCheck = F, showInfo = T)
```

Arguments

`lesions.list` list of antsImages (faster) or filenames (slower)

`mask` (default=NA) a mask image to restrict the search for patches. Will be automatically calculated if not provided. Normally the mask restricts the search only to voxels lesioned in >10% of subejcts.

`returnPatchMatrix` (default=FALSE) logical, should the matrix of patches be returned. This is used in [lesymap](#) to run the analyses.

`thresholdPercent` (default=0.1) voxels with lesions in less than this proportion of subjects will not be considered. I.e., 0.1 = 10%.

`binaryCheck` (default=FALSE) set this to TRUE to verify that maps are binary.

`showInfo` (default=TRUE) logical indicating whether to display information.

Value

List of objects named as follows:

- `patchimg` - antsImage with every voxel assigned a patch number
- `patchimg.samples` - antsImage mask of one representative voxel for each patch. Can be used to extract the patchmatrix.
- `patchimg.size` - antsImage with the patch size at every voxel
- `patchimg.mask` - antsImage of full mask with all voxels. Can be used to put back results in combination with `patchindx`.
- `patchindx` - vector of patch membership for each voxel. Can be used to put back results in an image.

- `npatches` - number of unique patches in the image
- `nvoxels` - total number of lesioned voxels in `patchimg.mask`
- `patchvoxels` - vector of voxel count for each patch
- `patchvolumes` - vector of volume size for each patch
- `patchmatrix` - matrix of patches. This is used in `lesymap` to save time when running repetitive analyses.

Author(s)

Dorian Pustina

Examples

```
lesydata = file.path(find.package('LESYMAP'), 'extdata')

filenames = Sys.glob(file.path(lesydata, 'lesions', '*.nii.gz'))
patchinfo = getUniqueLesionPatches(filenames[1:10]) # slower

lesions = imageFileNames2ImageList(filenames[1:10])
patchinfo = getUniqueLesionPatches(lesions) # faster
```

<code>lesyload_mricron</code>	<i><code>lesyload_mricron</code></i>
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Description

Function to load data from a previous analysis in MRICron/npm in a ready format for use in `lesymap`

Usage

```
lesyload_mricron(valfile, imageFolder = NA, returnFileNames = F,
  checkHeaders = T, showInfo = T)
```

Arguments

<code>valfile</code>	mricron filename with extention <code>.val</code> . The function will search for images in the same folder where <code>valfile</code> is located, unless you specify explicitly <code>imageFolder</code> . If any of the files listed in the <code>.val</code> file are not found in the folder, an error will be displayed.
<code>imageFolder</code>	(default=NA) folder to look for the image files
<code>returnFileNames</code>	(default=FALSE) By default the function will load the images in memory to speed up things in <code>lesymap</code> . This may require too much RAM memory in some cases, and you may want to use filenames instead, which requires less memory but is slower in <code>lesymap</code> .
<code>checkHeaders</code>	(default=TRUE) Headers will be checked to make sure all images have the same dimension/origin/resolution, etc.
<code>showInfo</code>	(default=TRUE) show information upon successful load

Value

List with the following information lesions - list of antsImages or vector of filenames behavior - vector of behavioral scores

Author(s)

Dorian Pustina

lesymap

Lesion to Symptom Mapping

Description

Lesymap uses univariate and multivariate methods to map functional regions of the brain that, when lesioned, cause specific cognitive deficits. All is required is a set of Nifti images with the lesion of each subject and the vector of behavioral scores. Lesions must be already registered in template space, use 'antsRegistration' or other ANTs tools to achieve this. Lesymap will check that lesions are in the same space before running. By default, voxels with identical lesion patterns are grouped together in unique patches, and analysis are run on patches. Patch-based mapping decreases the number of multiple comparisons and speeds up the analyses. Multivariate mapping is performed using an optimized version of sparse canonical correlations (SCCAN).

Usage

```
lesymap(lesions.list, behavior, mask = NA, patchinfo = NA, method = "BM",
        correctByLesSize = "none", multipleComparison = "fdr",
        pThreshold = 0.05, flipSign = F, minSubjectPerVoxel = "10%",
        nperm = 1000, saveDir = NA, binaryCheck = F, noPatch = F,
        showInfo = T, ...)
```

Arguments

`lesions.list` list of antsImages, or a vector of filenames, or a single antsImage with 4 dimensions.

`behavior` vector of behavioral scores or filename pointing to a file with a single column of numbers.

`mask` (default=NA) binary image to select the area where analysis will be performed. If not provided will be computed automatically by thresholding the average lesion map at minSubjectPerVoxel.

`patchinfo` (default=NA) an object obtained with getUniqueLesionPatches or from a previous analyses. Useful for repetitive analysis to save time and avoid the computation of patches each time.

`method` what tests to run, one of 'BM' (default), 'BMfast', 'ttest', 'welch', 'regres', 'regresfast', 'regresPerm', 'sccan', 'sccanRaw'.

BM - Brunner-Munzel non parametric test, also called the Generalized Wilcoxon Test. The BM test is the same test used in the npm/Mricron software. See (see [Rorden \(2007\)](#)).

BMfast - ultrafast Brunner-Munzel with compiled code. Requires Rcpp and RcppArmadillo packages. BMfast can be combined with multipleComparison='FWERperm' to perform permutation based thresholding in a short time.

`ttest` - Regular single tailed t-test. Variances of groups are assumed to be equal. This is the test used in the voxbo software. Relies on `t.test` function in R. It is assumed that 0 voxels are healthy, i.e., higher behavioral scores. See the "alternative" parameter for inverted cases. (see [Bates \(2003\)](#)).

`welch` - t-test that assumes unequal variance between groups. Relies on `t.test` function in R.

`regres` - linear model between voxel values and behavior. Uses the `lm` function in R. This is equivalent to a t-test, but is useful when voxels are continuous, or when you want to know the direction of relationship without making assumptions. No covariates are allowed, but see below.

`regresfast` - ultrafast linear regressions with compiled code. Requires `Rcpp` and `RcppArmadillo` packages. You can set covariates. The effect of each voxel will be estimated with the formula:

```
behavior ~ voxel + covar1 + covar2 + ...
```

This method allows permutation based thresholding with `FWERperm` and `clusterPerm`. If covariates are used, permutations are performed with the Freedman-Lane method (see [Winkler \(2014\)](#)).

`regresPerm` - linear model between voxel values and behavior. P-values are computed through permutations with the `lmPerm` function in `lmPerm` package.

`chisq` - chi-square test between voxel values and behavior. The method is used when your behavior data are binary. Relies on the `chisq.test` R function and corrects individual voxel p-values with the Yates method (similar to the voxbo software).

`chisqPerm` - chi-square test between voxel values and behavior. The method is used when your behavior data are binary. P-values are established through permutation tests. Relies on the `chisq.test` R function.

`sccan` - sparse canonical correlations (NEW). Multivariate method that considers all voxels at once. By default, `lesymap` will run a lengthy procedure to determine the optimal sparseness value (how extensive the results should be). You can set `optimizeSparseness=FALSE` if you want to skip this optimization. The search for optimal sparseness provides a cross-validated correlation measure that shows how well SCCAN can predict new patients. If this correlation has $p > pThreshold$, the entire solution will be ignored and a NULL result will be returned. `Lesymap` returns normalized (0-1) voxel weights converted to positive; you can use `rawStat=TRUE` to retain the original voxel weights. Note that `lesymap` scales and centers both lesion and behavior data prior to processing (hardcoded in `lsm_sccan`).

`correctByLesSize`

whether to correct for lesion size in the analysis. Options are "none", "voxel", "behavior":

- "none": (default) no correction
- "voxel": divide voxel values by $1/\sqrt{\text{lesionsize}}$. This is the method used in [Mirman \(2015\)](#) and [Zhang \(2014\)](#). This correction works only with 'regres' methods. Two sample comparisons (t-tests and Brunner-Munzel) use binary voxels and will ignore this correction.
- "behavior": residualize behavioral scores by removing the effect of lesion size. This works on all methods, but is more aggressive on results.

`multipleComparison`

(default='fdr') method to adjust p-values. Standard methods include "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr". (see `p.adjust`)

Permutation methods include:

"FWERperm" (permutation based family-wise threshold) is enabled with methods 'BMfast' and 'regresfast'. In this case, many analysis are run with permuted behavioral scores, and the peak score is recorded each time (see Winkler 2014). The optimal threshold is established at 95th percentile of this distribution (or whatever pThreshold you choose). You can choose to use as reference another voxel lower in the ranks by specifying another 'v' value (i.e., lesymap(..., v=10) will record the 10th highest voxel).

"clusterPerm" (permutation based cluster correction) is enabled for 'regresfast'. It records the maximal cluster size from many random permutations of the behavior score and sets a cluster threshold based on that distribution. You must select pThreshold (voxel-wise, default=0.05) and clusterPermThreshold (cluster-wise, default 0.05) to achieve optimal with this method.

pThreshold	(default=0.05) threshold statistics at this p-value (after corrections or permutations)
flipSign	logical (default=FALSE), invert the sign in the statistics image.
minSubjectPerVoxel	(default='10%') remove voxels/patches with lesions in less than X subjects. Value can be specified as percentage ('10%') or exact number of subjects (10).
nperm	(default=1000) number of permutations to run when necessary.
saveDir	(default=NA) save results in the specified folder.
binaryCheck	logical (default=FALSE), make sure the lesion matrix is 0/1.
noPatch	logical (default=FALSE), if True avoids using patch information and will analyze all voxels. It will take longer and results will be worse due to more multiple comparison corrections. This argument is ignored when performing SCCAN analyses.
showInfo	logical (default=TRUE), display time-stamped info messages
...	arguments that will be passed down to other functions (i.e., sparseness=0.045)

Details

Several other parameters can be specified to lesymap() which will be passed to other called functions. Here are some examples:

permuteNthreshold - (default=9) for Brunner-Munzel tests only. Voxels lesioned in less than this number of subjects will undergo permutation-based p-value estimation. Useful because the BM test is not valid when comparing groups with $N < 9$. Note, permuted BM tests require the package 'nparcomp'.

clusterPermThreshold - threshold used to find the optimal cluster size when using 'clusterPerm' multiple comparison correction.

alternative - (default='greater') for two sample tests (ttests and BM). LESYMAP computes single tailed p-values, assuming that non-lesioned 0 voxels have higher behavioral scores. You can specify the opposite relationship with alternative='less' or compute two tailed p-values with alternative='two.sided'.

covariates - (default=NA) enabled for method = 'regresfast'. This will allow to model the effect of each voxel in the context of other covariates, i.e., formula "behavior ~ voxel + covar1 + covar2 + ...".

I.e., lesymap(lesions, behavior, method='regresfast', covariates=cbind(lesionsize, age)).

If you choose permutation based thresholding with covariates, lesymap will use the Freedman-Lane method for extracting the unique effect of each voxel (see Winkler 2014, Freedman 1983)

template - antsImage or filename used for plotting the results if a saving directory is specified (see saveDir)

v - (default=1) which voxel to record for permutation based thresholding. Normally the peak voxel is used (1), but other voxels can be recorded. See Mirman 2017 for this approach.

Value

The following objects are typically found in the returned list:

- stat.img - statistical map
- pval.img - p-values map
- zmap.img - zscore map
- mask.img - mask used for the analyses
- average.img - map of all lesions averaged. Map is produced only if no mask is defined.
- callinfo - list of details of how you called lesymap
- perm.vector - the values obtained from each permutation
- perm.clusterThreshold - threshold computed for cluster thresholding
- perm.FWERthresh - threshold computed for FWERperm thresholding
- patchinfo - list of variables describing patch information:
 - patchimg - antsImage with the patch number each voxels belongs to
 - patchimg.samples - antsImage mask with a single voxel per patch
 - patchimg.size - antsImage with the patch size at each voxel
 - patchimg.mask - the mask within which the function will look for patches
 - npatches - number of unique patches in the image
 - nvoxels - total number of lesioned voxels in mask
 - patchvoxels - vector of voxel count for each patch
 - patchvolumes - vector of volume size for each patch
 - patchmatrix - the lesional matrix, ready for use in analyses. Matrix has size NxP (N=number of subjects, P=number of patches)

Author(s)

Dorian Pustina

Examples

```
lesydata = file.path(find.package('LESYMAP'), 'extdata')
filenames = Sys.glob(file.path(lesydata, 'lesions', 'Subject*.nii.gz'))
behavior = Sys.glob(file.path(lesydata, 'behavior', 'behavior.txt'))
template = antsImageRead(
  Sys.glob(file.path(lesydata, 'template', 'ch2.nii.gz')))
lsm = lesymap(filenames, behavior, method = 'BMfast')
plot(template, lsm$stat.img, window.overlay = range(lsm$stat.img))

## Not run:
# Same analysis with SCCAN
lsm = lesymap(filenames, behavior, method = 'sccan',
  sparseness=0.045, optimizeSparseness=FALSE)
plot(template, lsm$stat.img, window.overlay = range(lsm$stat.img))
save.lesymap(lsm, saveDir='/home/dp/Desktop/SCCANresults')
```

```
## End(Not run)
```

lsm_BM

lsm_BM

Description

Lesion to symptom mapping performed on a prepared matrix. Brunner-Munzel tests are performed using each column of the matrix to split the behavioral scores in two groups.

Usage

```
lsm_BM(lesmat, behavior, permuteNthreshold = 9, nperm = 10000,
       alternative = "greater", showInfo = TRUE, ...)
```

Arguments

lesmat	binary matrix (0/1) of voxels (columns) and subjects (rows).
behavior	vector of behavioral scores.
permuteNthreshold	(default=9) Voxels lesioned in less than this number will undergo permutation based thresholding. See Medina et al 2010.
nperm	Number of permutations to perform when needed.
alternative	(default="greater") It is assumed that healthy voxels (0) have greater behavioral scores. If your data follow an inverted relationship choose "less" or "two.sided".
showInfo	display info messages when running the function.
...	other arguments received from lesymap .

Value

List of objects returned:

- `statistic` - vector of statistical values
- `pvalue` - vector of pvalues
- `zscore` - vector of zscores

Author(s)

Dorian Pustina

Examples

```
{
  set.seed(123)
  lesmat = matrix(rbinom(200,1,0.5), ncol=2)
  set.seed(123)
  behavior = rnorm(100)
  result = lsm_BM(lesmat, behavior)
}
```

lsm_BMfast

*lsm_BMfast***Description**

Lesion to symptom mapping performed on a prepared matrix. Brunner-Munzel tests are performed using each column of the matrix to split the behavioral scores in two groups. This function relies on a compiled version for fast processing.

Usage

```
lsm_BMfast(lesmat, behavior, permuteNthreshold = 9, alternative = "greater",
  statOnly = F, nperm = 1000, FWERperm = F, v = 1, pThreshold = 0.05,
  showInfo = F, ...)
```

Arguments

lesmat	binary matrix (0/1) of voxels (columns) and subjects (rows).
behavior	vector of behavioral scores.
permuteNthreshold	(default=9) Voxels lesioned in less than this number will undergo permutation based thresholding. See Medina et al 2010.
alternative	(default="greater") It is assumed that healthy voxels (0) have greater behavioral scores. If your data follow an inverted relationship choose "less" or "two.sided".
statOnly	logical (default=FALSE), skips some computations, don't use unless you know it's effects
nperm	(default=1000) Number of permutations to perform when needed.
FWERperm	logical (default=FALSE) whether to perform permutation based FWER thresholding.
v	(default=1) which voxel to record at each permutation, first or other voxels (i.e., v=10 for 10 highest voxel)
pThreshold	(default=0.05) what threshold to use for FWER
showInfo	display info messages when running the function.
...	other arguments received from lesymap .

Value

List of objects returned:

- `statistic` - vector of statistical values
- `pvalue` - vector of pvalues
- `zscore` - vector of zscores
- `perm.vector` - (optional) vector of permuted statistics
- `perm.FWERthresh` - (optional) permutation threshold established from the distribution of `perm.vector`

Author(s)

Dorian Pustina

Note on zscores qnorm gives same values as MRICron and relies on the normal distribution. however, we are computing t-scores, and should have relied on that distribution, which is the t-score itself.

Examples

```
{
  set.seed(123)
  lesmat = matrix(rbinom(200,1,0.5), ncol=2)
  set.seed(123)
  behavior = rnorm(100)
  result = lsm_BMfast(lesmat, behavior)
}
```

lsm_chisq

lsm_chisq

Description

Lesion to symptom mapping performed on a prepared matrix. The behavior must be a binary vector. Chi square tests are performed at each voxel. By default the Yates correction is performed, use `correct=FALSE` if you need to disable it. The behavior must be a binary vector. Exact p-values can be obtained with permutation based estimatins.

Usage

```
lsm_chisq(lesmat, behavior, YatesCorrect = TRUE, runPermutations = F,
  nperm = 2000, showInfo = TRUE, ...)
```

Arguments

lesmat	binary matrix (0/1) of voxels (columns) and subjects (rows).
behavior	vector of behavioral scores (must be binary).
YatesCorrect	(default=T) logical whether to use Yates correction.
runPermutations	logical (default=FALSE) whether to use permutation based p-value estimation.
nperm	(default=2000) The number of permutations to run.
showInfo	display info messages when running the function.
...	other arguments received from lesymap .

Value

List of objects returned:

- `statistic` - vector of statistical values
- `pvalue` - vector of pvalues
- `zscore` - vector of zscores

Author(s)

Dorian Pustina

Examples

```
{
  set.seed(123)
  lesmat = matrix(rbinom(200,1,0.5), ncol=2)
  set.seed(1234)
  behavior = rbinom(100,1,0.5)
  result = lsm_chisq(lesmat, behavior)
}
```

lsm_regres

*lsm_regres***Description**

Lesion to symptom mapping performed on a prepared matrix. Regressions are performed between behavior and each column in the lesmat matrix.

Usage

```
lsm_regres(lesmat, behavior)
```

Arguments

lesmat	matrix of voxels (columns) and subjects (rows).
behavior	vector of behavioral scores.

Value

List of objects returned:

- `statistic` - vector of statistical values
- `pvalue` - vector of pvalues
- `zscore` - vector of zscores

Author(s)

Dorian Pustina

Examples

```
{
  set.seed(123)
  lesmat = matrix(rbinom(200,1,0.5), ncol=2)
  set.seed(123)
  behavior = rnorm(100)
  result = lsm_regres(lesmat, behavior)
}
```

<code>lsm_regresfast</code>	<i><code>lsm_regresfast</code></i>
-----------------------------	------------------------------------

Description

Lesion to symptom mapping performed on a prepared matrix. Regressions are performed between behavior and each column of the lesmat matrix. Fast function based on compiled code.

Usage

```
lsm_regresfast(lesmat, behavior, covariates = NA, FWERperm = F,
  nperm = 1000, v = 1, pThreshold = 0.05, clusterPerm = F, mask = NA,
  voxindx = NA, samplemask = NA, clusterPermThreshold = 0.05,
  showInfo = T, ...)
```

Arguments

<code>lesmat</code>	matrix of voxels (columns) and subjects (rows).
<code>behavior</code>	vector of behavioral scores.
<code>covariates</code>	(default=NA) vector of matrix of covariates.
<code>FWERperm</code>	logical (default=FALSE) whether to run permutation based FWER thresholding.
<code>nperm</code>	Number of permutations to perform when needed.
<code>v</code>	(default=1) what voxel to record for FWER thresholding.
<code>pThreshold</code>	(default=0.05) Voxel-wise threshold.
<code>clusterPerm</code>	logical (default=FALSE), whether to perform permutation based cluster thresholding.
<code>mask</code>	(default=NA) antsImage reference mask used for cluster computations.
<code>voxindx</code>	(default=NA) indices of voxels to put in mask
<code>samplemask</code>	(default=NA) antsImage used to extract voxels back in a matrix.
<code>clusterPermThreshold</code>	(default=0.05) threshold for cluster selection after obtaining cluster size distribution.
<code>showInfo</code>	display info messages when running the function.
<code>...</code>	other arguments received from lesymap .

Value

List of objects returned:

- `statistic` - vector of statistical values
- `pvalue` - vector of pvalues
- `zscore` - vector of zscores
- `perm.vector` - (optional) vector of permuted statistics
- `perm.FWERthresh` - (optional) permutation threshold established from the distribution of `perm.vector`
- `perm.clusterThreshold` - (optional) permutation threshold established from the distribution of `perm.vector`

Author(s)

Dorian Pustina

Examples

```
{
  set.seed(123)
  lesmat = matrix(rbinom(200,1,0.5), ncol=2)
  set.seed(123)
  behavior = rnorm(100)
  result = lsm_regresfast(lesmat, behavior)
}
```

lsm_regresPerm

lsm_regresPerm

Description

Lesion to symptom mapping performed on a prepared matrix. Regressions are performed between behavior and each column in the lesmat matrix. This function relies on the lmPerm package to run. The number of permutations required to reach stable p-values is established automatically. For this reason, the user cannot specify a predefined number of permutations.

Usage

```
lsm_regresPerm(lesmat, behavior)
```

Arguments

lesmat	matrix of voxels (columns) and subjects (rows).
behavior	vector of behavioral scores.

Value

List with vectors of statistic, pvalue, and zscore.

Author(s)

Dorian Pustina

lsm_sccan

*Sparse canonical correlations for symptom mapping.***Description**

Multivariate SCCAN adapted for lesion to symptom mapping purposes. By default an optimization routine is used to find the best sparseness value. If you specify sparseness manually, it will be validated to find the cross-validated correlation that can be obtained with that sparseness. You can skip the entire optimization/validation by choosing `optimizeSparseness=FALSE`. To understand SCCAN arguments, see [sparseDecom2](#).

Usage

```
lsm_sccan(lesmat, behavior, mask, rawStat = F, showInfo = T,
  optimizeSparseness = T, tstamp = "%H:%M:%S", pThreshold = 0.05,
  mycoption = 1, robust = 1, sparseness = 0.045, nvecs = 1,
  cthresh = 150, its = 20, npermsSCCAN = 0, smooth = 0.4, ...)
```

Arguments

lesmat	matrix of voxels (columns) and subjects (rows).
behavior	vector of behavioral scores.
mask	antsImage binary mask to put back voxels in image.
rawStat	logical (default=FALSE) whether to skip the normalization of values and thresholding at 0.1. If TRUE, the raw voxel weights will be returned.
showInfo	logical (default-TRUE) display messages
optimizeSparseness	logical (default=TRUE) whether to run the sparseness optimization routine. If false, the default sparseness value will be used. If sparseness is manually set this flag decides if the manual sparseness will be checked with cross validations.
tstamp	timestamp format used in LESYMAP
pThreshold	(default=0.05) If cross validated correlations show significance below this value the results are considered null and an empty map is returned.
mycoption	(default=1) SCCAN parameter, see sparseDecom2
robust	(default=1) SCCAN parameter, see sparseDecom2
sparseness	(default=1) SCCAN parameter, see sparseDecom2
nvecs	(default=1) SCCAN parameter, see sparseDecom2
cthresh	(default=150) SCCAN parameter, see sparseDecom2
its	(default=20) SCCAN parameter, see sparseDecom2
npermsSCCAN	(default=0) SCCAN permutations, see sparseDecom2
smooth	(default=0.4) SCCAN parameter, see sparseDecom2
...	other arguments received from lesymap .

Value

List of objects returned:

- `statistic` - vector of statistical values
- `pvalue` - vector of pvalues
- `optimalSparseness` - (optional) optimal value found for sparseness
- `CVcorrelation.stat` - (optional) Correlation between true and predicted score with k-fold validation using the optimal sparseness value
- `CVcorrelation.pval` - (optional) p-value of the above correlation

Author(s)

Dorian Pustina

Examples

```
{
## Not run:
lesydata = file.path(find.package('LESYMAP'),'extdata')
filenames = Sys.glob(file.path(lesydata, 'lesions', '*.nii.gz'))
behavior = Sys.glob(file.path(lesydata, 'behavior', 'behavior.txt'))
behavior = read.table(behavior,header=FALSE)[,1]
avg = antsAverageImages(filenames)
mask = thresholdImage(avg, 0.1, Inf)
lesmat = imagesToMatrix(filenames,mask)
result = lsm_sccan(lesmat, behavior,
  optimizeSparseness=F, sparseness=0.8, mask = mask)

## End(Not run)
}
```

lsm_ttest

lsm_ttest

Description

Lesion to symptom mapping performed on a prepared matrix. T-tests are performed using each column of the matrix to split the behavioral scores in two groups. If `var.equal=TRUE` the Welch test is performed instead.

Usage

```
lsm_ttest(lesmat, behavior, var.equal = T, alternative = "greater", ...)
```

Arguments

<code>lesmat</code>	binary matrix (0/1) of voxels (columns) and subjects (rows).
<code>behavior</code>	vector of behavioral scores.
<code>var.equal</code>	logical (default=TRUE) should the variance between groups considered equal (t-test) or unequal (Welch test).
<code>alternative</code>	(default='greater') Sets the expected relationship between voxel value and behavior. By default voxels with zero are not lesioned, and behavior is expected to be higher, thus <code>alternative='greater'</code> . If the relationship in your data is inverted, use <code>alternative='less'</code> , and if you don't know your data, use <code>alternative='two.sided'</code> .
<code>...</code>	other arguments received from lesymap .

Value

List of objects returned:

- `statistic` - vector of statistical values
- `pvalue` - vector of pvalues
- `zscore` - vector of zscores

Author(s)

Dorian Pustina

Examples

```
{
  set.seed(123)
  lesmat = matrix(rbinom(200,1,0.5), ncol=2)
  set.seed(123)
  behavior = rnorm(100)
  result = lsm_ttest(lesmat, behavior)
}
```

minSegDistance

minSegDistance

Description

This function computes the metric displacement between two binary masks

Usage

```
minSegDistance(manual, predict, get = "all", binarize = F, label = 1)
```

Arguments

manual	manual segmentation of class antsImage, used as reference
predict	other antsImage to compare to manual
get	(default='all') one of 'mean', 'max', 'min', or 'all'
binarize	logical (default=FALSE) whether to binarize the input images
label	(default=1) integer or vector of labels to binarize I.e., label=c(2,4) means label 2 from manual, and 4 from predict will be compared.

Value

Scalar (for 'mean', 'max', 'min') or list (for 'all'). Note, results are in milimeters

Note

max = Hausdorff distance

Author(s)

Dorian Pustina

optimize_SCCANsparseness

Optimization of SCCAN sparseness

Description

Function used to optimize SCCAN sparseness for lesion to symptom mapping.

Usage

```
optimize_SCCANsparseness(lesmat, behavior, mask, nfolds = 4,
  sparsenessPenalty = 0.03, lower = 0.005, upper = 0.9, tol = 0.03,
  justValidate = F, cvRepetitions = 3, mycoption = 1, robust = 1,
  sparseness = NA, nvecs = 1, cthresh = 150, its = 30,
  npermsSCCAN = 0, smooth = 0.4, sparseness.behav = -0.99, ...)
```

Arguments

lesmat	lesion matrix
behavior	behavior vector
mask	antsImage mask
nfolds	how many folds to use
sparsenessPenalty	penalty term
lower	minimum searched sparseness
upper	maximum searched sparseness
tol	tolerance value, see optimize() in R
justValidate	just check the CV of provided sparseness


```

cvRepetitions      number of cross-validations
mycoption          standard SCCAN parameter
robust             standard SCCAN parameter
sparseness         standard SCCAN parameter
nvecs             standard SCCAN parameter
cthresh           standard SCCAN parameter
its               standard SCCAN parameter
npermsSCCAN       SCCAN permutations
smooth            standard SCCAN parameter
sparseness.behav   what sparsness to use for behavior
...               other arguments received from lesymap or lsm_sccan.

```

Value

List with:

minimum - best sparseness value

objective - minimum value of objective function

CVcorrelation - cross-validated correlation of optimal sparsness

Author(s)

Dorian Pustina

the optimization function Will run SCCAN on each training fold, compute behavior prediction on the test fold, and finally return a cross validated correlation from entire sample

end of optimfun

```
print.lesymap
```

```
print.lesymap
```

Description

Funciton to display some meaningful summary when a lesymap output is called in command line.

Usage

```
## S3 method for class 'lesymap'
print(x, ...)
```

Arguments

```

x                the output from a lesymap() call.
...             useless for compatibility with default print.

```

Author(s)

Dorian Pustina

regresfast	<i>Fast linear regressions</i>
------------	--------------------------------

Description

Takes a matrix of voxels and a vector of behavior and runs fast regressions for each voxel. Covariates can be defined (i.e. age) to find the effect of each voxel on behavior within the context of other predictive factors.

Usage

```
regresfast(X, y, covariates, hascovar = FALSE)
```

Arguments

X	matrix of voxels (columns) for all subjects (rows).
y	vector of behavioral scores.
covariates	matrix with one or more columns. Must be of same length as behavior. This variable should always be set, and the next argument can tell if covariates should be used or not.
hascovar	logical to tell whether covariates should be used.

Value

List with (1) statistic, (2) n = number of subjects, (3) kxfrm = degrees of freedom.

Author(s)

Dorian Pustina

save.lesymap	<i>Save the output of lesymap.</i>
--------------	------------------------------------

Description

Function to save the output of lesymap.

Usage

```
save.lesymap(lsm, saveDir, infoFile = "Info.txt", template = NA,
  saveTemplate = F, savePatchImages = T, plot.alpha = 0.8,
  plot.axis = 3, plot.quality = 8, ...)
```

Arguments

<code>lsm</code>	object obtained with <code>lesymap()</code>
<code>saveDir</code>	folder to save to, will be created if it doesn't exist.
<code>infoFile</code>	(default='Info.txt') what should be the filename of the file with information.
<code>template</code>	(default=NA) an <code>antsImage</code> to overlay the results to. If the template is provided, results will be plotted and saved as image.
<code>saveTemplate</code>	(default=FALSE) should the template image also be saved? Useful when passing the results to a colleague.
<code>savePatchImages</code>	(default=TRUE) should the patch images be saved
<code>plot.alpha</code>	see <code>plot.antsImage</code>
<code>plot.axis</code>	see <code>plot.antsImage</code>
<code>plot.quality</code>	see <code>plot.antsImage</code>
<code>...</code>	other arguments to use for <code>plot()</code> .

Value

Nothing is returned. Files saved include resulting maps and a descriptive file with a lot of information about the `lesymap` run.

Author(s)

Dorian Pustina

<code>simulateBehavior</code>	<i>Simulation of behavior scores from lesion maps</i>
-------------------------------	---

Description

Function simulate behavioral scores based on the lesion load of specific brain areas. Used to run simulation studies.

Usage

```
simulateBehavior(lesions.list, parcellation, label = NA, mask = NA,
  errorWeight = 0.3, binaryCheck = F, exponent = 1)
```

Arguments

<code>lesions.list</code>	list of lesions (<code>antsImages</code>) or vector of filenames.
<code>parcellation</code>	mask or parcellation image. If a parcellation is passed, lesion load will be computed for each different label (value) in the image. Zero and non-affected labels are not returned by default. The parcellation input can be an <code>antsImage</code> or a character vector pointing to a file.
<code>label</code>	if the parcellation has multiple labels, you can select which labels to simulate behaviors for (i.e., <code>c(101,43)</code> to simulate behavior for labels with value 101 and 43 only)

mask	mask to restrict the count of lesioned voxels. It is not recommended to use a mask, because lesions should affect behavior as they are, without the user restricting the lesions to masks defined a posteriori.
errorWeight	the amount of error to be added (i.e., 0.5 means half of the simulation will be error, the other half signal)
binaryCheck	check to make sure all lesions are binary
exponent	power exponent to elevate behavior in order to increase non-linearity relationship with lesion load. 1 is default, and 3 is what Wang (2013) reported as lesion load relationship with behavior.

Value

List of three objects: - behavload - a matrix of simulated behavioral scores. Each column shows simulation for a single parcel. Column names indicate the label number in the parcellation file.
- lesload - same as behavload, but indicates lesions loads from which behavior was simulated.
- lesbehavCorrelation - vector of correlation values (Pearson) between lesion load and simulated scores.

Author(s)

Dorian Pustina

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