arasdar / DL

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1 contributor

844 lines (843 sloc) 597 KB

Brain-Computer Interfaces (Fall 2017, ELE 594)

Instructor: Yalda Shahriari

2nd homework, 10/8/17 (The homework, is due by Oct 18th

, 11:55 pm).

Instruction: All the data instructions are the same as homework 1.

1-

a) Perform PCA on broadband data using two time windows, one before and one after trial onset (e.g., - 500 to 0 ms and 100 to 600 ms).

Hint: Separate the requested epochs from the EEG data (e.g. [-500 0ms]).

Center the data by subtracting the mean of each epoch.

For each trial obtain the sample covariance matrix (refer to the lecture notes).

Get the average of the covariances over all the trials.

Perform eigenvalue decomposition, order the PCs and the eigenvalues in descending order, and proceed to answer the questions.

```
In [1]: import scipy.io as spio
        import numpy as np

        sampleEEGdata = spio.loadmat(file_name='../BCI-HW1/sampleEEGdata.mat')
```

```
In [2]: sampleEEGdata.keys()
```

```
Out[2]: dict_keys(['__version__', 'EEG', '__header__', '__globals__'])
```

```
In [3]: sampleEEGdata['EEG'].shape
```

```
Out[3]: (1, 1)
```

```
In [4]: sampleEEGdata['EEG'][0, 0].dtype
```

```
Out[4]: dtype([('setname', 'O'), ('filename', 'O'), ('filepath', 'O'), ('subject', 'O'), ('group', 'O'),
         ('condition', 'O'), ('session', 'O'), ('comments', 'O'), ('nbchan', 'O'), ('trials', 'O'), ('pnt
        s', 'O'), ('srate', 'O'), ('xmin', 'O'), ('xmax', 'O'), ('times', 'O'), ('data', 'O'), ('icaact',
         'O'), ('icawinv', 'O'), ('icasphere', 'O'), ('icaweights', 'O'), ('icachansind', 'O'), ('chanloc
        s', 'O'), ('urchanlocs', 'O'), ('chaninfo', 'O'), ('ref', 'O'), ('event', 'O'), ('urevent', 'O'),
         ('eventdescription', 'O'), ('epoch', 'O'), ('epochdescription', 'O'), ('reject', 'O'), ('stats',
         'O'), ('specdata', 'O'), ('specicaact', 'O'), ('splinefile', 'O'), ('icasplinefile', 'O'), ('dipf
        it', 'O'), ('history', 'O'), ('saved', 'O'), ('etc', 'O'), ('spedata', 'O')])
```

```
In [5]: sampleEEGdata['EEG'][0, 0]['data'].shape
```

```
Out[5]: (64, 640, 99)
```

```
In [6]: data = sampleEEGdata['EEG'][0, 0]['data']
        srate = sampleEEGdata['EEG'][0, 0]['srate'][0, 0]
        data.shape, srate
```

```
Out[6]: ((64, 640, 99), 256)
```

```
In [7]: # To separate the pre- and post- trial onset epochs: low limit and length/duration
        # duration= 500 ms, low1= -500 ms, low2 = 100ms
        # to convert the time point/loc to the sample number:
        # time/T gives you number of points
        # time * freq to get the number of samples
        # The overal timeline is -1500 to 1000
        # low1, low2, length =
        xmin = sampleEEGdata['EEG'][0, 0]['xmin'][0, 0]
        xmax = sampleEEGdata['EEG'][0, 0]['xmax'][0, 0]
        xmin, xmax, srate, data.shape[1], data.shape[1]/ (xmax - xmin)
```

```
Out[7]: (-1, 1.49609375, 256, 640, 256.40062597809077)
```

```
In [8]: # number of sample / (duration) == freq
        # -0.5 - 0.0 and 0.1 - 0.6
        # length = 0.5
        # low1 = -0.5, low2 = 0.1 temporally/ time-wise/ time-axis
        low1, length, low2 = int((-0.5 - xmin) * srate), int(0.5 * srate), int((0.1 - xmin) * srate)
        low1, length, low2
```

```
Out[8]: (128, 128, 281)
```

```
In [9]: # Extract the pre- and post- trial onset/stimuli event as segments/ epochs from the data
        data_pre, data_post = data[:, low1: low1+length, :], data[:, low2: low2+length, :]
        data_post.shape, data_pre.shape, data.shape # data.shape = (channels, time-points, trials) == (0,
         1, 2)
```

```
Out[9]: ((64, 128, 99), (64, 128, 99), (64, 640, 99))
```

```
In [10]: # Center the data by subtracting the mean of each epoch.
         # The mean should be the mean of all samples in the space of channels/ number axis or dimensions o
         r features
         data.shape[2], data[:, :, 0].shape, data[:, :, 0].mean(axis=1).shape
```

```
Out[10]: (99, (64, 640), (64,))
```

```
In [11]: # axis = 0 number of channels, axis= 1 number of points
         (data[:, :, 0] - data[:, :, 0].mean(axis=1).reshape(-1, 1)).shape
```

```
Out[11]: (64, 640)
```

```
In [12]: data_mean_list = []
         for idx_trial in range(data.shape[2]):
             data_trial_mean = data[:, :, idx_trial] - data[:, :, idx_trial].mean(axis=1).reshape(-1, 1)
         #     print(data_trial_mean.shape)
             data_mean_list.append(data_trial_mean)
         len(data_mean_list), data_mean_list[0].shape
```

```
Out[12]: (99, (64, 640))
```

```
In [13]: np.array(data_mean_list).shape, np.array(data_mean_list, dtype=float).dtype
```

```
Out[13]: ((99, 64, 640), dtype('float64'))
```

```
In [14]: data_mean = np.array(data_mean_list, dtype=float)
```

```
In [15]: # normalize the data: 0-mean (zero-mean) and 1-std (uni-cov/std)
         def normalize_data(data):
             data_norm_list = []
             for idx_trial in range(data.shape[2]):
                 data_trial_norm = data[:, :, idx_trial] - data[:, :, idx_trial].mean(axis=1).reshape(-1,
         1)
                 data_trial_norm /= data[:, :, idx_trial].std(axis=1).reshape(-1, 1)
                 data_norm_list.append(data_trial_norm)
             data_norm_list = np.array(data_norm_list, dtype=float)
             return data_norm_list
```

```
In [16]: data_pre_norm, data_norm, data_post_norm = normalize_data(data=data_pre),
         normalize_data(data=data), normalize_data(data=data_post)
```

```
In [17]: data_norm.shape, data_post_norm.shape, data_pre_norm.shape
```

```
Out[17]: ((99, 64, 640), (99, 64, 128), (99, 64, 128))
```

```
In [18]: # # make sure the mean was calculated correctly
         # for idx_trial in range(data_mean.shape[0]):
         #     if data_mean[idx_trial].mean(axis=1).sum(axis=0) > 1e-4:
         #         print(data_mean[idx_trial].mean(axis=1).sum(axis=0))
         #     if data_post_mean[idx_trial].mean(axis=1).sum(axis=0) > 0.01:
         #         print(data_post_mean[idx_trial].mean(axis=1).sum(axis=0))
         #     if data_pre_mean[idx_trial].mean(axis=1).sum(axis=0) > 0.01:
         #         print(data_pre_mean[idx_trial].mean(axis=1).sum(axis=0))
```

```
In [19]: # For each trial obtain the sample covariance matrix (refer to the lecture notes).
         def cov_data(data_norm):
             data_cov_list = []
             for idx_trial in range(data_norm.shape[0]):
```

```
        data_trial_cov = data_norm[idx_trial] @ data_norm[idx_trial].T # X_nxt @ X_nxt.T = conv_nx
n
        data_cov_list.append(data_trial_cov)
    data_cov = np.array(data_cov_list, dtype=float)
    return data_cov
```

In [20]:
```
data_pre_cov, data_cov, data_post_cov = cov_data(data_norm=data_pre_norm), cov_data(data_norm=data
_norm), cov_data(data_norm=data_post_norm)
```

In [21]:
```
data_cov.shape, data_pre_cov.shape, data_post_cov.shape
```

Out[21]:
```
((99, 64, 64), (99, 64, 64), (99, 64, 64))
```

In [22]:
```
# Get the average of the covariances over all the trials.
data_cov_mean, data_pre_cov_mean, data_post_cov_mean = data_cov.mean(axis=0), data_pre_cov.mean(ax
is=0), data_post_cov.mean(axis=0)
```

In [23]:
```
data_cov_mean.shape, data_pre_cov_mean.shape, data_post_cov_mean.shape
```

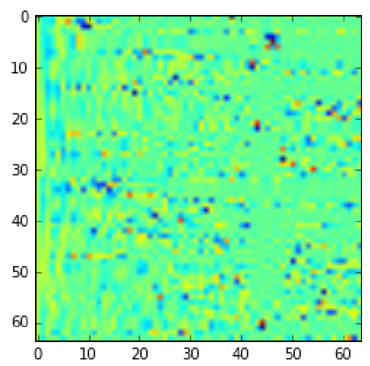
Out[23]:
```
((64, 64), (64, 64), (64, 64))
```

In [24]:
```
# Perform eigenvalue decomposition,
# order the PCs and the eigenvalues in descending order,
# and proceed to answer the questions.
def pca_sorted(data_cov_mean):
    w, v = np.linalg.eig(a=data_cov_mean)
    # w.shape, v.shape, w.reshape(-1, 1).shape, np.hstack(tup=(w.reshape(-1, 1), v)).shape
    # wv = np.column_stack(tup=(w, v))
    # w.shape, v.shape, np.array([w, v]).shape
    # sorted(wv[:, 0], reverse=True)

    # create a dict for sorting the eigen vevctors based eigen values
    w_to_v =  {w: v for w, v in zip(w, v)} # output is a dictionary {}
    w_sorted = sorted(w, reverse=True) # output is a list for python data structure []

    # Getting the sorted eigenvector according to eigvalues
    # w_to_v[w_sorted[0]]
    v_sorted = []
    for each_w in w_sorted:
        v_sorted.append(w_to_v[each_w])

    v_sorted = np.array(v_sorted, dtype=float)
    w_sorted = np.array(w_sorted, dtype=float)
    #     v_sorted.shape, v_sorted.dtype

    return w_sorted, v_sorted
```

In [25]:
```
w, v = pca_sorted(data_cov_mean=data_cov_mean)
# w.shape, v.shape
```

In [26]:
```
w_pre,v_pre = pca_sorted(data_cov_mean=data_pre_cov_mean)
w_post,v_post = pca_sorted(data_cov_mean=data_post_cov_mean)
```

In [27]:
```
import matplotlib.pyplot as mplot

# mplot.imshow(X=v)
# mplot.imshow(X=v_post)
mplot.imshow(X=v_pre)
mplot.show()
```



b) Plot topographical maps and time courses of the first four components.

To construct the PCA time courses, multiply the PCA weights defined by the pre- and post-trial time windows with the electrode time courses from the entire trial.

Do you notice any differences in the topographical maps or time courses from before versus after stimulus onset?

How would you interpret differences and/or similarities?

Note: Make the colormaps in ‘jet’ format and keep the color limit for the topoplots for both conditions (i.e. pre- and post-stimulus) the same

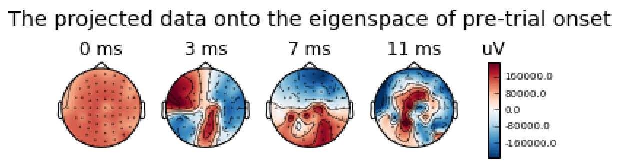
In [28]:

```python
# Use the topoplot.m function for plotting the head plots.
# Creating mne Objects from numpy arrays for Visualizing the epochs/ topomap plot
import mne as mne

labels = []
XYZs = []
eeg = sampleEEGdata['EEG'][0, 0]
eeg['chanlocs']['labels'][0, 0][0]
eeg['chanlocs']['labels'].shape[1]
for idx in range(eeg['chanlocs']['labels'].shape[1]):
    # channel labels or electrode labels
    label = eeg['chanlocs']['labels'][0, idx][0]
    #     print(label)
    labels.append(label)

    # channel location or electrode location
    X = eeg['chanlocs']['X'][0, idx][0][0]
    Y = eeg['chanlocs']['Y'][0, idx][0][0]
    Z = eeg['chanlocs']['Z'][0, idx][0][0]
    XYZs.append(np.array([X, Y, Z], dtype=float))

ch_location = np.array(XYZs, dtype=float) # channels or electrodes location
ch_names = labels # mat['ch_names'].tolist(): channels or electrodes names/ labels
dig_ch_pos = dict(zip(ch_names, ch_location))
montage = mne.channels.DigMontage(dig_ch_pos=dig_ch_pos)

sfreq = eeg['srate'][0, 0]

# It is also possible to use info from another raw object.
info = mne.create_info(ch_names=ch_names, ch_types='eeg', montage=montage, sfreq=sfreq)

tmin = eeg['xmin'][0, 0]
tmax = eeg['xmax'][0, 0]
picks = mne.pick_types(info=info, eeg=True)
```

In [78]:

```python
# It is also possible to use info from another raw object.
# info = mne.create_info(ch_names, sfreq, ch_types=None, montage=None, verbose=None)
# info = mne.create_info(ch_names=4, sfreq=sfreq, ch_types='eeg')
info = mne.create_info(ch_names=ch_names, ch_types='eeg', montage=montage, sfreq=sfreq)
evoked = mne.EvokedArray(data=v_pre[:, :4], info=info)
# times = np.arange(0.0, 2.5, 0.25)
evoked.plot_topomap(show=False, title='The projected data onto the eigenspace of pre-trial onset')
# evoked.plot_joint(show=False, title='The projected data onto the eigenspace of pre-trial onset')
# evoked.plot(show=False, window_title='window title', titles='The first four PCs for pre-onset da
ta')
```

Out[78]:

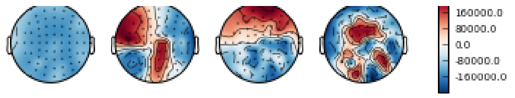


In [40]:

```python
# It is also possible to use info from another raw object.
# info = mne.create_info(ch_names, sfreq, ch_types=None, montage=None, verbose=None)
# info = mne.create_info(ch_names=4, sfreq=sfreq, ch_types='eeg')
info = mne.create_info(ch_names=ch_names, ch_types='eeg', montage=montage, sfreq=sfreq)
evoked = mne.EvokedArray(data=v[:, :4], info=info)
# times = np.arange(0.0, 2.5, 0.25)
evoked.plot_topomap(show=False, title='The projected data onto the eigenspace of full-trial includ
ing onset')
# evoked.plot(show=False, window_title='window title', titles='The first four PCs for pre-onset da
ta')
```

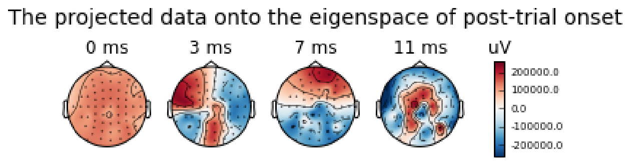
Out[40]:

The projected data onto the eigenspace of full-trial including onset
0 ms
3 ms
7 ms
11 ms
uV



In [41]:
```
# It is also possible to use info from another raw object.
# info = mne.create_info(ch_names, sfreq, ch_types=None, montage=None, verbose=None)
# info = mne.create_info(ch_names=4, sfreq=sfreq, ch_types='eeg')
info = mne.create_info(ch_names=ch_names, ch_types='eeg', montage=montage, sfreq=sfreq)
evoked = mne.EvokedArray(data=v_post[:, :4], info=info)
# times = np.arange(0.0, 2.5, 0.25)
evoked.plot_topomap(show=False, title='The projected data onto the eigenspace of post-trial
onset')
# evoked.plot(show=False, window_title='window title', titles='The first four PCs for pre-onset da
ta')
```

Out[41]:

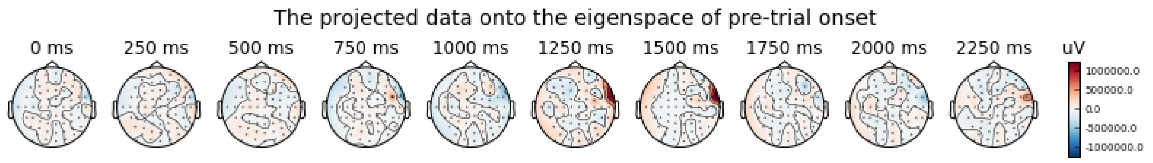


In [44]:
```
# v.shape, data_norm.shape
proj, proj_post, proj_pre = 0, 0, 0
for idx_trial in range(data_norm.shape[0]):
    proj += (v.T @ data_norm[idx_trial])/ data_norm.shape[0]
    proj_pre += (v_pre.T @ data_norm[idx_trial])/ data_norm.shape[0]
    proj_post += (v_post.T @ data_norm[idx_trial])/ data_norm.shape[0]

proj.shape, proj_pre.shape, proj_post.shape
```

Out[44]:
```
((64, 640), (64, 640), (64, 640))
```

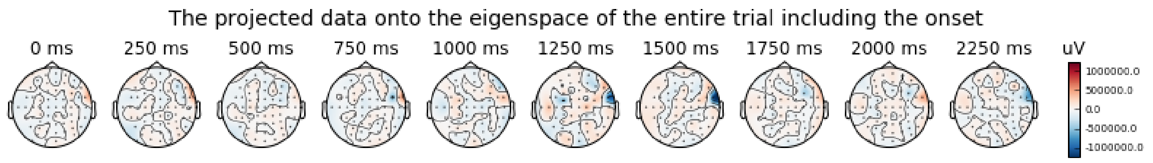
In [45]:
```
# It is also possible to use info from another raw object.
# info = mne.create_info(ch_names, sfreq, ch_types=None, montage=None, verbose=None)
# info = mne.create_info(ch_names=4, sfreq=sfreq, ch_types='eeg')
info = mne.create_info(ch_names=ch_names, ch_types='eeg', montage=montage, sfreq=sfreq)
evoked = mne.EvokedArray(data=proj_pre, info=info)
times = np.arange(0.0, 2.5, 0.25)
evoked.plot_topomap(show=False, times=times, title='The projected data onto the eigenspace of pre-
trial onset')
# evoked.plot(show=False, window_title='window title', titles='The first four PCs for pre-onset da
ta')
```

Out[45]:



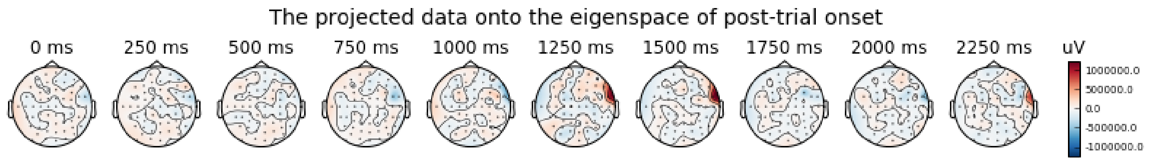
In [46]:
```
# It is also possible to use info from another raw object.
# info = mne.create_info(ch_names, sfreq, ch_types=None, montage=None, verbose=None)
# info = mne.create_info(ch_names=4, sfreq=sfreq, ch_types='eeg')
info = mne.create_info(ch_names=ch_names, ch_types='eeg', montage=montage, sfreq=sfreq)
evoked = mne.EvokedArray(data=proj, info=info)
evoked.plot_topomap(show=False, times=times, title='The projected data onto the eigenspace of the
 entire trial including the onset')
# evoked.plot(show=False, window_title='window title', titles='The first four PCs for pre-onset da
ta')
```

Out[46]:



In [47]:
```
# It is also possible to use info from another raw object.
# info = mne.create_info(ch_names, sfreq, ch_types=None, montage=None, verbose=None)
# info = mne.create_info(ch_names=4, sfreq=sfreq, ch_types='eeg')
info = mne.create_info(ch_names=ch_names, ch_types='eeg', montage=montage, sfreq=sfreq)
evoked = mne.EvokedArray(data=proj_post, info=info)
evoked.plot_topomap(show=False, times=times, title='The projected data onto the eigenspace of post
-trial onset')
# evoked.plot(show=False, window_title='window title', titles='The first four PCs for pre-onset da
ta')
```

Out[47]:


The projected data onto the eigenspace of post-trial onset
0 ms
250 ms
500 ms
750 ms
1000 ms
1250 ms
1500 ms
1750 ms
2000 ms
2250 ms
uV
1000000.0
500000.0
0.0
-500000.0
-1000000.0

In [ ]: