NeuroRA: A Python Toolbox of Representational Analysis from Multi-modal Neural Data

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Running title: NeuroRA: RSA toolbox in Python

Abstract

In studies of cognitive neuroscience, multivariate pattern analysis (MVPA) is widely used as it offers richer information than traditional univariate analysis. Representational similarity analysis (RSA), as one method of MVPA, has become an effective decoding method based on neural data by calculating the similarity between different representations in the brain under different conditions. Moreover, RSA is suitable for researchers to compare data from different modalities, and even bridge data from different species. However, previous toolboxes have been made to fit for specific datasets. Here, we develop a novel and easy-to-use toolbox based on Python named NeuroRA for representational analysis. Our toolbox aims at conducting cross-modal data analysis from multi-modal neural data (e.g. EEG, MEG, fNIRS, ECoG, sEEG, neuroelectrophysiology, fMRI), behavioral data, and computer simulated data. Compared with previous software packages, our toolbox is more comprehensive and powerful. By using NeuroRA, users can not only calculate the representational dissimilarity matrix (RDM), which reflects the representational similarity between different conditions, but also conduct a representational analysis among different RDMs to achieve a cross-modal comparison. In addition, users can save the results as NIfTI files based on fMRI data and plot the results as they wish. We introduce the structure, modules, features, and algorithms of NeuroRA in this paper, as well as examples applying the toolbox in published datasets.

Keywords:

Representational similarity analysis; multivariate pattern analysis; multi-modal; python; correlation analysis.

Introduction

In recent years, research on brain science based on neural data has shifted from univariate analysis towards multivariate pattern analysis (MVPA) (Norman et al., 2006). In contrast to the former, the latter accounts for the population coding for neurons. The decoding of neural activity can help scientists better understand the encoding process of neurons. As in David Marr's model, representation bridges the gap between a computation goal and implementation machinery (Marr, 1982). Representational similarity analysis (RSA) (Kriegeskorte et al., 2008a) is an effective MVPA method that can successfully describe the relationship between representations of different modalities of data, bridging gaps between human and animals. Therefore,

RSA has been rapidly applied in investigating various cognitive functions, including perception (Evans et al., 2015; Henriksson et al., 2019), memory (Xue et al., 2010), language (Chen et al., 2016), and decision-making (Yan et al., 2016).

With the technological development in brain science, various neural recording methods have emerged rapidly. Noninvasive neurophysiological recordings such as electroencephalography (EEG) and magnetoencephalography (MEG) with high temporal resolution, and neuroimaging methods such as functional near-infrared spectroscopy (fNIRS) and functional magnetic resonance imaging (fMRI) with high spatial resolution, have been widely used for basic research. Meanwhile, invasive techniques such as electrocorticography (ECoG), stereo-electro-encephalography (sEEG), and neuroelectrophysiology have been applied to patients or non-human primates. The interpretation of results across different recording modalities becomes difficult. The RSA method, however, uses a representation dissimilarity matrix (RDM) to bridge data from different modalities. For example, studies have attempted to combine fMRI results with electrophysiological results (Kriegeskorte et al., 2008b) or MEG results with electrophysiological results (Cichy et al., 2014). Moreover, it can connect behavioral and neural representational matrices (Wang et al., 2018). Furthermore, with the rapid development of artificial intelligence (AI) (Jordan and Mitchell, 2015; Kriegeskorte and Golan, 2019), RSA can be used to compare representations in artificial neural networks (ANN) with those in EEG (Greene and Hansen, 2018). In summary, RSA is a useful tool to combine the results of behavior and multi-modal neural data, which can lead to a better understanding of the brain, and even further, can help us establish a clearer link between the brain and artificial intelligence (Khaligh-Razavi and Kriegeskorte, 2014; Güçlü and van Gerven, 2015; Eickenberg et al., 2017; Greene and Hansen, 2018b; Kuzovkin et al., 2018).

Some existing tools for RSA include a module in MNE-Python, a module in PyMVPA, and a toolbox for RSA by Kriegeskorte (Nili et al., 2014). However, they all have some shortcomings. MNE can only perform RSA for MEG and EEG data. PyMVPA can only implement some basic functions, such as calculating the correlation coefficient and data conversion. Kriegeskorte's toolbox attached to their paper is designed mainly based on their own research data (Kriegeskorte et al., 2008b), which makes it difficult to generate to other datasets. We considered build a comprehensive and universal toolbox for RSA, and Python was chosen as a suitable programming language. Python is a rapidly rising programming language having great advantages for scientific computing (Sanner, 1999; Koepke, 2011). Because of its strong expansibility, it is more accommodating to use Python for computing and incorporate a toolbox inside it. NumPy (Van et al., 2011), Scikit-learn (Pedregosa et al.,

2013), and some other extensions can realize and simplify various basic computing functions. Thus, a number of researchers select Python to develop toolkits in psychology and neuroscience, such as PsychoPy (Peirce, 2007) for designing psychological experiment programs, MNE-Python (Gramfort et al., 2013) for EEG/MEG data analysis, and PyMVPA (Hanke et al., 2009) for utilizing MVPA in data from different modalities.

In the present toolbox, we have developed a novel and easy-to-use Python toolbox, NeuroRA (neural representational analysis), for comprehensive representation analysis. NeuroRA aims at using powerful computational resources with Python and conducting cross-modal data analyses for various types of neural data (e.g. EEG, MEG, fNIRS, fMRI), as well as behavioral data and computer stimulation data. NeuroRA requires some basic Python packages to function, including NumPy, Nibabel (Brett et al., 2016), and Matplotlib (Hunter, 2007). In the following sections, we detail the structure and function of NeuroRA and further apply it to an open dataset from a published study (Kriegeskorte, 2008).

Overview of NeuroRA

The structure and functions of NeuroRA are illustrated in **Fig. 1**. It can analyze all types of neural (including EEG, MEG, fNIRS, ECoG, sEEG, electrophysiological and fMRI data) and behavioral data. By utilizing the powerful computational toolbox in Python, NeuroRA gives users the ability to mine neural data thoroughly and efficiently.

First, NeuroRA can calculate RDMs from different modalities. An RDM reflects the representation similarity between different conditions/stimuli with neural data from a given modality. All values in the matrix are normalized, and the value at any point in the matrix reflects the dissimilarity of the data representation under the two conditions corresponding to the row and column respectively. Because the points on the diagonal are compared under the same conditions, they are identical, which implies that the dissimilarity value is 0. Second, NeuroRA performs a correlation analysis between RDMs from different modalities to compare representations across modalities. This procedure can be applied according to different parameters; for example, the calculation can be applied for each subject, for each channel, for each time-point, or a combination of all of them. Third, NeuroRA provides a unique and handy approach to saving the result of a representational analysis specific to fMRI data. Users can define the threshold of output parameters, and a NIfTI file can be obtained afterwards. Fourth, NeuroRA also provides some functions to visualize the results, such as RDMs and correlation coefficients across different time points.

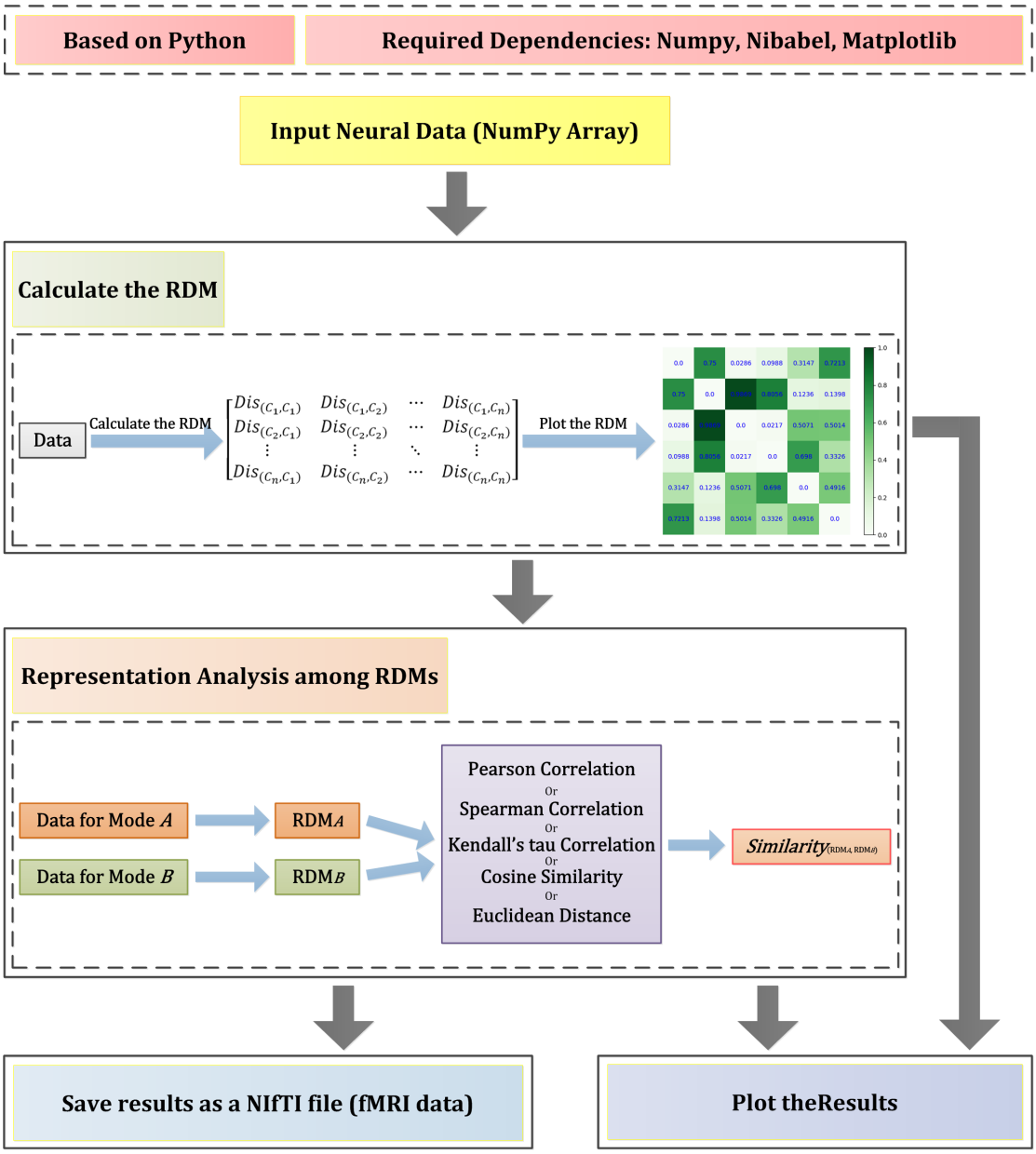

Fig. 1 Overview of NeuroRA. NeuroRA is a Python-based toolbox and requires some extension packages, including NumPy, Nibabel, and Matplotlib. It contains four main functions: calculating the RDM, comparing representations among different modalities using RDMs, saving results as a NIfTI file for fMRI data, and plotting the results. The specific implementation of these features is listed in the main text.

The pre-required packages for NeuroRA include NumPy, NiBabel, and Matplotlib. NumPy assists with matrix-based computation. NiBabel is used to generate NIfTI files. Matplotlib is employed for the plotting functions. Users can download NeuroRA through only one line of command: *pip install neurora*. The website for our toolbox is https://neurora.github.io/NeuroRA/, and the GitHub URL for its source code is https://github.com/neuora/NeuroRA.

Data Structures in NeuroRA

The calculations in NeuroRA are all based on multidimensional matrices, including deformation, transposition, decomposition, standardization, addition, and subtraction. The data type in NeuroRA is *ndarray*, an array class of NumPy. Therefore, users first convert their neural data into a matrix (*ndarray* type) as the input of NeuroRA, with information on the different dimensions of the matrix, such as the number of subjects, number of conditions, number of channels, and size of the image (see instructions in the software for details). Here, we give users some feasible methods for data conversion for different kinds of neural data in **Tabel 1**.The outputs of the functions in NeuroRA are square matrices with the same dimensions as the input matrix. The input and output data structures of the NeuroRA functions are shown in the tutorial attached in the website.

Table 1. Recommeded data conversion scheme

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	

NeuroRA's Modules and Features

NeuroRA attains various functions to process the representational analysis. Usually, data must be processed in multi-step ways, and this toolkit highly integrates these intermediate processes, making it easy to implement. In NeuroRA, only a simple function is required to complete the following processes. Users can obtain the required results after a necessary conversion of the data format.

Meanwhile, we attempt to add some adjustable parameters to meet the calculation requirements for different experiments and different modalities of data. Users can flexibly change the input parameters in the function to match their data format and computing goals.

NeuroRA mainly includes the following core modules, and more modules could be added in the future or as requested.

rdm_cal: A module to calculate RDM based on multi-modal neural data.

rdm_corr: A module to calculate the correlation coefficient between two RDMs, based on different algorithms, including Pearson correlation, Spearman correlation, Kendalls tau correlation, cosine similarity, and Euclidean distance.

corr_cal & corr_cal_byrdm: Two modules to calculate the representational similarities among the data or RDMs under different different conditions.

corr_to_nii: A module to save the correlation coefficients in a .nii file.

rsa_plot: A module to plot the RSA results. It contains the functions of plotting the RDM, plotting the correlation coefficients obtained from different

time points and the hotmap of correlation results by time sequence based on EEG/MEG data.

➢ Calculate the RDM

An RDM is a typical approach for comparing representations in neural data. By extracting data from two different conditions and calculating the correlations between them, we will obtain the similarity between the two representations under the two conditions. Subtract the obtained similarity index from 1 and get the values of the dissimilarity index in RDM (**Fig. 2**). In Fig 2, Different grating stimuli were observed to product different neural activity signals, and the value in RDM presented the dissimilarity of neural activities between two different stimuli. As shown in the figure, the closer the two grating orientations were, the lower the dissimilarity would be. In a typical object recognition experiment, humans and monkeys were allowed to watch the same sets of visual stimuli (Kriegeskorte, 2008). Researchers calculated the humans' RDM based on fMRI data and the monkeys' RDM based on electrophysiological data. The results indicated that the neural patterns in RDMs were similar when humans and monkeys observed stimuli belonged to the same category (animate or inanimate).

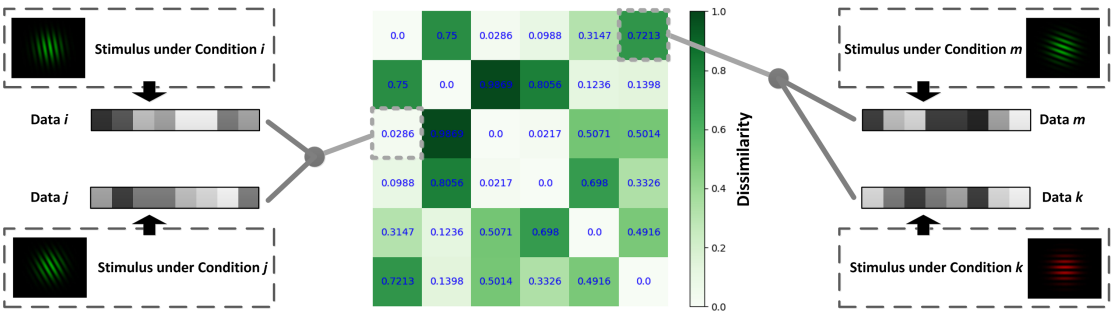

Fig. 2 Schematic diagram for calculating the RDM. Different data can be obtained under different conditions. The value of the point [*i*, *j*] in RDM is obtained by calculating the dissimilarity (1-correlation coefficient *r*) between the data under condition *i* and that under condition *j*.

The application of calculating RDM is not restricted. NeuroRA achieves computations based on multiple modal neural data from behavioral data to brain imaging data (**Fig. 3**).

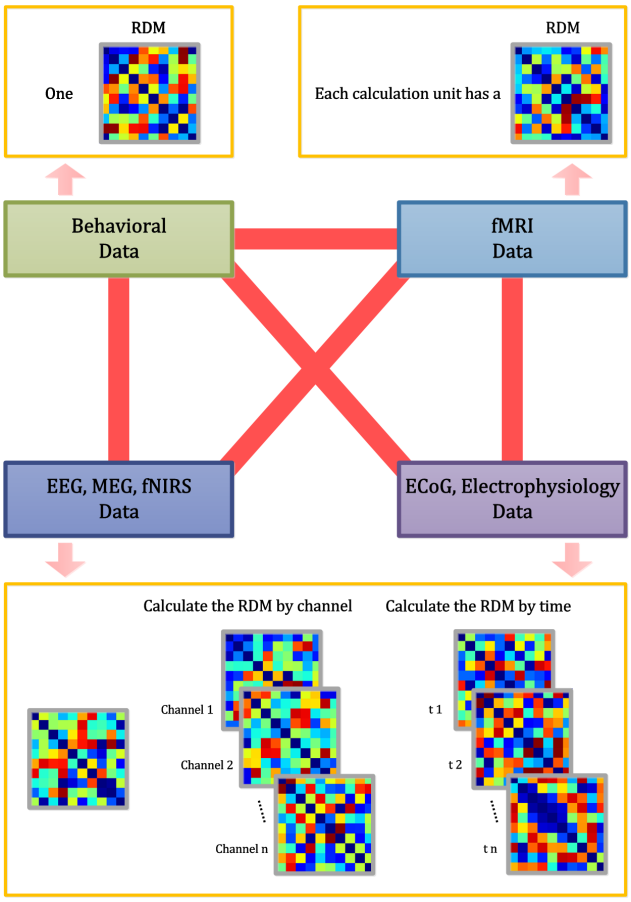

Fig. 3 Range of the feature of calculating the RDM. NeuroRA is capable of calculating data in a variety of modes, including behavior, fMRI, EEG, MEG, fNIRS, ECoG, sEEG, and electrophysiology. The red bold lines denote the ability to perform calculations between two modes.

Assuming that the measured data from a certain condition under a total of *n* experimental conditions are denoted as $d_1, d_2, \ldots, d_n$, then the following RDM of $n \times n$ can be calculated by the corresponding function under the rdm_cal module from our toolkit:

$$RDM = \begin{pmatrix} D_{11} & D_{12} & \cdots & D_{1n} \\ \vdots & \vdots & \ddots & \vdots \\ D_{n1} & D_{n2} & \cdots & D_{nn} \end{pmatrix}$$

where D_{ij} denotes the dissimilarity between the data under condition *i* and that under condition *j*. The dissimilarity (D_{ij}) is calculated as follows:

$$D_{ij} = 1 - correlation(d_i, d_j)$$

In certain cases, researchers must calculate RDM separately for each participant, or they may calculate RDM independently for each channel or

each time point (Henriksson et al., 2019; Hall-McMaster et al., 2019) (**Fig. 3**). We resolve these issues at the beginning of NeuroRA. The toolkit provides several input parameters in the functions that allow users to make the corresponding changes. Users can change the calculation parameters according to their requirements, and consequently, the corresponding output formats change.

➢ Representational Analysis among different RDMs

NeuroRA provides a convenient way to calculate cross-modality similarity by computing the similarities between two RDMs from different modalities. We offer several solutions to calculate the similarity (or correlation coefficient), including Pearson correlation, Spearman correlation, Kendalls tau correlation, cosine similarity, and Euclidean distance. Users can freely change parameters to select different computing methods.

In these calculation process, we first reform the square matrices into vectors and then calculate similarities (**Fig. 4**). Some previous studies calculated the correlation coefficient between two RDMs by using the diagonal values, which makes the result deceptively high (Ritchie et al., 2017). We avoid this by removing the diagonal values and include only half of the matrix to reduce the duplication, as the upper and lower halves of the RDM are actually identical (**Fig. 4**).

Furthermore, NeuroRA provides a permutation test to determine whether the two RDMs are related. The permutation test is based on random shuffling of data and is suitable for data with a small sample size (Efron and Tibshirani, 1994). We first shuffle the values in the two RDMs and re-calculate the similarity matrix between the two RDMs. By repeating this procedure 1000 times (the number of iterations here can be defined by users), a distribution of the null similarity matrix is obtained. We then compare the result from the data and the obtained random distribution, and we obtain the *p*-values for the similarity obtained from the real data.

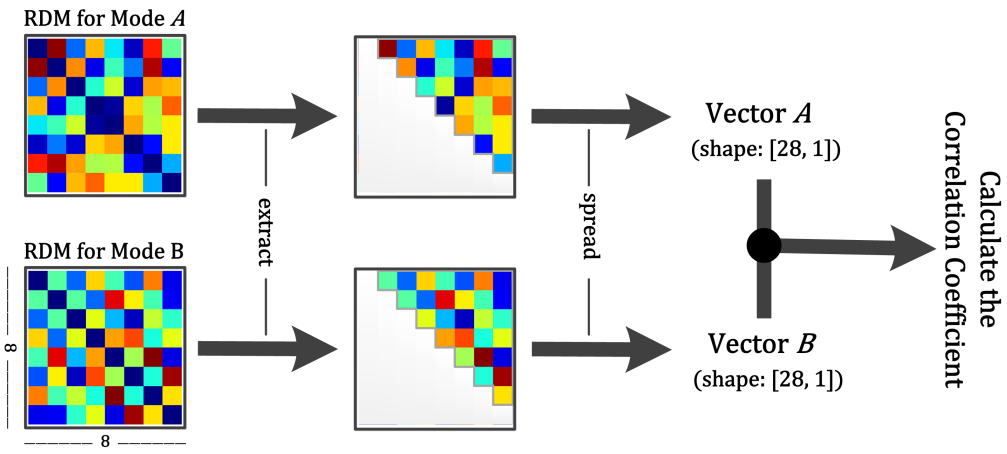

Fig. 4 Schematic diagram for calculation between two RDMs. Step 1: Obtain two RDMs from different modal data. Step 2: Extract the points of the upper diagonal (within the grey line). Step 3: Spread them as vectors. Step 4: Calculate the correlation coefficient or conduct a permutation test between two vectors. The former returns the correlation coefficient and the *p*-value, and the latter returns only the *p*-value.

NeuroRA can also perform calculations based on multiple RDMs. Consequently, we can expand it to conditions with multiple RDMs. When you obtain a behavioral RDM from behavioral data and wish to compare it with other modal data, a problem may arise as more than one RDM can be obtained based on other modal data, such as EEG or fMRI. Typically, calculations based on EEG data can obtain one RDM per channel or time interval. To determine which brain region or time interval is more relevant to behavior, our toolbox provides ergodic computations (**Fig. 3**). A simple example is when the users want to see which brain regions are highly correlated with behavioral performance, they can get one behavioral RDM based on behavioral response time or accuracy and they may also get many fMRI RDMs from different regions. Users can just put these two kinds of data (behavioral data and fMRI data) into our function, and they will get results showing the high-correlated regions (**Tabel 2**). These convenient functions of ergodic computation cover the vast majority of cross-modal research needs.

To maximally simplify users' experience, our toolbox offers a one-step option (**Tabel 2 Scheme 2**). Users can input data from two modalities, and the toolbox will return the final results of representation analysis. This will be very convenient and efficient when the users do not need to obtain the RDMs in the intermediate stages.

➢ Save Results as a NIfTI file for fMRI data

In the field of cognitive neuroscience, fMRI research constitutes a large proportion. Researchers typically wish to calculate RDMs for different brain

regions and overlay the statistical results with images obtained from other software such as SPM, BrainVoyager, and FreeSurfer. NeuroRA provides a unique function to return the statistics in a NIfTI file (**Fig 5**, **Table 3**). Users can then overlay the output .nii file calculated by our toolbox onto a standard template in other software to clearly observe the statistics across different brain regions.

Users can customize the size of the basic calculation unit $[k_x, k_y, k_z]$. Each *k* indicates the number of voxels along the corresponding axis. The strides between different calculation unit must be decided as $[s_x, s_y, s_z]$. The strides refer to how far the calculation unit is moved before another computation is made. Each *s* indicates how many voxels exist between two adjacent calculation units along the corresponding axis. For the fMRI data of size [*X*, *Y*, *Z*], the kernel size is usually set to be more than one voxel, so each voxel can exist in multiple kernels (calculation units). Therefore, *N* computations are required here:

$$N = (\lfloor (X - k_x)/s_x \rfloor + 1) \times (\lfloor (Y - k_y)/s_y \rfloor + 1) \times (\lfloor (Z - k_z)/s_z \rfloor + 1)$$

This implies that *N* RDMs must be calculated, which are each related to the target RDM. In NeuroRA, the final correlation coefficient of one voxel is the mean value of the correlation coefficients calculated by all kernels that contain this voxel.

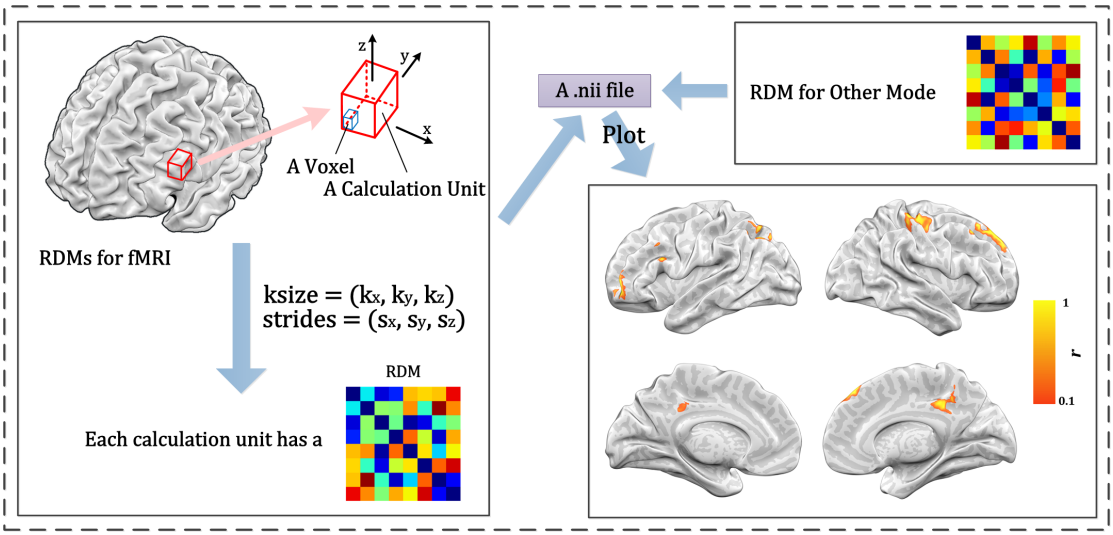

Fig. 5 Schematic diagram for calculation based on fMRI data. Users define the size and strides of the calculation unit. After computations between the RDMs for fMRI and the RDM for other modes (e.g. behavioral data, computer simulated data), a NIfTI file can be obtained by NeuroRA. At the bottom right is a demo of the resulting NIfTI file drawn with NeuroELF (http://neuroelf.net), and color-coded regions indicate strength of representation correlation

between two modes.

Table 2 Script of representational analysis between behavioral data and fMRI data in NeuroRA. Here are two schemes to achieve, and the calculation parameters of fMRI data are *ksize-[3, 3, 3]* and *strides-[1, 1, 1].* Users can just input there different data and obtain the correlation results between two modes.

Scheme 1

```
from neurora.rdm_cal import bhvRDM
from neurora.rdm_cal import fmriRDM
from neurora.corr_cal_byrdm import fmrirdms_corr

# the shape of bhv_data should be: [N_conditions, N_subs]
bhv_rdm = bhvRDM(bhv_data, sub_opt=0)
# the shape of bhv_rdm will be: [N_conditions, N_conditions]
# the shape of fmri_data should be: [N_conditions, N_subs, N_x, N_y, N_z],
# here N_x, N_y and N_z represent the size of the fMRI data.
fmri_rdms = fmriRDM(fmri_data, ksize=[3, 3, 3], strides=[1, 1, 1])
# the shape of fmri_rdms will be: [n_x, n_y, n_z, N_conditions, N_conditions],
# n_x, n_y and n_z represent the numbers of calculation units along x, y, z.

corrs = fmrirdms_corr(bhv_rdm, fmri_rdms, method='Spearman')
# the shape of corrs will be: [n_x, n_y, n_z, 2].
# That means each calculation unit gets a t-value and a p-value
# which reflect the correlation between fMRI data and behavioral data.
```

Scheme 2

```
from neurora.corr_cal import bhvANDfmri_corr

corrs = bhvANDfmri_corr(bhv_data, fmri_data, ksize=[3, 3, 3],
                        strides=[1, 1, 1], method='spearman')
# the shape of corrs will be: [n_x, n_y, n_z, 2].
```

NeuroRA provides thresholding parameters as well (**Table 3**). Users can set certain thresholds for *p*-values or *r*-values. For example, if the threshold for *p* value is set as 0.05, the final NIfTI file returned will be filtered with $p < 0.05$, and all voxels with $p>=0.05$ will be set as 0.

Table 3 Script of saving the calculation results as a NIfTI file for fMRI data. Users can get the correlation results based on the script in **Tabel 2**. The NIfTI file can be obtained by entering some necessary parameters.

```
from neurora.corr_to_nii import corr_save_nii
from neurora.stuff import get_affine

# the file name with full address of the NIfTI file you want to save
filename = "demo.nii"
# get affine matrix from a sample file
```

```
affine = get_affine("sample.nii")

# corrs can be obtained by previous steps in Table 2
# ksize and strides must be consistent with previous steps
# if the threshold is p < 0.01
corr_save_nii(corrs, filename, affine, size=[50, 60, 50], ksize=[3, 3, 3],
              strides=[1, 1, 1], p=0.01)
# if the threshold is r > 0.6
corr_save_nii(corrs, filename, affine, size=[50, 60, 50], ksize=[3, 3, 3],
              strides=[1, 1, 1], r=0.6)
# the final NIfTI file will be saved at the specified address
```

➢ Visualization of Results

NeuroRA provides several functions to visualize the results. The first option is to visualize RDMs (**Fig. 6a**) by function *plot_rdm()*. Users can select different colormaps and set up the threshold for correlation coefficients to appear. Here, we use the results from Kriegeskorte et al. 2008 as an example (**Fig. 6a**). In this study, 92 real-world images were presented to monkeys and humans, and researchers recorded responses in the inferior temporal cortex with both single-cell recoding and fMRI. Additionally, we obtained the Spearman correlation coefficient (*r*-value = 0.439, *p*-value<0.001) from the function in the *rsa_corr* module, which fit the results in their original paper. The second option is to visualize the results across different time points (**Fig. 6b**) by function *plot_corrs_by_time()* in the *rsa_plot* module. The similarity index is obtained from each time point and cascaded together. The third options is to visualize the similarity results for each channel based on the time series (**Fig. 6c**) by function *plot_corrs_hotmap()* in the *rsa_plot* module. The implementation of visualization requires the Pyplot module in the Matplotlib package.

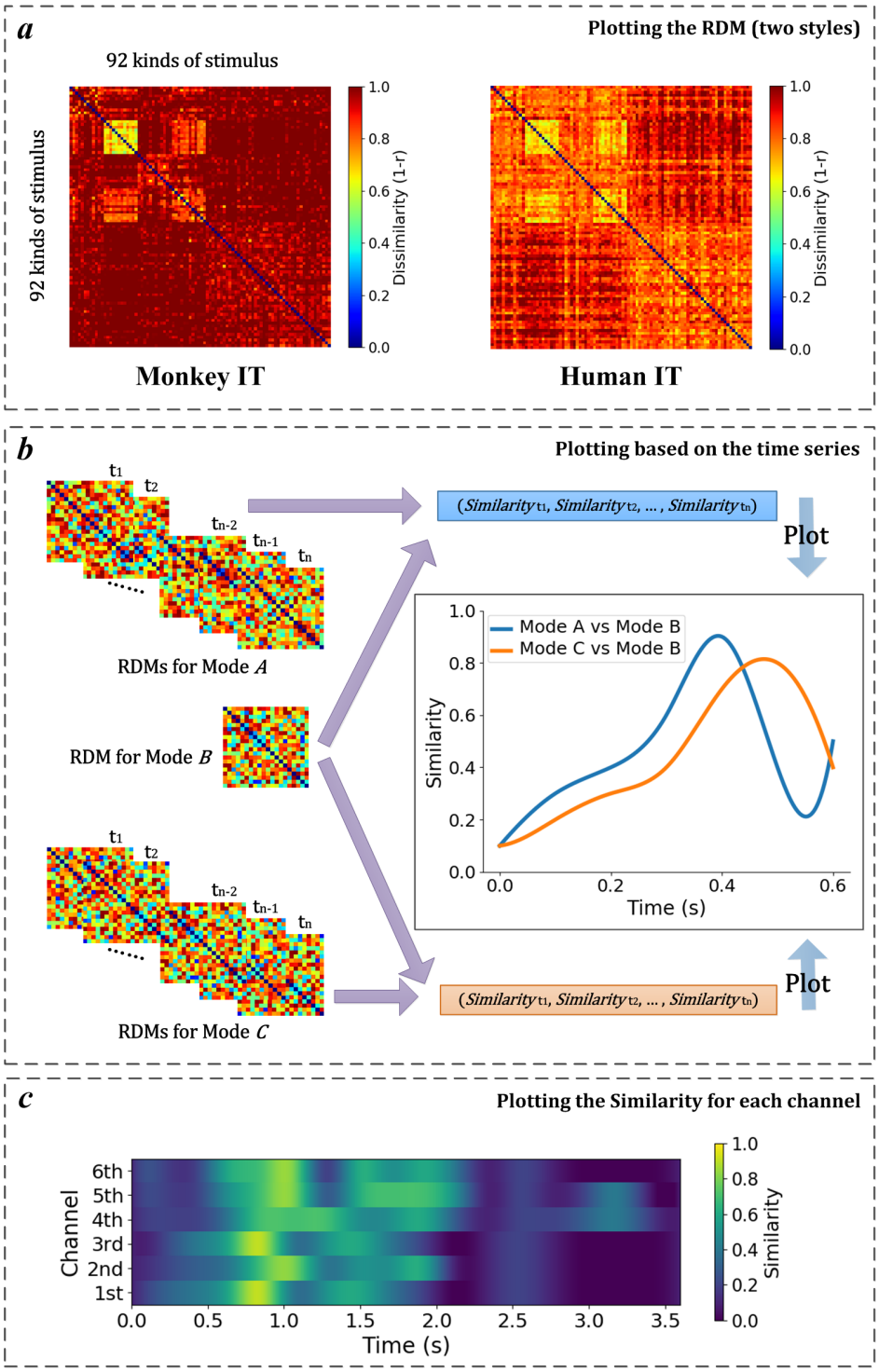

Fig. 6 Feature of visualization. (a) Example RDMs plotted by NeuroRA based on the results from Kriegeskorte et al. 2008 (Neuron). (b) Plot the results of representational similarity between different modes based on time series. (c) Plot the results of representational similarity for each channel based on time series.

We also provide a code demo on the publicly available visual-92-categories-task MEG datasets (Cichy et al., 2014). In this demo,

user can learn how to use NeuroRA to perform RSA and plot the essential results, including RDMs from different time points (**Fig 7a**), correlations over the time series (**Fig 7b**) and so on. This demo contains several critical sections: loading data & preprocessing, calculating RDMs, calculating the similarity matrix and plotting. Users can download the tutorial in NeuroRA website and find further details.

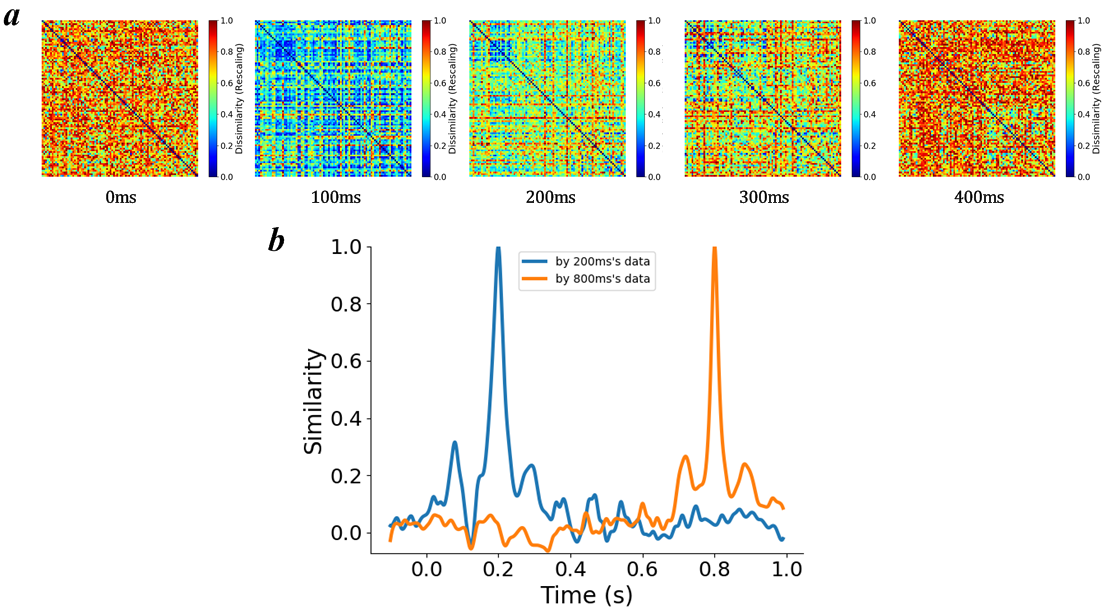

Figure 7 Demo results. (a) The RDMs of 0ms, 100ms, 200ms, 300ms and 400ms based on all 302 channels' MEG data. (b) Use the neural representations of 200ms and 800ms to calculate the similarities with all time-points' neural representations.

User Support

To report any bugs in the code or submit any queries or suggestions about our toolbox, users can use the issue tracker on GitHub: https://github.com/neurora/NeuroRA/issues. We will reply and act accordingly as soon as possible.

Discussion

RSA provides a novel way of observing big data, which is powerful in the field of cognitive neuroscience. An increasing number of studies have used such multivariate analysis to obtain novel information that could not be observed through univariate analysis (Mahmoudi et al., 2012; Sui et al., 2012; Haxby et al., 2014). More importantly, research based on different modalities must be assessed simultaneously, and RSA offers a perfect way to quantitatively compare results from different modalities with distinctive dimensions,

resolutions, and even different species (Cichy and Pantazis, 2017; Salmela et al., 2016).

In the present study, we have developed a Python-based toolbox that can perform representation analysis for neural data from many different modalities. Compared with other toolkits or modules that can also implement RSA, our toolbox has much wider application, stronger computational performance, and more convenient and complete functions, especially for the analysis of multi-modal data and cross-modal comparisons. Moreover, it is open source, free to use, and cross-platform.

For detailed information on each module and function in our toolbox, including the format of input data, the choice of parameters, and the format of output data, users can refer to our toolbox tutorial. To further understand the specific implementation of each function in the toolbox, people can read the source code directly. If users encounter any problems or difficulties during use, they can consult NeuroRA's tutorials and email our developers.

Although NeuroRA has already realized the essential functions for RSA analysis, there are still several limitations to be addressed in the future. First, NeuroRA is not yet designed to process the raw data. However, users can utilize other toolbox such as EEGLAB (Delorme and Makeig, 2004), MNE (Gramfort et al., 2013), and Nibabel (Brett et al., 2016), to import data and transfer them into a format fit for NeuroRA. We plan to develop an integrated format conversion function in the next version. Second, there is still significant room for improving the computational performance of NeuroRA, especially in the iterative calculation of fMRI data, which is often slow. This is due to nested loops in the code structure when we need to traverse the data from the entire brain and iterate the random shuffle many times. In the future, we will reduce the time by optimizing functions with GPUs. Third, there is currently no graphical user interface (GUI) right now, which we plan to design and implement based on PyQt in a future version. Users could then obtain the final results by dragging the data file to a specific location in the GUI with the mouse and filling in the relevant parameters.

Through NeuroRA, for the first time, we provide a method for researchers to perform representation analysis with neural data from many different modalities. However, this is only a starting point. With the development of the algorithm to compute RSA, we will include new methods, as well as new visualization tools. We hope that many interesting findings can be observed through our toolbox and we would like to collaborate with researchers that are interested in this tool to improve the toolbox further.

Information Sharing Statement

NeuroRA is available at https://pypi.org/project/neurora/. The website for NeuroRA is https://neurora.github.io/NeuroRA/, and the tutorial of the toolbox can be download here. The code for our toolbox NeuroRA can be accessed on GitHub: https://github.com/neurora/NeuroRA.

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