

# Tutorial of NeuroRA Version 1.0.7.4

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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](mailto: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

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## Part 1: Introduction

**NeuroRA** 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 providing 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.

## **Paper**

Lu, Z., & Ku, Y. *NeuroRA: A Python toolbox of representational analysis from multi-modal neural data*. (bioRxiv: <https://doi.org/10.1101/2020.03.25.008086>)

## Part 2: Data Conversion

Type of Neural Bata	Data Conversion Scheme
<b>fMRI</b>	<p>Use <i>Nibabel</i> (<a href="https://nipy.org/nibabel/">https://nipy.org/nibabel/</a>) to load fMRI data.</p> <pre>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 .....</pre>
<b>EEG/MEG</b>	<p>Use <i>MATLAB EEGLab</i> (<a href="http://sccn.ucsd.edu/eeglab/">http://sccn.ucsd.edu/eeglab/</a>) to do preprocessing and obtain .mat files, and use <i>Scipy</i> (<a href="https://www.scipy.org">https://www.scipy.org</a>) to load EEG data (.mat).</p> <pre>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 .....</pre> <p>Or use <i>MNE</i> (<a href="https://mne-tools.github.io">https://mne-tools.github.io</a>) to do preprocessing and return <i>ndarray</i>-type data.</p>
<b>fNIRS</b>	<p>For raw data from device, use <i>Numpy</i> (<a href="http://www.numpy.org">http://www.numpy.org</a>) to load fNIRS data (.txt or .csv).</p> <pre>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) .....</pre>
<b>ECoG/sEEG</b>	<p>Use <i>Brainstorm</i> (<a href="https://neuroimage.usc.edu/brainstorm/">https://neuroimage.usc.edu/brainstorm/</a>) to do preprocessing and obtain .mat files, and use <i>Scipy</i> to load ECoG data (.mat).</p>
<b>Electrophysiology</b>	<p>Use <i>pyABF</i> (<a href="https://github.com/sw Harden/pyABF">https://github.com/sw Harden/pyABF</a>) to load electrophysiology data (.abf).</p> <pre>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 .....</pre>
<p>Two functions, <i>NumPy.reshape()</i> &amp; <i>NumPy.transpose()</i>, are recommended for further data transformation</p>	

## 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\_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**

◆ **eegrdsms\_corr**(demo\_rdm, EEG\_rdsms, 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\_rdm, 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*

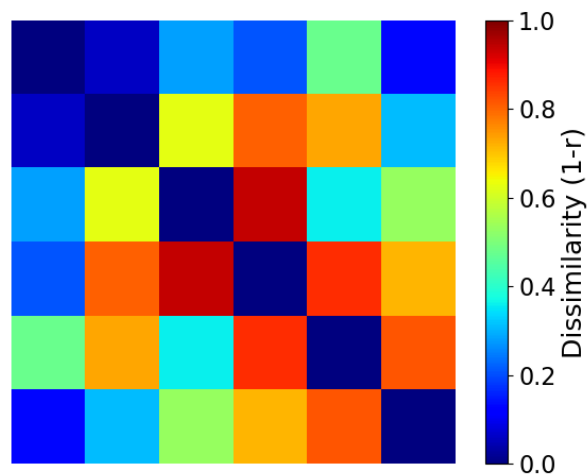
Parameters:

`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*

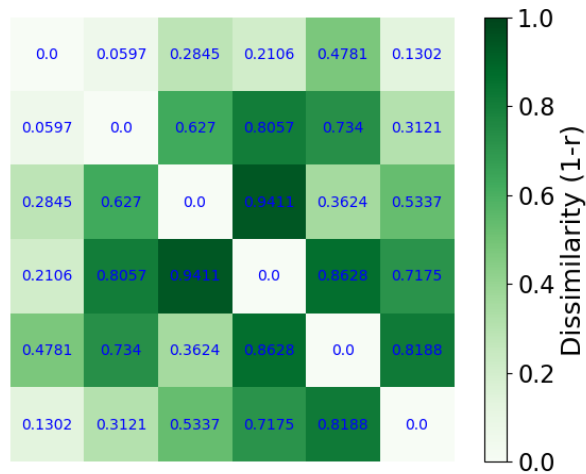
Parameters:

`rdm:` *array*

A representational dissimilarity matrix.

`fontsize:` *int / float*

Font size of the visible values



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

*A function for plotting the correlation coefficients by time sequence*

Parameters:

**corr:** *array*

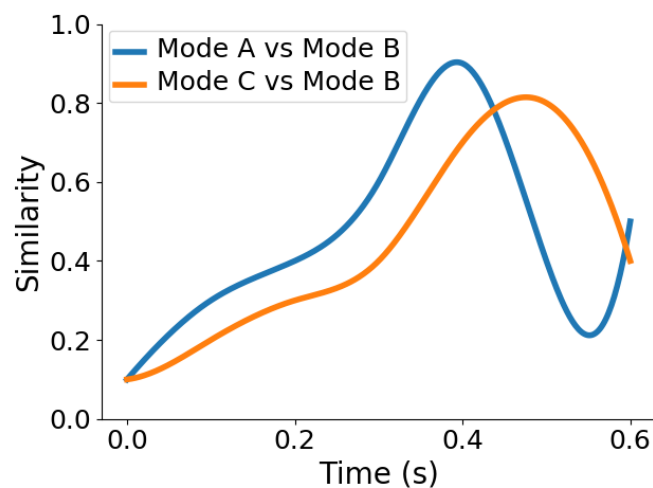
**corr** represent the correlation coefficients point-by-point. Its shape must be `[n_cons, ts, 2]` or `[n_cons, ts]`.

**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*

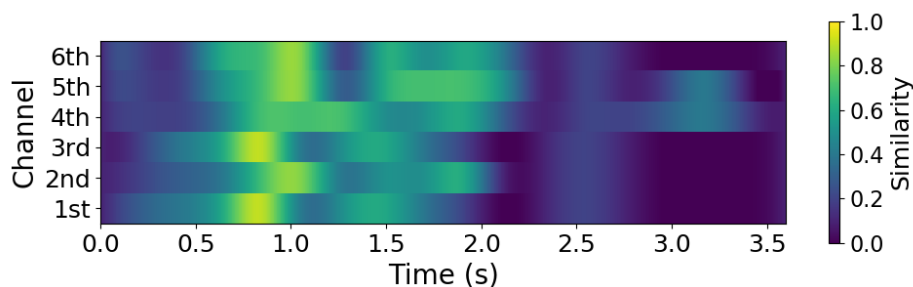
`labels` represent the names of channels.

`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:

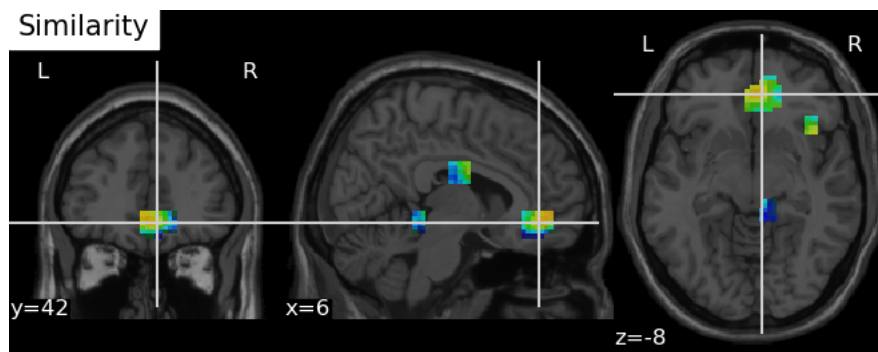
`img`: *Niimg-like object or the filename*

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*

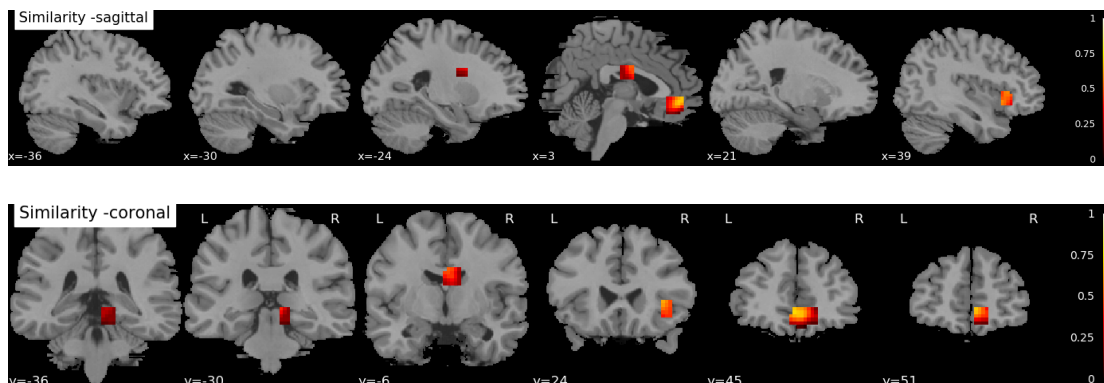
A 3-D image of the RSA result.

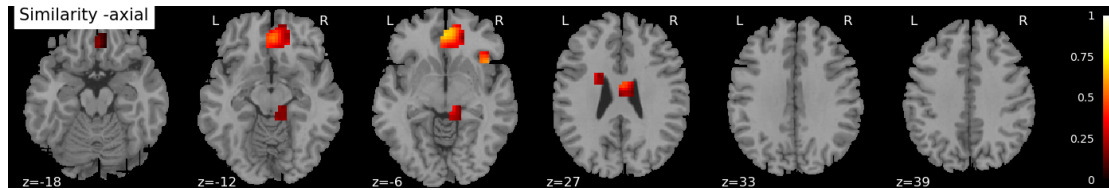
**threshold:** *None or int*

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*

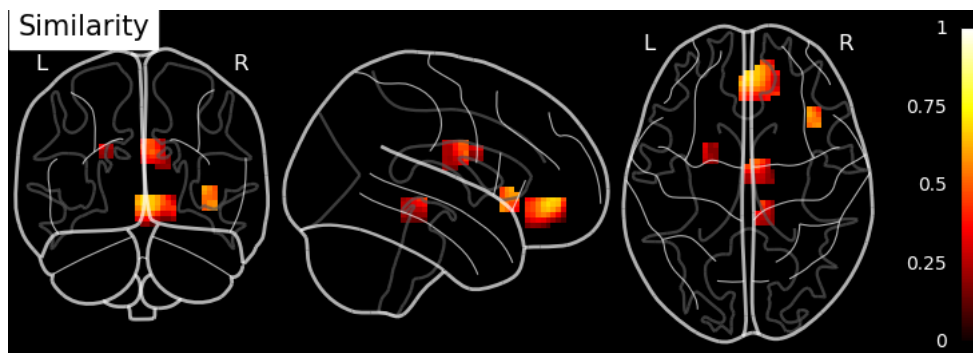
Parameters:

**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*

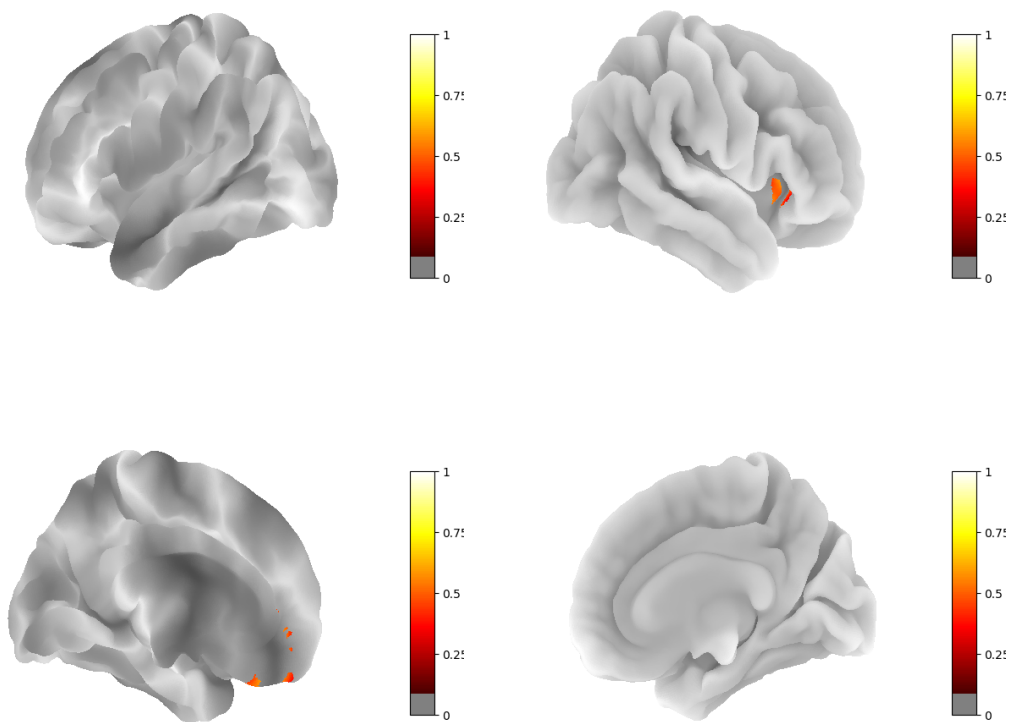
Parameters:

**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(corr, 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:

`corr:` *array*

`corr` 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      """

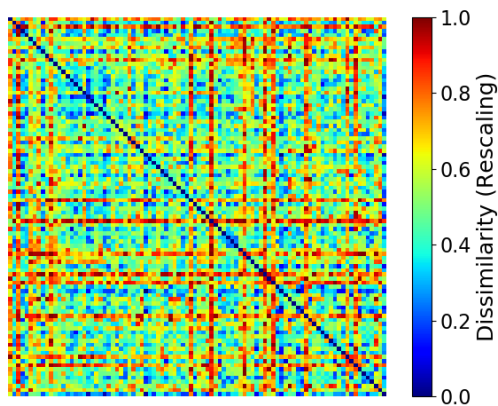
# shape of megdata: [n_subs, n_cons, n_chls, n_ts] -> [n_cons, n_subs,
n_chls, n_ts]
megdata = np.transpose(megdata, (1, 0, 2, 3))

# 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)

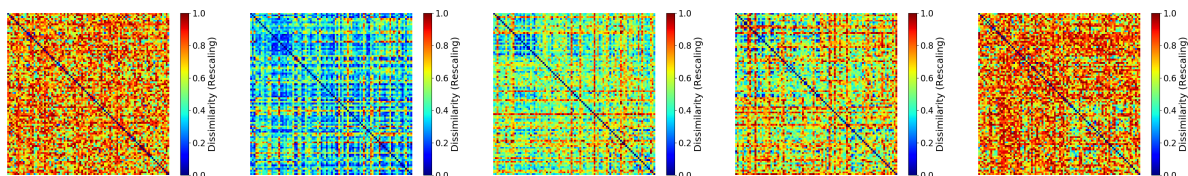
```



### Section 3: Calculating RDMs and Plotting

```
# Calculate the RDMs by a 10ms time-window
# (raw sampling frequency 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)
```

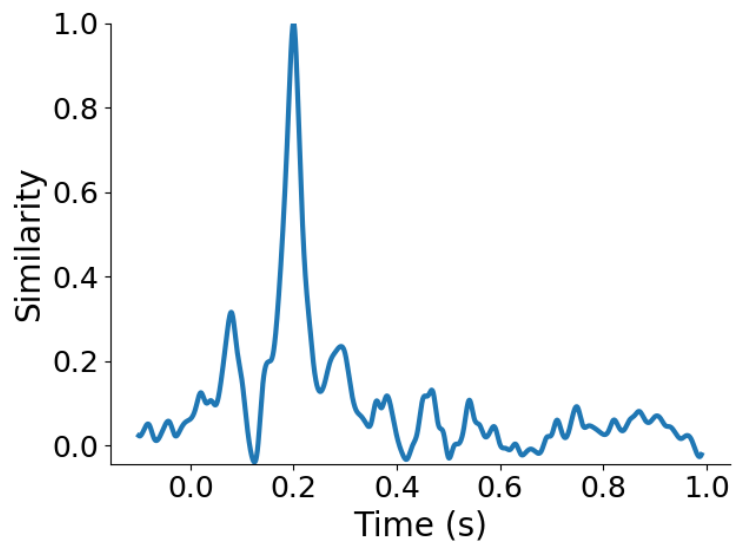
SpearmanrResult(correlation=0.02665680483550596, pvalue=0.08462337954774739)

### 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])
```

