

Script Demo for EEG/MEG based on NeuroRA

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April 09, 2020

Users can learn how to use [NeuroRA](#) to do research by representational analysis based on EEG/MEG data.

This demo is 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 '
# Users can learn how to use Neurora to do research based on EEG/MEG etc
data.

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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.nps_cal import nps
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, plot_corrs_by_time,
plot_nps_hotmap, plot_corrs_hotmap

"""*****          Section 1: loading example data          *****"""
""" Here, we use MNE-Python toolbox for loading data and processing """
""" 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
        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: Preprocessing                               *****"""

# 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])

"""**** Section 3: Calculating the neural pattern similarity ****"""

# Get data under different condition
# Here we calculate the neural pattern similarity (NPS) between two
stimulus
# Seeing Humanface vs. Seeing Non-Humanface

# get data under "humanface" condtion
megdata_humanface = megdata[12:24]
# get data under "nonhumanface" condition
megdata_nonhumanface = megdata[36:48]

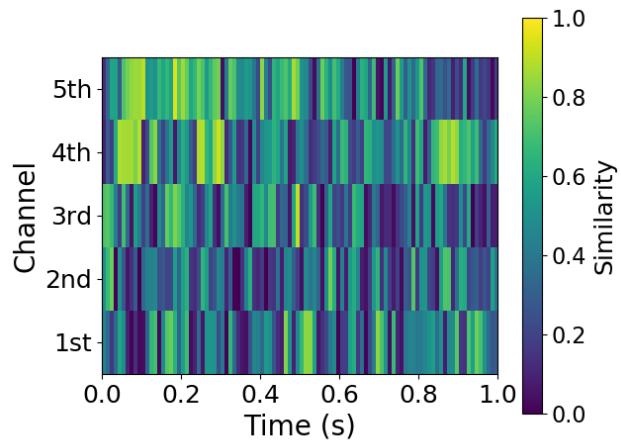
# Average the data
avg_megdata_humanface = np.average(megdata_humanface, axis=0)
avg_megdata_nonhumanface = np.average(megdata_nonhumanface, axis=0)

# Create NPS input data
# Here we extract the data from first 5 channels between 0ms and 1000ms
nps_data = np.zeros([2, 3, 1, 5, 1000]) # n_cons=2, n_subs=3, n_chls=5,
n_ts=1000
nps_data[0] = avg_megdata_humanface[:, :, :5, 100:1100] # the start time
of the data is -100ms
nps_data[1] = avg_megdata_nonhumanface[:, :, :5, 100:1100] # so 100:1200
corresponds 0ms-1000ms

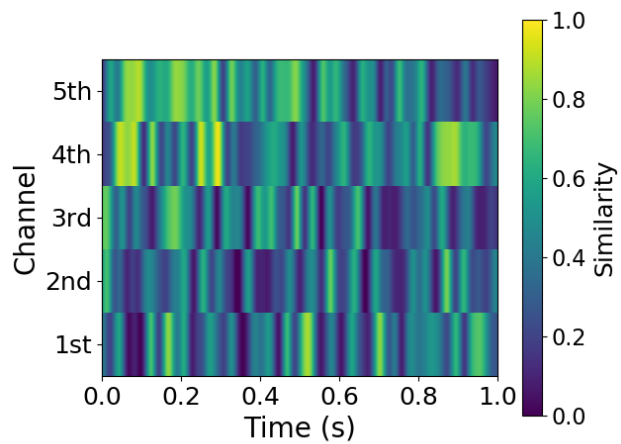
# Calculate the NPS with a 10ms time-window
# (raw sampling requency is 1000Hz, so here
time_win=10ms/(1s/1000Hz)/1000=10)
nps = nps(nps_data, time_win=10, time_step=10)

# Plot the NPS results
plot_nps_hotmap(nps, time_unit=[0, 0.01], abs=True)

```



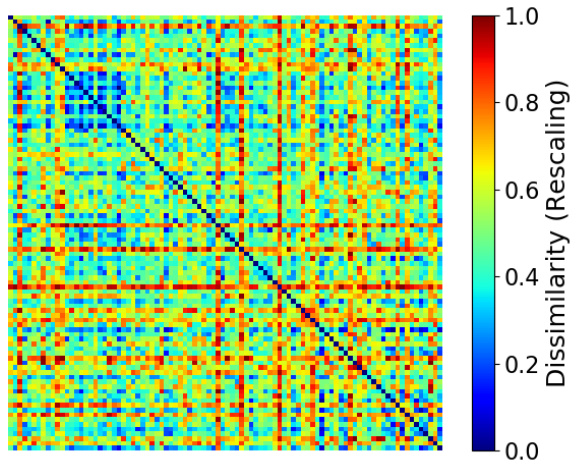
```
# Smooth the results and plot
plot_nps_hotmap(nps, time_unit=[0, 0.01], abs=True, smooth=True)
```



```
***** Section 4: Calculating single RDM and Plotting *****

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

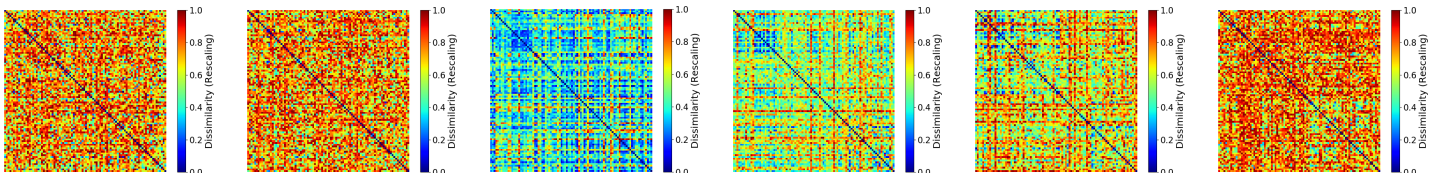
# Plot this RDM
plot_rdm(rdm, rescale=True)
```



***** Section 5: 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_opt=1, time_win=10, time_step=10)

# Plot the RDM of -100ms, 0ms, 100ms, 200ms, 300ms, 400ms
times = [0, 10, 20, 30, 40, 50]
for t in times:
    plot_rdm(rdms[t], rescale=True)
```



***** Section 6: Calculating the Similarity between two RDMs *****

```
# RDM of 200ms
rdm_sample1 = rdms[30]
# RDM of 800ms
rdm_sample2 = rdms[90]

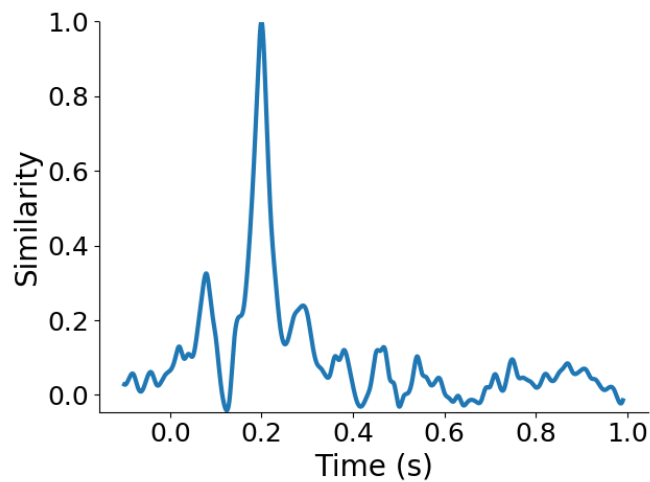
# calculate the correlation coefficient between these two RDMs
corr = rdm_correlation_spearman(rdm_sample1, rdm_sample2, rescale=True)
print(corr)
```

SpearmanrResult(correlation=0.02665680483550596, pvalue=0.08462337954774739)

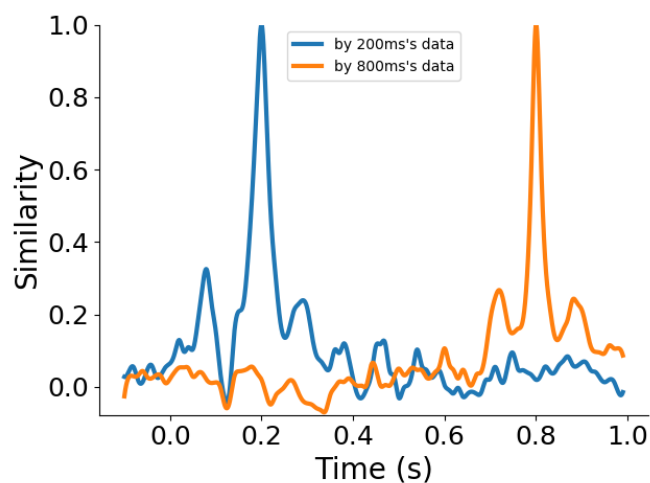
***** Section 7: Calculating the Similarity and Plotting *****

```
# 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])
```



```

*****      Section 8: Calculating the RDMs for each channels      *****

```

```

# Calculate the RDMs for the first six channels by a 10ms time-window
between 0ms and 1000ms

```

```

rdms_chls = eegRDM(megdata[:, :, :, :6, 100:1100], chl_opt=1,
time_opt=1, time_win=10, time_step=10)

```

```

# Create a 'human-related' coding model RDM

```

```

model_rdm = np.ones([92, 92])

```

```

for i in range(92):

```

```

    for j in range(92):

```

```

        if (i < 24) and (j < 24):

```

```

            model_rdm[i, j] = 0

```

```

        model_rdm[i, i] = 0

```

```

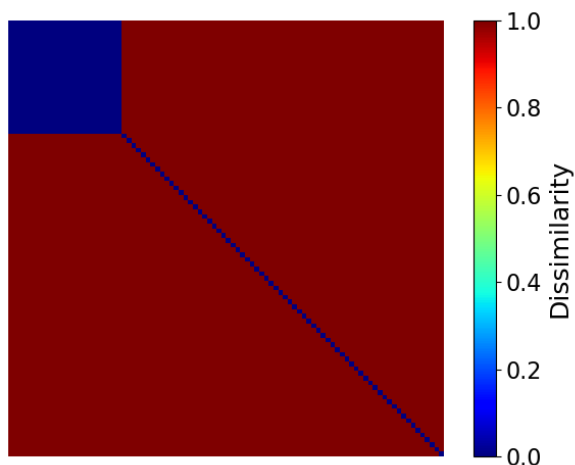
# Plot this coding model RDM

```

```

plot_rdm(model_rdm)

```



```

# Calculate the representational similarity between the neural
activities and the coding model for each channel

```

```

corrs_chls = rdms_corr(model_rdm, rdms_chls)

```

```

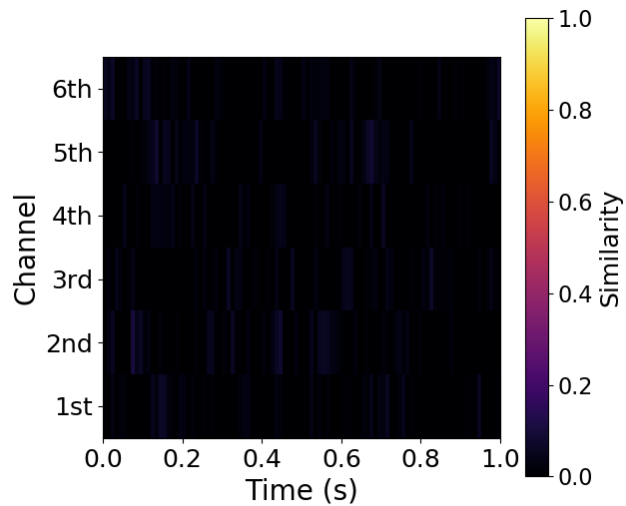
# Plot the representational similarity results

```

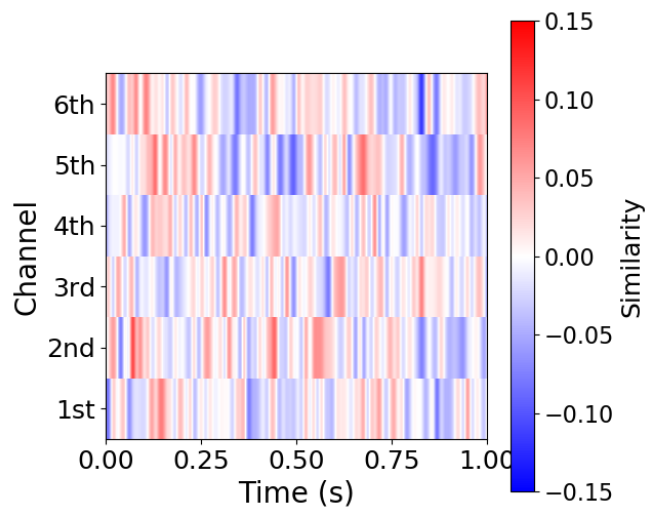
```

plot_corrs_hotmap(corrs_chls, time_unit=[0, 0.01])

```



```
# Set more parameters and re-plot
plot_corrs_hotmap(corrs_chls, time_unit=[0, 0.01], lim=[-0.15, 0.15],
smooth=True, cmap='bwr')
```



Users can see more details below:

GitHub Website: <https://github.com/neurora/NeuroRA>

NeuroRA Website: <https://neuroragithub.io/NeuroRA/>

PyPi Website: <https://pypi.org/project/neurora/>

BioRxiv Paper: <https://doi.org/10.1101/2020.03.25.008086>