

Package ‘mand’

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Type Package

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Imports oro.nifti, oro.dicom, imager, caret

Description Several functions can be used to analyze neuroimaging data using multivariate methods based on the 'msma' package. The functions used in the book entitled "Multivariate Analysis for Neuroimaging Data" (2021, ISBN-13: 978-0367255329) are contained. Please also see Kawaguchi et al. (2017) <[doi:10.1093/biostatistics/kxx011](https://doi.org/10.1093/biostatistics/kxx011)> and Kawaguchi (2019) <[DOI:10.5772/intechopen/90444](https://doi.org/10.5772/intechopen/90444)>

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mand-package	<i>Multivariate Analysis for Neuroimaging Data Package</i>
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Description

A Package for implementation of multivariate data analysis for neuroimaging data.

Author(s)

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References

Kawaguchi A, Yamashita F (2017). Supervised Multiblock Sparse Multivariable Analysis with Application to Multimodal Brain Imaging Genetics. *Biostatistics*, 18(4) 651-665.

atlas	<i>Atlas set</i>
-------	------------------

Description

The data is the atlas image data. An image whose element is "ROIid" is stored for each atlas.

Usage

data(atlas)

Format

A list of array

atlasdatasets	<i>Atlas data set</i>
---------------	-----------------------

Description

The data is the atlas data. Various atlases are stored. Each matrix has "ROIid" and "ROIname" as column names.

Usage

```
data(atlasdatasets)
```

Format

A list of matrix

atlastable	<i>Result report with atlas data</i>
------------	--------------------------------------

Description

This function refers to the results obtained by the analysis in an atlas image, and reports a summary of the results for each anatomical region.

Usage

```
atlastable(x, y, atlasdataset = NULL, ROIids = NULL, ...)
```

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

Arguments

x	an array for the atlas image.
y	an array for the result image.
atlasdataset	a matrix or data.frame. The colnames should include "ROIid" and "ROIname".
ROIids	a vector indicating ROI id shown in the result.
...	further arguments passed to or from other methods.

Details

atlastable requires the atlas image and data frame including the ROI id and the name.

Examples

```

data(diffimg)
data(atlasdatasets)
data(atlas)
atlasname = "aal"
atlasdataset = atlasdatasets[[atlasname]]
tmpatlas = atlas[[atlasname]]
atlastable(tmpatlas, diffimg, atlasdataset=atlasdataset, ROIids = c(1:2, 37:40))

```

baseimg

Base Brain Data

Description

The data is the base brain data. This is an average image of a healthy person, and is used when generating artificial data.

Usage

```
data(baseimg)
```

Format

A array

basisprod

Product Radial Basis Function

Description

This is a function to product the output for the rbfunc function with data matrix for a dimension reduction.

Usage

```
basisprod(A, B)
```

Arguments

A a list or a matrix corresponding to the output for the rbfunc function with the argument hispec=FALSE or data matrix, respectively.

B a list or a matrix.

Details

basisprod requires one list and one matrix.

Value

a producted matrix

Examples

```

imagedim1=c(10,10,10)

B1 = rbfunc(imagedim=imagedim1, seppix=4, hispec=TRUE)
B2 = rbfunc(imagedim=imagedim1, seppix=4, hispec=FALSE)

n = 50
S = matrix(rnorm(n*prod(imagedim1)), nrow = n, ncol = prod(imagedim1))

SB1 = S %**% B1
SB12 = tcrossprod(S, t(B1))
all(SB1-SB12 == 0)

SB2 = basisprod(S, B2)
all(SB1-SB2 == 0)

BS1 = t(B1) %**% t(S)
BS2 = basisprod(B2, S)
all(BS1-t(BS2) == 0)

```

 coat

Coat Function

Description

This is a function for plotting an image. The analysis result can be overcoated on the template.

Usage

```

coat(
  x,
  y = NULL,
  pseq = NULL,
  xyz = NULL,
  col.x = gray(0:64/64),
  col.y = NULL,
  breaks.y = NULL,
  zlim.x = NULL,
  zlim.y = NULL,
  rownum = 5,
  colnum = NULL,
  plane = c("axial", "coronal", "sagittal", "all")[1],

```

```

xlab = "",
ylab = "",
axes = FALSE,
oma = rep(0, 4),
mar = rep(0, 4),
bg = "black",
paron = TRUE,
cross.hair = FALSE,
chxy = NULL,
color.bar = TRUE,
regionplot = FALSE,
atlasdataset = NULL,
regionname = c("atlas", "stat")[1],
regionlegend = FALSE,
atlasname = "",
ROIids = 1:9,
...
)

```

Arguments

x	image1. Base image.
y	image2 to be overcoated.
pseq	a vector plot sequence.
xyz	a vector position to be plotted.
col.x	a color vector for image1.
col.y	a color vector for image2.
breaks.y	a vector breaks value for y.
zlim.x	a vector plot limitation values for z of x.
zlim.y	a vector plot limitation values for z of y.
rownum	a numeric, the number of row for the plot.
colnum	a numeric, the number of colnum for the plot.
plane	a vector plot sequence.
xlab	a character for a label in the x axis.
ylab	a character for a label in the y axis.
axes	a logical. TRUE presents the axes.
oma	a vector for outer margin area.
mar	a vector for margin.
bg	a character for color of background.
paron	a logical. TRUE means par is used.
cross.hair	a logical.
chxy	a vector cross hair position to be plotted.

color.bar	a logical.
regionplot	a logical.
atlasdataset	a matrix or data.frame. colnames should include "ROIid" and "ROIname".
regionname	a character.
regionlegend	a logical.
atlasname	a character.
ROIids	a vector
...	further arguments passed to or from other methods.

Details

coat requires a image array.

Examples

```
data(exbrain)
coat(exbrain)
```

diffimg

Difference Brain Data

Description

The data is the difference brain data. This represents the difference between the average images of healthy subjects and patients with Alzheimer's disease, and is used when generating artificial data.

Usage

```
data(diffimg)
```

Format

A array

exbrain	<i>Example Brain Data</i>
---------	---------------------------

Description

The data are from a MRI gray matter brain data for one subject.

Usage

```
data(exbrain)
```

Format

A array

imgdatamat	<i>Creat Data Matrix Function</i>
------------	-----------------------------------

Description

This is a function that creates a data matrix for analysis from a file saved in image format.

Usage

```
imgdatamat(
  imgfnames,
  mask = NULL,
  ROI = FALSE,
  atlas = NULL,
  atlasdataset = NULL,
  ROIids = NULL,
  zeromask = FALSE,
  schange = FALSE,
  ...
)
```

Arguments

imgfnames	a vector for (nifti) file names to be used.
mask	a vector for brain mask data.
ROI	a logical for roi data set.
atlas	an array for the atlas.
atlasdataset	a matrix or data.frame. colnames shold include "ROIid" and "ROIname".
ROIids	a vector

zeromask a logical for masking voxel with all zeros.
schange a logical for change dimension.
... further arguments passed to or from other methods.

Details

imgdatamat requires image file names.

Value

S data matrix
brainpos binary brain position.
imagedim three dimensional vector for image dimension

Examples

```
# imgfnames1 = c("img1.nii", "img2.nii")  
# imgdata = imgdatamat(imgfnames1)
```

mask

Brain Mask

Description

The data is the brain mask. This is used to exclude extra-brain regions from the analysis.

Usage

```
data(mask)
```

Format

A array

 multicomplot

Multi components plot

Description

This is a function that plots the vectorized image returned to its original dimensions by the `multirec` function.

Usage

```
multicomplot(
  object,
  x,
  comps = NULL,
  row4comp = 6,
  col4comp = 1,
  pseq4comp = NULL,
  ...
)
```

Arguments

<code>object</code>	an object of class "multirec." Usually, a result of a call to <code>multirec</code>
<code>x</code>	template image
<code>comps</code>	a component sequence to be plotted.
<code>row4comp</code>	the number of rows per a component
<code>col4comp</code>	the number of columns per a component
<code>pseq4comp</code>	the number of images per a component
<code>...</code>	further arguments passed to or from other methods.

Details

`multicomplot` requires the output result of `msma` function.

Examples

```
data(baseimg)
data(diffimg)
data(mask)
data(template)
img1 = simbrain(baseimg = baseimg, diffimg = diffimg, mask=mask)
B1 = rbfunc(imagedim=img1$imagedim, seppix=2, hispec=FALSE, mask=img1$brainpos)
SB1 = basisprod(img1$S, B1)
fit111 = msma(SB1, comp=2)
ws = multirec(fit111, imagedim=img1$imagedim, B=B1, mask=img1$brainpos)
multicomplot(ws, template)
```

multirec *Multi components reconstruction*

Description

This is a function that returns the weight vector of multiple components obtained by the msma function applied after dimension reduction by the radial basis function to the same dimension as the original image.

Usage

```
multirec(
  object,
  imagedim,
  B = NULL,
  mask = NULL,
  midx = 1,
  comps = NULL,
  XY = c("X", "Y", "XY")[1],
  signflip = FALSE
)
```

Arguments

object	an object of class msma. Usually, a result of a call to msma
imagedim	a vector for original dimension.
B	a list or a matrix.
mask	a list or a matrix.
midx	a block number.
comps	a component sequence to be plotted.
XY	a character, indicating "X" or "Y". "XY" for the scatter plots using X and Y scores from msma.
signflip	a logical if the sign in the block is flipped to pose the super as positive.

Details

multirec requires the output result of msma function.

Examples

```
data(baseimg)
data(diffimg)
data(mask)
img1 = simbrain(baseimg = baseimg, diffimg = diffimg, mask=mask)
B1 = rbfunc(imagedim=img1$imagedim, seppix=2, hispec=FALSE, mask=img1$brainpos)
```

```
SB1 = basisprod(img1$$S, B1)
fit111 = msma(SB1, comp=2)
ws = multirec(fit111, imagedim=img1$imagedim, B=B1, mask=img1$brainpos)
```

ptest

Prediction Model Function

Description

This is the function that creates and evaluates the predictive model.

Usage

```
ptest(
  object,
  Z = Z,
  newdata = NULL,
  testZ = NULL,
  regmethod = "glm",
  methods1 = c("boot", "boot632", "cv", "repeatedcv", "LOOCV", "LGOCV")[4],
  metric = "ROC",
  number1 = 10,
  repeats1 = 5,
  params = NULL
)
```

Arguments

object	a matrix indicating the explanatory variable(s), or an object of class msma, which is a result of a call to msma .
Z	a vector, response variable(s) for the construction of the prediction model. The length of Z is the number of subjects for the training.
newdata	a matrix for the prediction.
testZ	a vector, response variable(s) for the prediction evaluation. The length of testZ is the number of subjects for the validation.
regmethod	a character for the name of the prediction model. This corresponds to the method argument of the train function in the caret package.
methods1	a character for the name of the evaluation method.
metric	a character for the name of summary metric to select the optimal model.
number1	a number of folds or number of resampling iterations
repeats1	a number of repeats for the repeated cross-validation
params	a data frame with possible tuning values.

Details

ptest requires the output result of msma function.

Value

predict results

Examples

```
data(baseimg)
data(diffimg)
data(mask)
data(template)
img1 = simbrain(baseimg = baseimg, diffimg = diffimg, mask=mask)
B1 = rbfunc(imagedim=img1$imagedim, seppix=2, hispec=FALSE, mask=img1$brainpos)
SB1 = basisprod(img1$S, B1)
fit111 = msma(SB1, comp=2)
predmodel = ptest(fit111, Z=img1$Z)
```

rbfunc

Radial Basis Function

Description

This makes a radial basis function.

Usage

```
rbfunc(imagedim, seppix, hispec = FALSE, mask = NULL)
```

Arguments

imagedim	a vector indicating image three dimension.
seppix	a numeric. distance between knots.
hispec	a logical. TRUE produces a matrix output. FALSE produces a list output to reduce the data memory.
mask	a vector.

Details

rbfunc requires the dimensions of the original image to be applied and the knot interval. The output is obtained as a matrix, with the number of rows corresponding to the number of voxels in the original image and the number of columns determined by the knot spacing. By setting hispec = TRUE, you can get the output in list format with a smaller memory.

Examples

```
imagedim1=c(10,10,10)

B1 = rbfunc(imagedim=imagedim1, seppix=4, hispec=TRUE)
B2 = rbfunc(imagedim=imagedim1, seppix=4, hispec=FALSE)
```

rec

Reconstruction

Description

This is a function that restores the vectorized image to its original dimensions, reduced in dimension by the radial basis function.

Usage

```
rec(Q, imagedim, B = NULL, mask = NULL)
```

Arguments

Q	a vector for reduced data.
imagedim	a vector for original dimension.
B	a list or a matrix indicating the basis function used in the dimension reduction.
mask	a list or a matrix indicating the mask image used in the dimension reduction.

Details

rec requires a vector to be converted to a array.

Value

a reconstructed array

Examples

```
imagedim1=c(10,10,10)
recvec = rec(rnorm(prod(imagedim1)), imagedim1)
```

sdevimg	<i>Standard Deviation Brain Data</i>
---------	--------------------------------------

Description

The data is the standard deviation brain data. This represents the common standard deviation between the average images of healthy subjects and patients with Alzheimer's disease, and is used when generating artificial data.

Usage

```
data(sdevimg)
```

Format

A array

simbrain	<i>Generate simulation data Function</i>
----------	------------------------------------------

Description

This is a function for simulation data based on the real base brain image data and difference in brain between healthy and disease groups.

Usage

```
simbrain(  
  baseimg,  
  diffimg,  
  sdevimg = NULL,  
  mask = NULL,  
  n0 = 10,  
  c1 = 0.5,  
  sd1 = 0.01,  
  zeromask = FALSE,  
  reduce = c("no", "rd1", "rd2")[1],  
  output = c("rdata", "nifti")[1],  
  seed = 1  
)
```

Arguments

baseimg	an array for the basis image.
diffimg	an array for the difference image.
sdevimg	an array for the standard deviation image.
mask	an array for the mask image.
n0	a numeric, which is a sample size per group.
c1	a numeric,
sd1	a numeric, standard deviation for the individual variation.
zeromask	a logical, whether mask the position with zero values for all subjects.
reduce	a vector.
output	a vector.
seed	a numeric for seed for random variables.

Details

simbrain requires a base brain image data and mean difference image data.

Value

S	data matrix
Z	binary group variable
brainpos	binary brain position.
imagedim	three dimensional vector for image dimension

Examples

```
data(baseimg)
data(diffimg)
sim1 = simbrain(baseimg = baseimg, diffimg = diffimg)
```

sizechange

Size change Function

Description

TThis is a function that changes the resolution of the image.

Usage

```
sizechange(img1, simscale = NULL, refsize = NULL, ...)
```


Arguments

img1 a array or nifti class, which is a image data to be changed the size.
simscale a numeric.
resize a vector with length 3, which is a size to be changed.
... further arguments passed to or from other methods.

Details

sizechange requires the array data.

Value

size changed image

Examples

```
data(exbrain)
exbrain2 = sizechange(exbrain, simscale=1/2)
```

template

Brain Template

Description

The data is the brain template. This is an average brain image, and is mainly used for overlaying analysis results.

Usage

```
data(template)
```

Format

A array

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