Script Demo for fMRItual based on NeuroRA

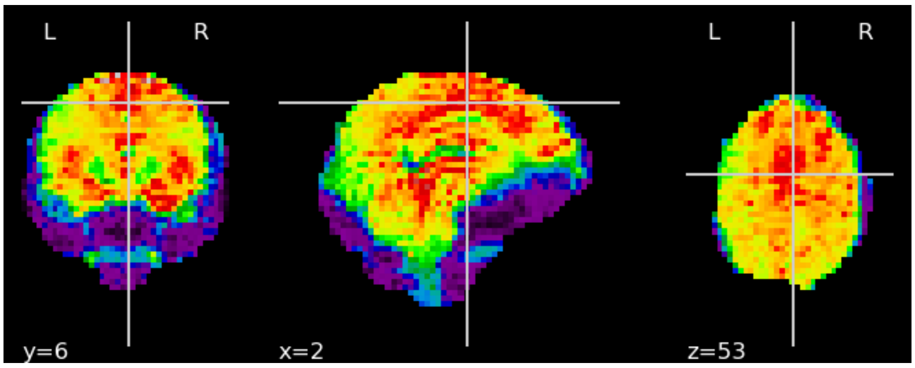
by Zitong Lu
Dec 22, 2020

Users can learn how to use NeuroRA to do research by representational analysis based on fMRI data.

This demo is based on the publicly available Haxby fMRI datasets. (*Reference:* Haxby, J. V. (2001). Distributed and Overlapping Representations of Faces and Objects in Ventral Temporal Cortex. Science, 293(5539), 2425–2430.) Nilearn has been used to load this dataset and plot some results in this demo.

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

' a demo based on Haxby fMRI data '
# Users can learn how to use Neurora to do research based on fMRI data.

__author__ = 'Zitong Lu'

from nilearn import datasets, plotting
from nilearn.image import index_img, mean_img
import numpy as np
import pandas as pd
import nibabel as nib
from neurora.stuff import get_affine, datamask
from neurora.nps_cal import nps_fmri, nps_fmri_roi
from neurora.rsa_plot import plot_rdm
from neurora.rdm_cal import fmriRDM_roi, fmriRDM
from neurora.corr_cal_by_rdm import fmrirdms_corr
from neurora.nii_save import corr_save_nii


""""**********       Section 1: Loading example data       **********"""
""" Here, we use Nilearn toolbox for loading data and processing """
""" you can learn this process from Nilearn
(http://nilearn.github.io/index.html) """
```

```
# load Haxby dataset (here, we only use subject2's data for this
example)
haxby_dataset = datasets.fetch_haxby()

# load the fMRI data filename & mask data filename
func_filename = haxby_dataset.func[0]
mask_filename = haxby_dataset.mask

# read label information of the experiment
labelinfo = pd.read_csv(haxby_dataset.session_target[0], sep=' ')
labels = labelinfo['labels']



"""**********          Section 2: Preprocessing          **********"""

# get mask data NumPy array
maskdata = nib.load(mask_filename).get_fdata()

# get the size of the data
nx, ny, nz = maskdata.shape

# labels of seven ategories
categories = ["face", "cat", "house", "chair", "shoe", "bottle",
"scissors"]
# numbe of conidtions: 7
ncon = len(categories)

# get fmri data under 7 conditions
# here we average the data under different conditions
fmri_data = np.full([ncon, nx, ny, nz], np.nan)

for i in range(ncon):
    img = mean_img(index_img(func_filename,
labels.isin([categories[i]])))
    fmri_data[i] = datamask(img.get_fdata(), maskdata)

# get fmri data under 'face'-condition
face_img = nib.Nifti1Image(fmri_data[0], affine=img.affine)
# have a look
plotting.plot_epi(face_img)
plotting.show()
```

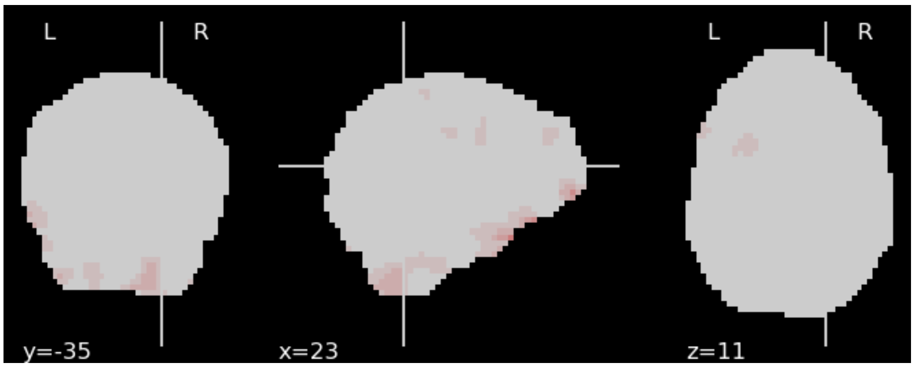


```
# reshaoe the data: [ncon, nx, ny, nz] -> [ncon, nsubs, nx, ny, nz]
# here just one subject's data
fmri_data = np.reshape(fmri_data, [ncon, 1, nx, ny, nz])



"""**Section 3: Calculating the neural pattern similarity (for ROI)**"""

# get mask of 'mask_face' in the dataset
mask_face_filename = haxby_dataset.mask_face[0]
mask_face_data = nib.load(mask_face_filename).get_fdata()

# get input data under two condition
# here, "face"-condition vs. "scissors"-condition
nps_fmri_data = fmri_data[[0, 6]]

# calculate the neural pattern similarity (NPS) for ROI between two
stimulus
nps_roi = nps_fmri_roi(nps_fmri_data, mask_face_data)

# print the NPS result
print(nps_roi)
```

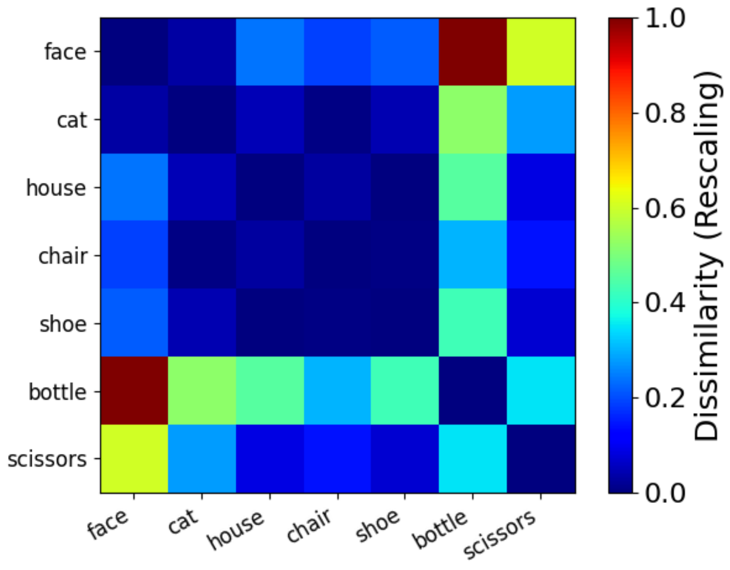
```
9.994484681410596982e-01, 5.880839542727496111e-43
```

```
"""Section 4: Calculating the neural pattern similarity (Searchlight)"""

# calculate the neural pattern similarity (NPS) between two stimulus
nps = nps_fmri(nps_fmri_data)

# convert the NPS results into a .nii file
savefilename = "nps_img"
affine = get_affine(mask_filename)
```

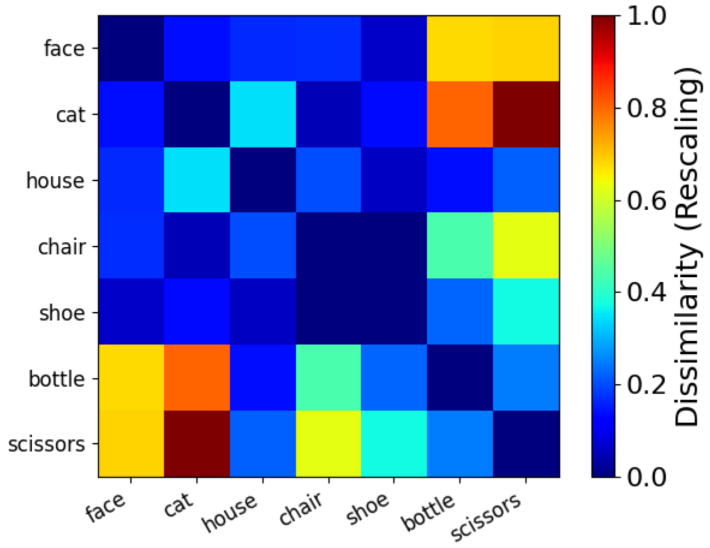
```
corr_save_nii(nps[0], filename=savefilename, affine=affine, size=[nx, ny, nz], smooth=False, plotrlt=False)

# have a look
plotting.plot_epi(savefilename+".nii")
plotting.show()
```



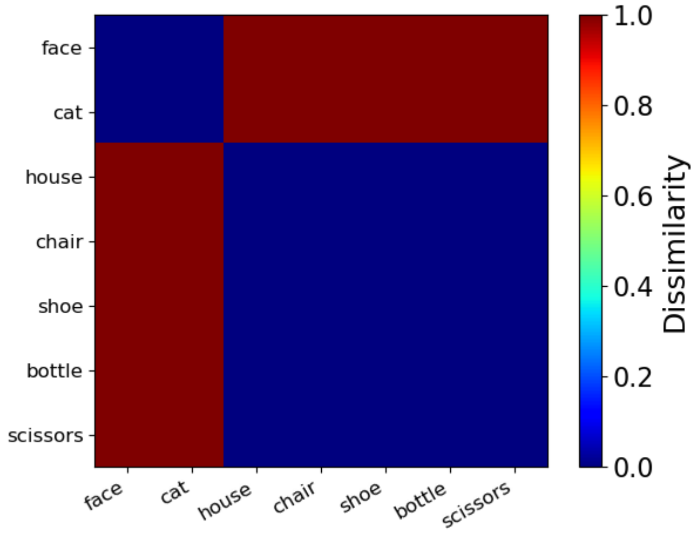
```
"""***    Section 5: Calculating the RDM for ROI and Plotting    ***"""

# get mask of "mask_vt" in the dataset
mask_vt_filename = haxby_dataset.mask_face[0]
mask_vt_data = nib.load(mask_vt_filename).get_fdata()

# calculate the RDM for ROI
rdm_roi = fmriRDM_roi(fmri_data, mask_vt_data)

# plot the RDM
plot_rdm(rdm_roi, rescale=True, conditions=categories)
```



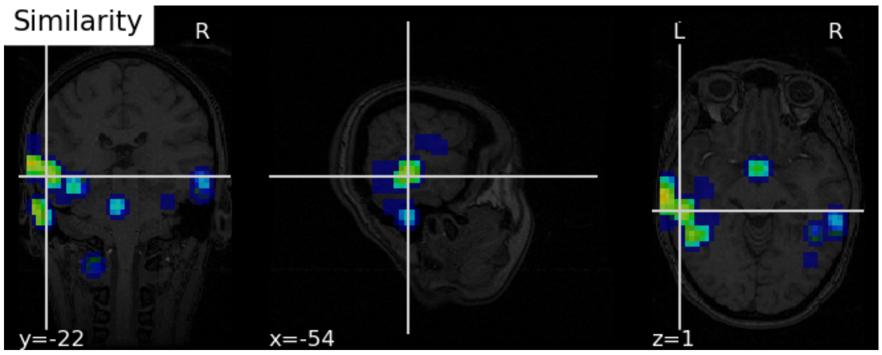
```
"""**  Section 6: Calculating the RDM by Searchlight and Plotting   **"""

# calculate the RDMs by Searchlight
fmri_RDMs = fmriRDM(fmri_data, sub_opt=0)

# plot one of the RDMs
plot_rdm(fmri_RDMs[20, 30, 30], rescale=True, conditions=categories)
```

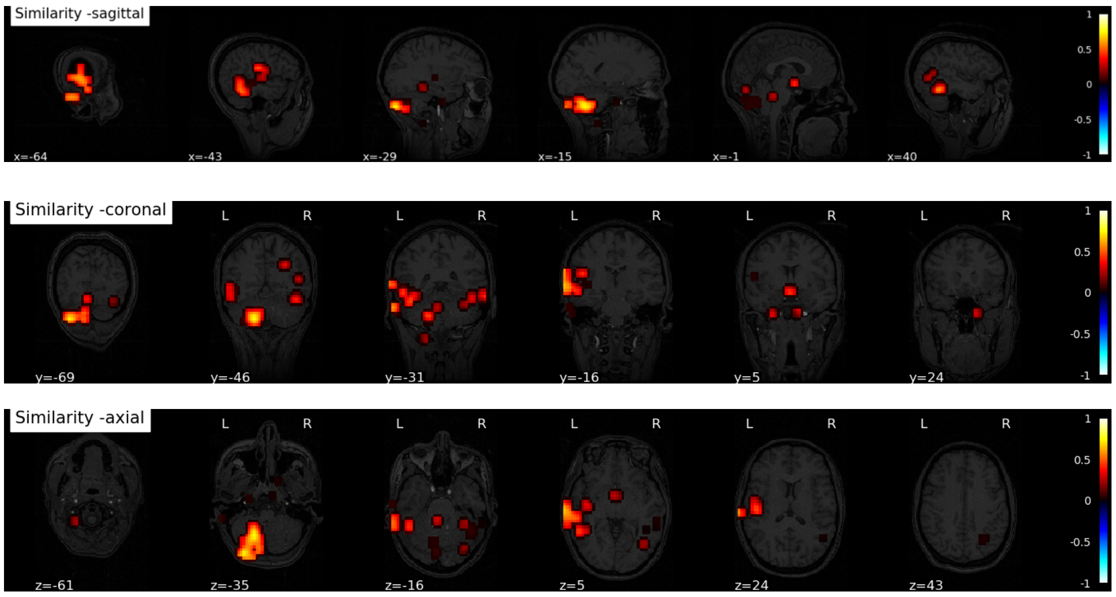


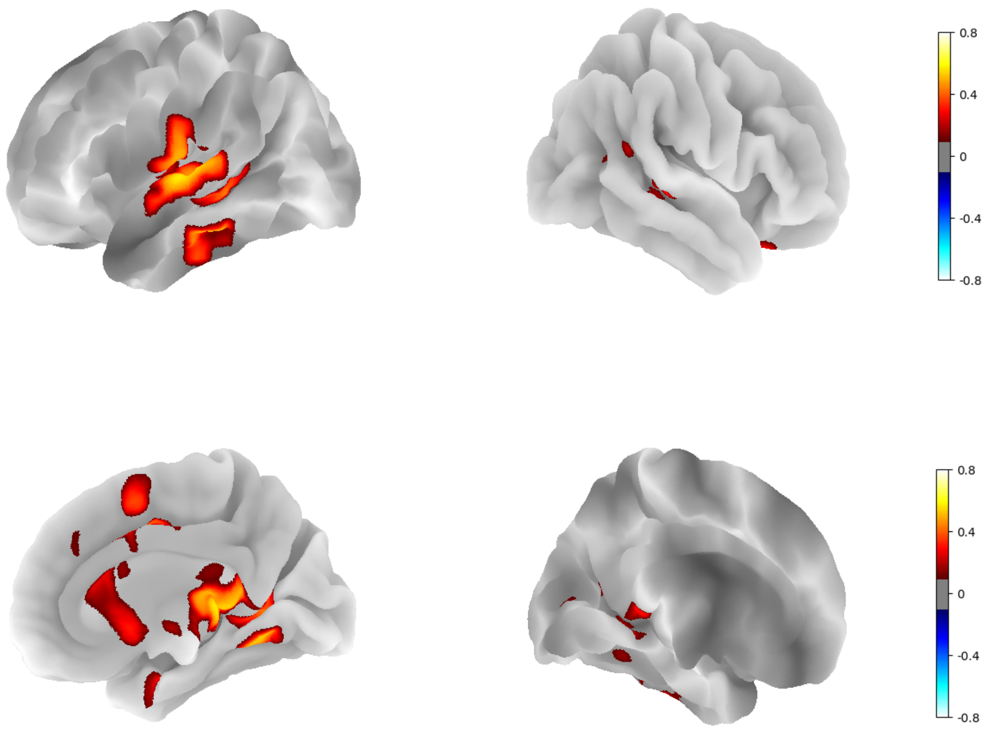
```
"""*** Section 7: Calculating the representational similarities    ***"""
"""***            between a coding model and neural activities    ***"""

# Create a RDM for "animate-inanimate" coding model
# which means the representations of animate matters are highly similar
# and the representations of inanimate matters are highly similar
model_RDM = np.array([[0, 0, 1, 1, 1, 1, 1],
                      [0, 0, 1, 1, 1, 1, 1],
                      [1, 1, 0, 0, 0, 0, 0],
                      [1, 1, 0, 0, 0, 0, 0],
                      [1, 1, 0, 0, 0, 0, 0],
                      [1, 1, 0, 0, 0, 0, 0],
                      [1, 1, 0, 0, 0, 0, 0]])

# plot the model RDM
plot_rdm(model_RDM, conditions=categories)
```



```
# calculate the similarities between model RDM and searchlight RDMs
corrs = fmrirdms_corr(model_RDM, fmri_RDMs)



""""*****      Section 8: Saving the RSA result and Plotting      *****"""

# load the filename of anatomical image as the background for plotting
ant_filename = haxby_dataset.anat[0]

# get the affine info
affine = get_affine(mask_filename)

# save the RSA result as a .nii file
# and visualize the result automatically
# p < 0.05, FDR-correct
rsarltfilename = "demo2_rsarlt_img"
img = corr_save_nii(corrs, filename=rsarltfilename, affine=affine,
corr_mask=mask_filename, size=[40, 64, 64], p=0.001, plotrlt=True,
img_background=ant_filename)
```

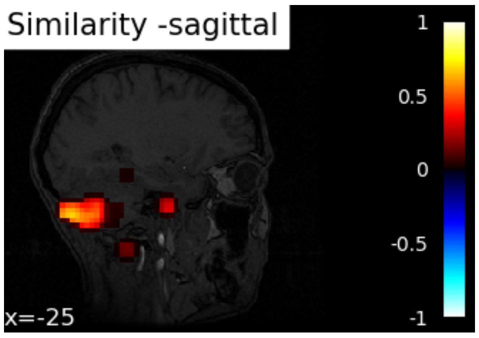




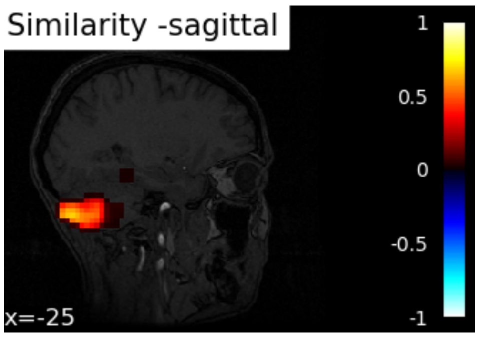


```
# Users can plot the RSA results independently by functions below
from neurora.rsa_plot import plot_brainrsa_regions
from neurora.rsa_plot import plot_brainrsa_montage
from neurora.rsa_plot import plot_brainrsa_glass
from neurora.rsa_plot import plot_brainrsa_surface

# here use a [5, 5, 5] cube to remove the significant area smaller than
it
```

```
# before filtering
plot_brainrsa_montage(rsarltfilename, slice=[[-25], 0, 0],
background=ant_filename)
```



```
# after filtering
plot_brainrsa_montage(rsarltfilename, threshold=125, slice=[[-25], 0,
0], background=ant_filename)
```



Users can see more details below:

GitHub Website: https://github.com/neurora/NeuroRA
NeuroRA Website: https://neurora.github.io/NeuroRA/
PyPi Website: https://pypi.org/project/neurora/
Paper: https://doi.org/10.3389/fninf.2020.563669