Tutorial of NeuroRA Version 1.0.7.4

Updated by 2020-04-02

This Tutorial of NeuroRA provides information on how to use the NeuroRA including its easy-to-use functions.

Before you read it, you only need to spend a little time learning the basic Python syntax and this toolkit is easy to understand. In addition, it would be better if you are familiar with Python, especially the matrix operations based on NumPy.

If there is anything wrong, difficult to understand or having any useful advice during reading it, you can contact me (zitonglu1996@gmail.com) and I will be happy and thankful to know about it.

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This tutorial consists of these parts:

- Introduction & Installation
- Data Conversion
- Calculate the RDM (Representational Dissimilarity Matrices)
- Calculate the correlation coefficient between RDMs
- Visualization for results
- Save as a NIfTI file (for fMRI)
- Others
- Demo

Content

Part 1: Introduction

NueorRA is a Python toolbox for multimode neural data representational analysis.

Overview

Representational Similarity Analysis (RSA) has become a popular and effective method to measure the representation of multivariable neural activity in different modes.

NeuroRA is a novel and easy-to-use toolbox based on Python, which can do some works about RSA among nearly all kinds of neural data, including behavioral, EEG, MEG, fNIRS, ECoG, electrophysiological and fMRI data.

Installation

- *pip install NeuroRA*

Required Dependencies

Numpy: a fundamental package for scientific computing
Matplotlib: a Python 2D plotting library
NiBabel: a package prividing read +/- write access to some common medical and neuroimaging file formats

Nilearn: a Python module for fast and easy statistical learning on NeuroImaging data.

MNE-Python: a Python software for exploring, visualizing, and analyzing human neurophysiological data.

Part 2: Data Conversion

Type of Neural Bata	Data Conversion Scheme
fMRI	Use *Nibabel* (https://nipy.org/nibabel/) to load fMRI data. *import nibabel as nib* *fmrifilename = "demo.nii" # the fmri data file name with full address* *data = nib.load(fmrifilename).get_fdata() # load fMRI data as ndarray* *……*
EEG/MEG	Use *MATLAB EEGLab* (http://sccn.ucsd.edu/eeglab/) to do preprocessing and obtain .mat files, and use *Scipy* (https://www.scipy.org) to load EEG data (.mat). *import scipy.io as sio* *filename = "demo.mat" # the EEG/MEG data file name with full address* *data = sio.loadmat(filename)["data"] # load EEG/MEG data as ndarray* *……* Or use *MNE* (https://mne-tools.github.io) to do preprocessing and return *ndarray*-type data.
fNIRS	For raw data from device, use *Numpy* (http://www.numpy.org) to load fNIRS data (.txt or .csv). *import numpy as np* *txtfilename = "demo.txt" # the fNIRS data file name with full address* *csvfilename = "demo.csv"* *data = np.loadtxt(txtfilename) # load fNIRS data as ndarray* *data = np.loadtxt(csvfilename, delimiter, usecols, unpack)* *……*
ECoG/sEEG	Use *Brainstorm* (https://neuroimage.usc.edu/brainstorm/) to do preprocessing and obtain .mat files, and use Scipy to load ECoG data (.mat).
Electrophysiology	Use *pyABF* (https://github.com/swharden/pyABF) to load electrophysiology data (.abf). *import pyabf* *abf = pyabf.ABF("demo.abf") # the electrophysiology data file name with full address* *abf.setSweep(sweepNumber, channel) # access sweep data* *data = abf.sweepY # get sweep data with sweepY* *……*
Two functions, *NumPy.reshape()* & *NumPy.transpose()*, are recommended for further data transformation	

Part 3: Calculate the RDM

Module ***rdm_cal.py***

- bhvRDM(bhv_data, sub_opt=0, data_opt=1)

  A function for calculating the RDM based on behavioral data

  Parameters:

  bhv_data: *array*

  The behavioral data. If data_opt=0, the shape of bhv_data must be [n_cons, n_subs]. n_cons, n_subs represent the number of conditions & the number of subjects.

  sub_opt: *int (0 / 1)*

  Calculate the RDM for each subject or not. 1 or 0.

  data_opt: *int (0 / 1)*

  If data_opt=1, each subject's each trial has a value of data. If data_opt=0, each subject has a value of data, here ignore the effect of trials.

  Returns:

  rdm/rdms: *array*

  If sub_opt=0, return only one rdm (shape: [n_cons, n_cons]).
  If sub_opt=1, return rdms (shape: [n_subs, n_cons, n_cons]).

- eegRDM(EEG_data, time_win=5, sub_opt=0, chl_opt=0, time_opt=0)

  A function for calculating the RDM based on EEG/MEG/fNIRS data

  Parameters:

  EEG_data: *array*

  The EEG/MEG/fNIRS data. The shape of EEG_data must be [n_cons, n_subs, n_trials, n_chls, n_ts]. n_cons, n_subs, n_trials, n_chls, n_ts represent the number of conditions, subjects, trials, channels, frequencies and time-points.

time_win: *int*

(Only when time_opt = 1, time_win works) The time-window for each calculation.

sub_opt: *int (0 / 1)*

Calculate the RDM for each subject or not. 1 or 0.

chl_opt: *int (0 / 1)*

Calculate the RDM for each channel or not. 1 or 0.

time_opt: *int (0 / 1)*

Calculate the RDM for each time-point or not. 1 or 0.

Returns:

rdm/rdms: *array*

If sub_opt=0 and chl_opt=0 and time_opt=0, return only one rdm (shape: [n_cons, n_cons]).

If sub_opt=0 and chl_opt=0 and time_opt=1, return rdms (shape: [int(n_ts/tim_win), n_cons, n_cons]).

If sub_opt=0 and chl_opt=1 and time_opt=0, return rdms (shape: [n_chls, n_cons, n_cons]).

If sub_opt=1 and chl_opt=0 and time_opt=0, return rdms (shape: [n_subs, n_cons, n_cons]).

If sub_opt=0 and chl_opt=1 and time_opt=1, return rdms (shape: [n_chls, int(n_ts/tim_win), n_cons, n_cons]).

If sub_opt=1 and chl_opt=0 and time_opt=1, return rdms (shape: [n_subs, int(n_ts/tim_win), n_cons, n_cons]).

If sub_opt=1 and chl_opt=1 and time_opt=0, return rdms (shape: [n_subs, n_chls, n_cons, n_cons]).

If sub_opt=1 and chl_opt=1 and time_opt=1, return rdms (shape: [n_subs, n_chls, int(n_ts/tim_win), n_cons, n_cons]).

◆ ecogRDM(ele_data, time_win=5, opt="all")

A function for calculating the RDM based on ECoG/electrophysiological data

Parameters:

ele_data: *array*

The ECoG/electrophysiological data. The shape of ele_data must be [n_cons, n_trials, n_chls, n_ts]. n_cons, n_trials, n_chls, n_ts represent the number of conditions, trials, channels, frequencies and time-points.

time_win: *int*

The time-window for each calculation.

opt: *string ("channels" or "time" or "all")*

Calculate the RDM for each channel or for each time-point or not. "channels" or "time" or "all".

Returns:

rdm/rdms: *array*

If opt="channels", return rdms (shape: [n_chls, n_cons, n_cons]).

If opt="time", return rdms (shape: [int(n_ts/time_win), n_cons, n_cons])

◆ fmriRDM(fmri_data, ksize=[3, 3, 3], strides=[1, 1, 1])

A function for calculating the RDM based on fMRI data

Parameters:

fmri_data: *array*

The fmri data. The shape of fmri_data must be [n_cons, n_subs, nx, ny, nz]. n_cons, n_subs, nx, ny, nz represent the number of conditions, the number of subjects, the size of the fMRI data.

ksize: *array*

ksize=[kx, ky, kz] represents that the calculation unit contains k1*k2*k3 voxels.

strides: *array*

strides=[sx, sy, sz] represents the moving steps along the x, y, z.

Returns:

rdms: *array*

Return rdms for each calculation unit. The shape of rdms is [n_x, n_y, n_z, n_cons, n_cons]. Here, n_x, n_y, n_z represent the number of calculation units along the x, y, z.

Part 4: Calculate the Correlation Coefficient

Module ***rdm_corr.py***

◆ rdm_correlation_spearman(RDM1, RDM2, rescale=False)

A function for calculating the Spearman correlation coefficient between two RDMs

Parameters:

RDM1: *array*

The shape of RDM1 must be [n_cons, n_cons].

RDM2: *array*

The shape of RDM2 must be [n_cons, n_cons].

rescale: *Boolean (True or False)*

Rescale the values in RDM or not. True or False.

Returns:

corr: *array*

The corr contains two values: correlation coefficient and p-value. The shape of corr is [2,].

◆ rdm_correlation_pearson(RDM1, RDM2, rescale=False)

A function for calculating the Pearson correlation coefficient between two RDMs

Parameters:

RDM1: The shape of RDM1 must be [n_cons, n_cons].

RDM2: The shape of RDM2 must be [n_cons, n_cons].

rescale: *Boolean (True or False)*

Rescale the values in RDM or not. True or False.

Returns:

corr: The corr contains two values: correlation coefficient and p-value. The shape of corr is [2,].

◆ rdm_correlation_kendall(RDM1, RDM2, rescale=False)

A function for calculating the Kendalls tau correlation coefficient between two RDMs

Parameters:

RDM1: The shape of RDM1 must be [n_cons, n_cons].

RDM2: The shape of RDM2 must be [n_cons, n_cons].

rescale: *Boolean (True or False)*

Rescale the values in RDM or not. True or False.

Returns:

corr: The corr contains two values: correlation coefficient and p-value. The shape of corr is [2,].

◆ rdm_similarity(RDM1, RDM2, rescale=False)

A function for calculating the Cosine Similarity between two RDMs

Parameters:

RDM1: The shape of RDM1 must be [n_cons, n_cons].

RDM2: The shape of RDM2 must be [n_cons, n_cons].

Returns:

similarity: The Cosine Similarity.

◆ rdm_distance(RDM1, RDM2, rescale=False)

A function for calculating the Euclidean Distances between two RDMs

Parameters:

RDM1: The shape of RDM1 must be [n_cons, n_cons].

RDM2: The shape of RDM2 must be [n_cons, n_cons].

rescale: *Boolean (True or False)*

Rescale the values in RDM or not. True or False.

Returns:

dist: The Euclidean Distance.

- rdm_permutation (RDM1, RDM2, iter=1000)

A function for permutation test between two RDMs

Parameters:

RDM1: The shape of RDM1 must be [n_cons, n_cons].

RDM2: The shape of RDM2 must be [n_cons, n_cons].

iter: The number of iterations.

Returns:

p: The p-value.

Module ***corr_cal.py***

- bhvANDeeg_corr(bhv_data, eeg_data, sub_opt=0, bhv_data_opt=1, time_win=5, chl_opt=0, time_opt=0, method="spearman", rescale=False)

A function for calculating the Similarity/Correlation Coefficient between behavioral data and EEG/MEG/fNIRS data

Parameters:

bhv_data: *array*

The behavioral data. If data_opt=0, the shape of bhv_data must be [n_cons, n_subs]. n_cons, n_subs represent the number of conditions & the number of subjects.

eeg_data: *array*

The EEG/MEG/fNIRS data. The shape of eeg_data must be [n_cons, n_subs, n_trials, n_chls, n_ts]. n_cons, n_subs, n_trials, n_chls, n_ts represent the number of conditions,

subjects, trials, channels, frequencies and time-points.

sub_opt: *int (0 / 1)*

Calculate the RDM for each subject or not. 1 or 0.

bhv_data_opt: *int (0 / 1)*

If bhv_data_opt=1, each subject's each trial has a value of data. If bhv_data_opt=0, each subject has a value of data, here ignore the effect of trials.

time_win: *int*

The time-window for each calculation.

chl_opt: *int (0 / 1)*

Calculate the RDM for each channel or not. 1 or 0.

time_opt: *int (0 / 1)*

Calculate the RDM for each time-point or not. 1 or 0.

method: *string ("spearman" or "pearson" or "kendall" or "similarity" or "distance")*

They correspond to different methods of calculation. "spearman" or "pearson" or "kendall" or "similarity" or "distance".

rescale: *Boolean (True or False)*

Rescale the values in RDM or not. True or False.

Returns:

corr/corrs: *array*

The correlation coefficients corresponding to the RDMs.

◆ bhvANDecog_corr(bhv_data, ele_data, time_win=5, ecog_opt="allin", method="spearman" , rescale=False)

A function for calculating the Similarity/Correlation Coefficient between behavioral data and ECoG/electricophysiological data

Parameters:

bhv_data: *array*

The behavioral data. If data_opt=0, the shape of bhv_data

must be [n_cons, n_subs]. n_cons, n_subs represent the number of conditions & the number of subjects.

ele_data: *array*

The ECoG/electrophysiological data. The shape of ele_data must be [n_cons, n_trials, n_chls, n_ts]. n_cons, n_trials, n_chls, n_ts represent the number of conditions, trials, channels, frequencies and time-points.

time_win: *int*

The time-window for each calculation.

opt: *string ("channels" or "time" or "all")*

Calculate the RDM for each channel or for each time-point or not. "channels" or "time" or "all".

method: *string ("spearman" or "pearson" or "kendall" or "similarity" or "distance")*

They correspond to different methods of calculation. "spearman" or "pearson" or "kendall" or "similarity" or "distance".

rescale: *Boolean (True or False)*

Rescale the values in RDM or not. True or False.

Returns:

corr/corrs: The correlation coefficients corresponding to the RDMs.

- bhvANDfmri_corr(bhv_data, fmri_data, bhv_data_opt=1, ksize=[3, 3, 3], strides=[1, 1, 1], method="spearman" , rescale=False)

A function for calculating the Similarity/Correlation Coefficient between behavioral data and fMRI data

Parameters:

bhv_data: *array*

The behavioral data. If data_opt=0, the shape of bhv_data must be [n_cons, n_subs]. n_cons, n_subs represent the number of conditions & the number of subjects.

fmri_data: *array*

The fmri data. The shape of fmri_data must be [n_cons,

n_subs, nx, ny, nz]. n_cons, n_subs, nx, ny, nz represent the number of conditions, the number of subjects, the size of the fMRI data.

bhv_data_opt: *int (0 / 1)*

If bhv_data_opt=1, each subject's each trial has a value of data. If bhv_data_opt=0, each subject has a value of data, here ignore the effect of trials.

ksize: *array*

ksize=[kx, ky, kz] represents that the calculation unit contains k1*k2*k3 voxels.

strides: *array*

strides=[sx, sy, sz] represents the moving steps along the x, y, z.

method: *string ("spearman" or "pearson" or "kendall" or "similarity" or "distance")*

They correspond to different methods of calculation. "spearman" or "pearson" or "kendall" or "similarity" or "distance".

rescale: *Boolean (True or False)*

Rescale the values in RDM or not. True or False.

Returns:

corrs: *array*

The correlation coefficients corresponding to the RDMs. The shape of corrs is [n_x, n_y, n_z, 2].

- eegANDfmri_corr(eeg_data, fmri_data, chl_opt=0, ksize=[3, 3, 3], strides=[1, 1, 1], method="spearman" , rescale=False)

A function for calculating the Similarity/Correlation Coefficient between EEG/MEG/fNIRS data and fMRI data

Parameters:

eeg_data: *array*

The EEG/MEG/fNIRS data. The shape of eeg_data must be [n_cons, n_subs, n_trials, n_chls, n_ts]. n_cons, n_subs,

n_trials, n_chls, n_ts represent the number of conditions, subjects, trials, channels, frequencies and time-points.

fmri_data: *array*

The fmri data. The shape of fmri_data must be [n_cons, n_subs, nx, ny, nz]. n_cons, n_subs, nx, ny, nz represent the number of conditions, the number of subjects, the size of the fMRI data.

chl_opt: *int (0 / 1)*

Calculate the RDM for each channel or not. 1 or 0.

ksize: *array*

ksize=[kx, ky, kz] represents that the calculation unit contains k1*k2*k3 voxels.

strides: *array*

strides=[sx, sy, sz] represents the moving steps along the x, y, z.

method: *string ("spearman" or "pearson" or "kendall" or "similarity" or "distance")*

They correspond to different methods of calculation. "spearman" or "pearson" or "kendall" or "similarity" or "distance".

rescale: *Boolean (True or False)*

Rescale the values in RDM or not. True or False.

Returns:

corrs: *array*

The correlation coefficients corresponding to the RDMs.

Module ***corr_cal_by_rdm.py***

◆ eegrdms_corr(demo_rdm, EEG_rdms, method="spearman" , rescale=False)

A function for calculating the Similarity/Correlation Coefficient between RDMs based on EEG/MEG/fNIRS data and a demo RDM

Parameters:

demo_rdm: *array*

The shape must be [n_cons, n_cons].

EEG_rdm: *array*

The shape must be [n_ts, n_cons, n_cons] or [n_chls, n_cons, n_cons].

method: *string ("spearman" or "pearson" or "kendall" or "similarity" or "distance")*

They correspond to different methods of calculation. "spearman" or "pearson" or "kendall" or "similarity" or "distance".

rescale: *Boolean (True or False)*

Rescale the values in RDM or not. True or False.

Returns:

corrs: *array*

The correlation coefficients corresponding to the RDMs.

◆ fmrirdms_corr(demo_rdm, fMRI_rdms, method="spearman" , rescale=False)

A function for calculating the Similarity/Correlation Coefficient between RDMs based on fMRI data and a demo RDM

Parameters:

demo_rdm: *array*

The shape must be [n_cons, n_cons].

fmri_rdm: *array*

The shape must be [n_x, n_y, n_z, n_cons, n_cons].

method: *string ("spearman" or "pearson" or "kendall" or "similarity" or "distance")*

They correspond to different methods of calculation. "spearman" or "pearson" or "kendall" or "similarity" or "distance".

rescale: *Boolean (True or False)*

Rescale the values in RDM or not. True or False.

Returns:

corrs: *array*

The correlation coefficients corresponding to the RDMs. The shape of corrs is [n_x, n_y, n_z, 2].

Part 4: Visualization for Results

Module ***rsa_plot.py***

- plot_rdm(rdm, rescale=False)

  A function for plotting the RDM

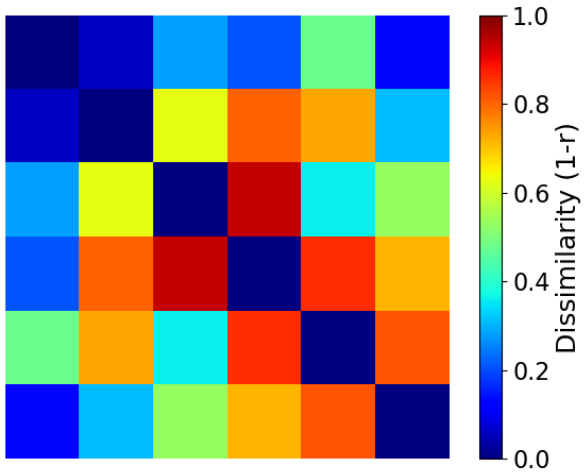
  Parameters:

  rdm: *array*

  A representational dissimilarity matrix.

  rescale: *Boolean (True or False)*

  Rescale the values in RDM or not. True or False.



- plot_rdm_withvalue(rdm, fontsize=10)

  A function for plotting the RDM with visible values

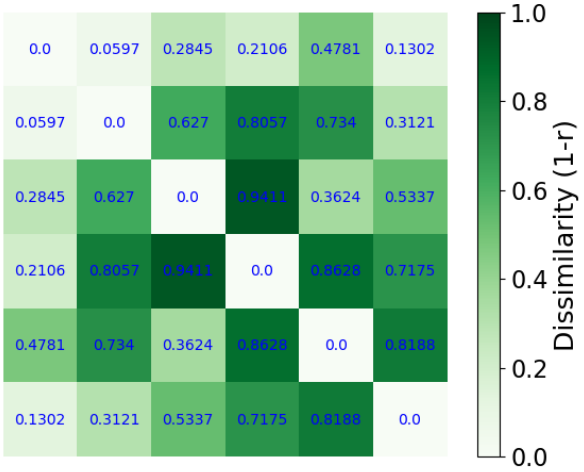
  Parameters:

  rdm: *array*

  A representational dissimilarity matrix.

  fontsize: *int / float*

  Font size of the visible values



◆ plot_corrs_by_time(corrs, labels=None, time_unit=[0, 1])

A function for plotting the correlation coefficients by time sequence

Parameters:

corrs: *array*

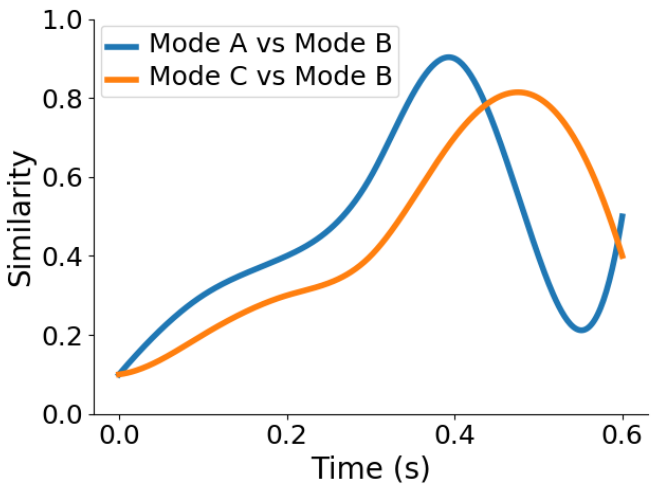
corrs represent the correlation coefficients point-by-point. Its shape must be [n_cons, ts, 2] or [n_cons, ts].

labels: array

labels represent the names of conditions of RSA results.

time_unit: *array*

time_unit=[start_t, t_step]. Here, start_t represents the start time and t_step represents the time between two adjacent time-points.



◆ plot_corrs_hotmap(eegcorrs, chllabels=None, time_unit=[0, 1], smooth=True)

A function for plotting the correlation coefficients by time sequence

Parameters:

eegcorrs: *array*

eegcorrs represent each channels' correlation coefficients point-by-point. Its shape must be [n_chls, ts, 2] or [n_chls, ts].

chllabels: *array*

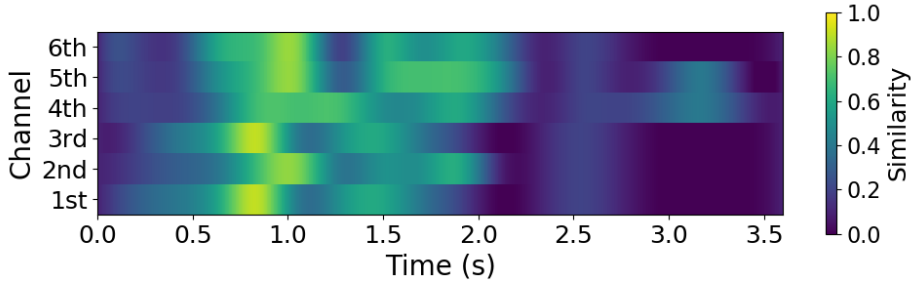
labels represent the names of channels.

time_unit: *array*

time_unit=[start_t, t_step]. Here, start_t represents the start time and t_step represents the time between two adjacent time-points.

smooth: *Boolean (True or False)*

True or False represents smoothing the results or not.



◆ plot_brainrsa_region(img, threshold=None)

A function for plotting the RSA-result regions by 3 cuts (frontal, axial, and lateral)

Parameters:

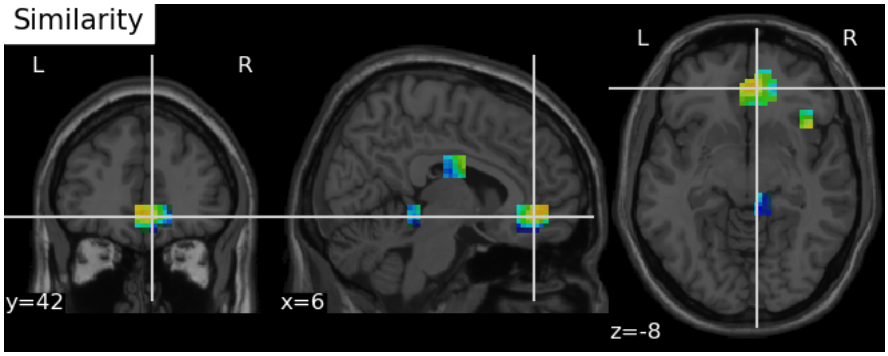
img: *Niimg-like object or the filename*

A 3-D image of the RSA result.

threshold: *None or int*

If it is an int, threshold is the number of voxels used in

correction. Only the similarity clusters consisting more than threshold voxels will be visualized. If it is None, the threshold-correction won't work.



- plot_brainrsa_montage (img, threshold=None, slice=[6, 6, 6])

A function for plotting the RSA-result by different cuts

Parameters:

img: *Niimg-like object or the filename*

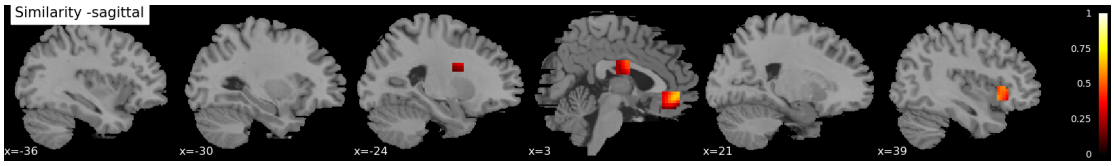
A 3-D image of the RSA result.

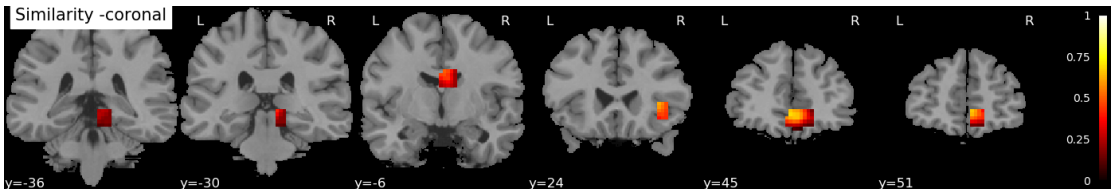
threshold: *None or int*

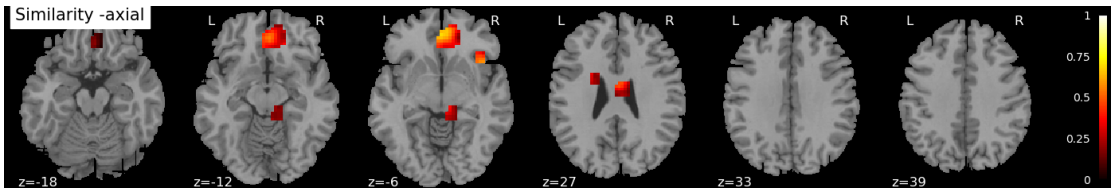
If it is an int, threshold is the number of voxels used in correction. Only the similarity clusters consisting more than threshold voxels will be visualized. If it is None, the threshold-correction won't work.

slice: *array*

slice=[nx, ny, nz]. The nx, ny, nz is the number of cuts in the x, y, z directions.







◆ plot_brainrsa_glass (img, threshold=None)

A function for plotting the 2-D projection of the RSA-result

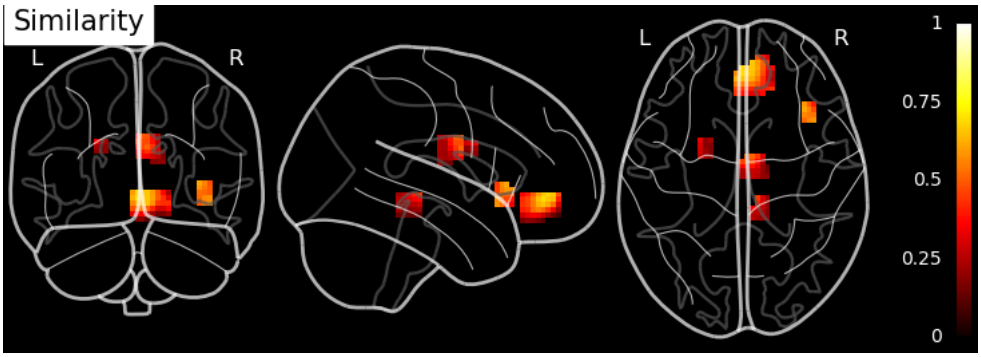
Parameters:

img: *Niimg-like object or the filename*

A 3-D image of the RSA result.

threshold: *None or int*

If it is an int, threshold is the number of voxels used in correction. Only the similarity clusters consisting more than threshold voxels will be visualized. If it is None, the threshold-correction won't work.



◆ plot_brainrsa_surface (img, threshold=None)

A function for plotting the RSA-result into a brain surface

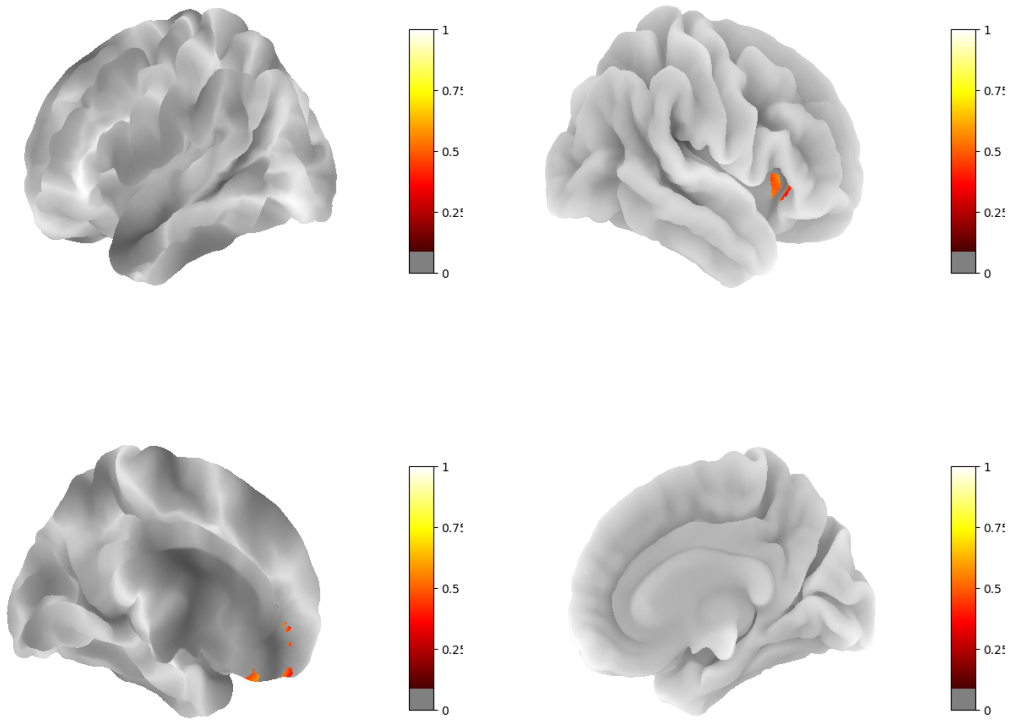
Parameters:

img: *Niimg-like object or the filename*

A 3-D image of the RSA result.

threshold: *None or int*

If it is an int, threshold is the number of voxels used in correction. Only the similarity clusters consisting more than threshold voxels will be visualized. If it is None, the threshold-correction won't work.



◆ plot_brainrsa_rlts (img, threshold=None, slice=[6, 6, 6])

A function for plotting the RSA-result by a set of images

Parameters:

img: *Niimg-like object or the filename*

A 3-D image of the RSA result.

threshold: *None or int*

If it is an int, threshold is the number of voxels used in correction. Only the similarity clusters consisting more than threshold voxels will be visualized. If it is None, the threshold-correction won't work.

slice: *array*

slice=[nx, ny, nz]. The nx, ny, nz is the number of cuts in the x, y, z directions.

Part 5: Save as a NIfTI file (for fMRI)

Module ***corr_to_nii.py***

- corr_save_nii(corrs, filename, affine, size=[60, 60, 60], ksize=[3, 3, 3], strides=[1, 1, 1], p=1, r=0, similarity=0, distance=0, correct_method=None, correct_n=27)

  A function for saving the correlation coefficients as a .nii file

  Parameters:

  corrs: *array*

  corrs represent the correlation coefficients. Its shape must be [n_x, n_y, n_z, 2].

  filename: *string*

  The filename of the NIfTI file. Don't need a suffix.

  affine: *array*

  An affine array that tells you the position of the image array data in a reference space.

  size: *array*

  size=[x, y, z] represents that the size of the original data.

  ksize: *array*

  ksize=[kx, ky, kz] represents that the calculation unit contains k1*k2*k3 voxels.

  strides: *array*

  strides=[sx, sy, sz] represents the moving steps along the x, y, z.

  p, r, similarity, distance: *float*

  They represent the threshold value for calculation.

  correct_method: *None / 'FWE' / 'FDR'*

  The method for correction.

  correct_n: *int*

  The number of voxels used in correction.

Returns:

img_nii: *array*

The matrix form of the NIfTI file.

Part 6: Others

Module ***stuff.py***

- limtozero(x)

  A function for zeroing the value close to zero.

  Parameters:

  x: *float*

  A value.

  Returns:

  0

- get_affine(file_name)

  A function for getting the affine.

  Parameters:

  file_name: *string*

  The file_name of a fMRI file.

  Returns:

  affine: *array*

  An affine array that tells you the position of the image array data in a reference space.

- fwe_correct(p, size=[60, 60, 60], n=64)

  A function for FWE correction.

  Parameters:

  p: *array*

  A 3-D array of p-values, the number of p-value is the same as

the number of RSA calculation units in fMRI. Users can get p by corrs (Code: *p = corrs[:, :, :, 1]*).

size: *array*

size=[x, y, z] represents that the size of the original data.

n: *array*

The number of voxels used in correction.

Returns:

correctp: *array*

The FWE corrected p-values. A 3-D array of p-values, the number of p-value is the same as the number of RSA calculation units in fMRI.

- fdr_correct(p, size=[60, 60, 60], n=64)

A function for FDR correction.

Parameters:

p: *array*

A 3-D array of p-values, the number of p-value is the same as the number of RSA calculation units in fMRI. Users can get p by corrs (Code: *p = corrs[:, :, :, 1]*).

size: *array*

size=[x, y, z] represents that the size of the original data.

n: *array*

The number of voxels used in correction.

Returns:

correctp: *array*

The FDR corrected p-values. A 3-D array of p-values, the number of p-value is the same as the number of RSA calculation units in fMRI.

- correct_by_threshold(img, threshold)

A function for fMRI correction by threshold (the number of voxels).

Parameters:

img: *array*

A 3-D array of the RSA result.

threshold: *n*

The number of voxels used in correction. Only the similarity clusters consisting more than threshold voxels will be visualized.

Returns:

img: *array*

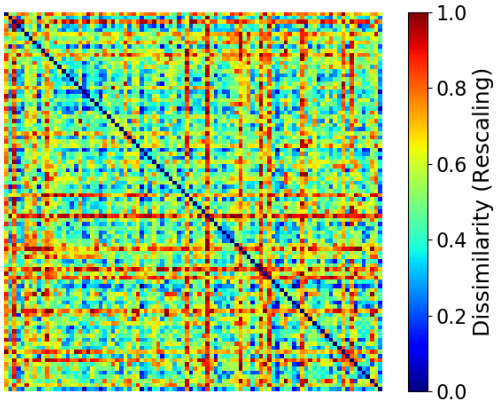
A 3-D array of the threshold-corrected RSA result.

Part 7: Demo

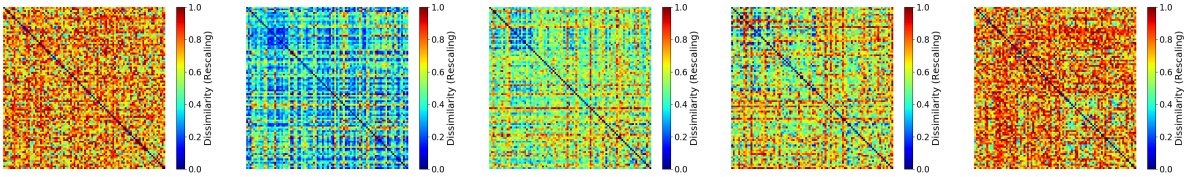
Here is a demo based on the publicly available visual-92-categories-task MEG datasets. (*Reference:* Cichy, R. M., Pantazis, D., & Oliva, A. "Resolving human object recognition in space and time." Nature neuroscience (2014): 17(3), 455-462.) MNE-Python has been used to load this dataset.

```
# -*- coding: utf-8 -*-

' a demo based on visual-92-categories-task MEG data '
# Here, we use MNE-Python toolbox for loading data and processing

__author__ = 'Zitong Lu'

import numpy as np
import os.path as op
from pandas import read_csv
import mne
from mne.io import read_raw_fif
from mne.datasets import visual_92_categories
from neurora.rdm_cal import eegRDM
from neurora.rdm_corr import rdm_correlation_spearman
from neurora.corr_cal_by_rdm import rdms_corr
from neurora.rsa_plot import plot_rdm
from neurora.rsa_plot import plot_corrs_by_time


"""       Section 1: loading data and preprocessing       """
""" you can learn this process from MNE-Python (https://mne-
tools.github.io/stable/index.html) """

data_path = visual_92_categories.data_path()
fname = op.join(data_path, 'visual_stimuli.csv')
conds = read_csv(fname)
conditions = []
for c in conds.values:
    cond_tags = list(c[:2])
    cond_tags += [('not-' if i == 0 else '') + conds.columns[k]
                  for k, i in enumerate(c[2:], 2)]
    conditions.append('/'.join(map(str, cond_tags)))
```

```
event_id = dict(zip(conditions, conds.trigger + 1))
print(event_id)
sub_id = [0, 1, 2]
megdata = np.zeros([3, 92, 306, 1101], dtype=np.float32)
subindex = 0
for id in sub_id:
    fname = op.join(data_path, 'sample_subject_'+str(id)+'_tsss_mc.fif')
    raw = read_raw_fif(fname)
    events = mne.find_events(raw, min_duration=.002)
    events = events[events[:, 2] <= 92]
    subdata = np.zeros([92, 306, 1101], dtype=np.float32)
    for i in range(92):
        epochs = mne.Epochs(raw, events=events, event_id=i + 1,
baseline=None,
                            tmin=-0.1, tmax=1, preload=True)
        data = epochs.average().data
        print(i, data.shape)
        subdata[i] = data
    megdata[subindex] = subdata
    subindex = subindex + 1

# the shape of MEG data: megdata is [3, 92, 306, 1101]
# n_subs = 3, n_conditions = 92, n_channels = 306, n_timepoints = 1101
(-100ms to 1000ms)


"""       Section 2: Calculating single RDM and Plotting        """

# shape of megdata: [n_subs, n_cons, n_chls, n_ts] -> [n_cons, n_subs,
n_chls, n_ts]
megdata = np.transpose(megdata, (1, 0, 2, 3))

# shape of megdata: [n_cons, n_subs, n_chls, n_ts] -> [n_cons, n_subs,
n_trials, n_chls, n_ts]
# here data is averaged, so set n_trials = 1
megdata = np.reshape(megdata, [92, 3, 1, 306, 1101])

# Calculate the RDM based on the data during 190ms-210ms
rdm = eegRDM(megdata[:, :, :, :, 290:310])

# Plot this RDM
plot_rdm(rdm, rescale=True)
```




```
"""      Section 3: Calculating RDMs and Plotting       """

# Calculate the RDMs by a 10ms time-window
# (raw sampling requency is 1000Hz, so here
time_win=10ms/(1s/1000Hz)/1000=10)
rdms = eegRDM(megdata, time_win=10, time_opt=1)

# Plot the RDM of 0ms, 50ms, 100ms, 150ms, 200ms
times = [10, 20, 30, 40, 50]
for t in times:
    plot_rdm(rdms[t], rescale=True)
```

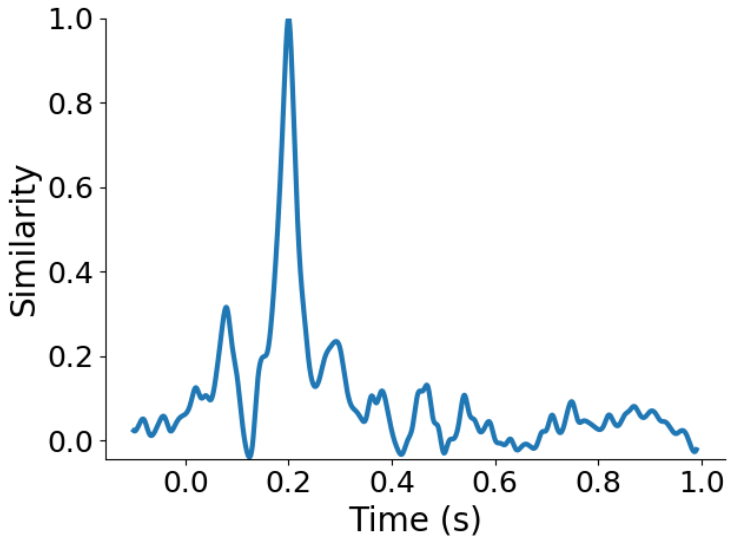


```
"""      Section 4: Calculating the Similarity between two RDMs     """

# RDM of 200ms
rdm_sample1 = rdms[20]
# RDM of 800ms
rdm_sample2 = rdms[90]

# calculate the correlation coefficient between these two RDMs
corr = rdm_correlation_spearman(rdm_sample1, rdm_sample2, rescale=True)
```

```
SpearmanrResult(correlation=0.02665680483550596, pvalue=0.08462337954774739)
```

```
"""      Section 5: Calculating the Similarity and Plotting       """
```

```
# Calculate the representational similarity between 200ms and all the
time points
corrs1 = rdms_corr(rdm_sample1, rdms)

# Plot the corrs1
corrs1 = np.reshape(corrs1, [1, 110, 2])
plot_corrs_by_time(corrs1, time_unit=[-0.1, 0.01])
```




```
# Calculate and Plot multi-corrs
corrs2 = rdms_corr(rdm_sample2, rdms)
corrs = np.zeros([2, 110, 2])
corrs[0] = corrs1
corrs[1] = corrs2
labels = ["by 200ms's data", "by 800ms's data"]
plot_corrs_by_time(corrs, labels=labels, time_unit=[-0.1, 0.01])
```