Neural Networks – Code

Line Kruse - 201608877 Study Group 6

```
1
 ##############################
 3 # LOAD DATA AND PREPARE TRAINING AND TEST SETS
 #############################
 5 from __future__ import print_function
 6 import keras
7 from keras datasets import mnist
8 from keras.models import Sequential
 9 from keras.layers import Dense, Dropout, Flatten
10 from keras.layers import Conv2D, MaxPooling2D
11 from keras import backend as K
12 import matplotlib.pyplot as plt
13
14 batch_size = 128
15 num_classes = 10
16 epochs = 5 # Original code has 12 epochs
17
18 # input image dimensions
19 img_rows, img_cols = 28, 28
20
21 # the data, split between train and test sets
22 (x_train, y_train), (x_test, y_test) = mnist.load_data()
23 print(x_train.shape)
24
25 if K.image data format() == 'channels first':
      x_train = x_train.reshape(x_train.shape[0], 1, img_rows, img_cols)
26
      x_test = x_test.reshape(x_test.shape[0], 1, img_rows, img_cols)
27
28
      input_shape = (1, img_rows, img_cols)
29 else:
30
      x_train = x_train.reshape(x_train.shape[0], img_rows, img_cols, 1)
31
      x_test = x_test.reshape(x_test.shape[0], img_rows, img_cols, 1)
32
      input_shape = (img_rows, img_cols, 1)
33
34 x_train = x_train.astype('float32')
35 x_test = x_test.astype('float32')
36 \times train /= 255
37 x_test /= 255
38
39 #Take 5000 out of 60000 subset of training data to improve speed
40 x_train =x_train[0:5000,:,:,:]
41 y_train=y_train[0:5000]
42 print(y_train[0:10])
43
44
45 #Take 1000 out of 10000 subset of test data to improve speed
46 x_test =x_test[0:1000,:,:,:]
47 y_test=y_test[0:1000]
48 print(y_test[0:10])
49
50 print('x_train shape:', x_train.shape)
51 print(x_train shape[0], 'train samples')
52 print(x_test shape[0], 'test samples')
53
```

```
54 # convert class label vectors to binary class matrices
55 y_train = keras.utils.to_categorical(y_train, num_classes)
56 y_test = keras.utils.to_categorical(y_test, num_classes)
57 print(v train[0])
58
59
60
############################
62 #CREATE MODEL 1 - FULLY CONNECTED FEEDFORWARD NETWORK
63 #Loss function: categorical crossentropy
64 #Optimizer: SGD
65
66 x_train_flat = x_train.reshape((x_train.shape[0], -1))
67 x test flat = x test.reshape((x test.shape[0], -1))
68
69 model = Sequential()
70 model.add(Dense(32, input_shape=(x_train_flat.shape[-1],),
   activation='relu'))
71 model.add(Dense(64, activation='relu'))
72 model.add(Dense(32, activation='relu'))
73 model.add(Dense(num_classes, activation='softmax'))
74
75 model.compile(loss=keras.losses.categorical_crossentropy,
76
                optimizer=keras.optimizers.Adadelta(),
                metrics=['accuracy'])
77
78 model.summary()
79
80 #TRAIN AND EVALUATE MODEL 1
81 model.fit(x_train_flat, y_train,
82
            batch_size=batch_size,
83
             epochs=epochs,
84
            verbose=1,
85
            validation_data=(x_test_flat, y_test))
86 score = model.evaluate(x_test_flat, y_test, verbose=0)
87 print('Test loss:', score[0])
88 print('Test accuracy:', score[1])
89
90
#############################
92 #CREATE MODEL 2 - CONVOLUTIONAL NETWORK
93 #Loss function: categorical crossentropy
94 #Optimizer: SGD
95
96 model = Sequential()
97 model.add(Conv2D(32, kernel_size=(3, 3),
98
                   activation='relu',
99
                   input_shape=input_shape))
100 model.add(Conv2D(64, (3, 3), activation='relu'))
101 model.add(MaxPooling2D(pool_size=(2,2)))
102 #model.add(Dropout(0.25)) #To prevent overfitting
103 model.add(Flatten()) #To input to fully connected layer
104 model.add(Dense(32, activation='relu')) #Fully connected layer
105 #model add(Dronout(0 5)) #To avoid overfitting
```

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TOO #HOUCE LAGUA DI OPOUCE OF STITE OF OF OF STITE CENTER
106 model.add(Dense(num classes, activation='softmax')) #Output layer
107
108 model.compile(loss=keras.losses.categorical_crossentropy,
                 optimizer=keras.optimizers.Adadelta(),
109
                 metrics=['accuracy'])
110
111 model.summary()
112
113 #TRAIN AND EVALUATE MODEL 2
114 model.fit(x_train_flat, y_train,
             batch_size=batch_size,
115
116
             epochs=epochs,
117
             verbose=1,
118
             validation data=(x test flat, y test))
119 score = model.evaluate(x_test_flat, y_test, verbose=0)
120 print('Test loss:', score[0])
121 print('Test accuracy:', score[1])
122
123
124
##############################
126 #COMPARE OPTIMIZERS
127
128 #MODEL 2 - Fully connected feedforward neural network:
129 #Loss function: categorical crossentropy
130 #Optimizer: Adadelta
131
132 x_train_flat = x_train.reshape((x_train.shape[0], -1))
133 x_test_flat = x_test.reshape((x_test.shape[0], -1))
134
135 model = Sequential()
136 model.add(Dense(32, input_shape=(x_train_flat.shape[-1],),
   activation='relu'))
137 model.add(Dense(64, activation='relu'))
138 model.add(Dense(32, activation='relu'))
139 model.add(Dense(num_classes, activation='softmax'))
141 model.compile(loss=keras.losses.categorical_crossentropy,
                 optimizer=keras.optimizers.Adadelta(),
142
143
                 metrics=['accuracy'])
144 model.summary()
145
146 #Train and evaluate model
147 model.fit(x train flat, y train,
             batch size=batch size,
148
149
             epochs=epochs,
150
             verbose=1.
             validation_data=(x_test_flat, y_test))
151
152 score = model.evaluate(x_test_flat, y_test, verbose=0)
153 print('Test loss:', score[0])
154 print('Test accuracy:', score[1])
155
156
157
```

```
159 #MODEL 4 - Convolutional neural network:
160 #Loss function: categorical crossentropy
161 #Optimizer: Adadelta
162 model = Sequential()
163 model.add(Conv2D(32, kernel_size=(3, 3),
                   activation='relu',
164
165
                    input_shape=input_shape))
166 model.add(Conv2D(64, (3, 3), activation='relu'))
167 model.add(MaxPooling2D(pool_size=(2, 2)))
168 #model.add(Dropout(0.25)) #To prevent overfitting
169 model.add(Flatten()) #To input to fully connected layer
170 model.add(Dense(32, activation='relu')) #Fully connected layer
171 #model.add(Dropout(0.5)) #To avoid overfitting
172 model.add(Dense(num_classes, activation='softmax')) #Output layer
173
174 model.compile(loss=keras.losses.categorical_crossentropy,
175
                 optimizer=keras.optimizers.Adadelta(),
                 metrics=['accuracy'])
176
177 model.summary()
178
179 #TRAIN AND EVALUATE MODEL 3
180 model.fit(x_train_flat, y_train,
             batch_size=batch_size,
181
182
             epochs=epochs,
183
             verbose=1,
184
             validation_data=(x_test_flat, y_test))
185 score = model.evaluate(x_test_flat, y_test, verbose=0)
186 print('Test loss:', score[0])
187 print('Test accuracy:', score[1])
188
189
190
191
192
193
194
195
```

MEG Analysis – Code

Study Group 6

```
1 | """
 2 MEG analysis - Classification algorithms
 4 @author: Martin, Christoffer, Line and Simon (Study Group 6)
 5
 6
7 # Import libraries
 8 import numpy as np
 9 import pandas as pd
10 from sklearn.naive_bayes import GaussianNB
11 from sklearn.model selection import cross val score
12 from sklearn.svm import SVC
13 from sklearn.neighbors import KNeighborsClassifier
14 import matplotlib.pyplot as plt
15 from sklearn.pipeline import make_pipeline
16 from sklearn.preprocessing import StandardScaler
17 import statsmodels.stats.api as sms
18
19 # Import data and labels
20 labels = np.load('pos_neg_img_labels.npy')
21 data = np.load('pos_neg_img_trials.npy')
23 # Loop through each sample and perform cross-validation (linear SVM)
24 n_samples = data.shape[2] # Get number of samples
25 index=np.arange(0)
26 Classification = pd.DataFrame(columns = ["Sample", "Score", "SD", "CI_low",
   "CI high"], index = index) # Create empty dataframe
27
28 for sample_index in range(n_samples):
29
       temp = data[:, :, sample_index] # Use all datapoints for the given sample index
       clf = SVC(kernel="linear", C=1) # Linear suport vector classifier
30
31
       clf = make_pipeline(StandardScaler(copy=False), clf) #Standardize data
32
       cv_score = cross_val_score(clf, temp, labels, cv=10) #perform 10-fold cross-
   validation
33
       mean_cv = np.mean(cv_score) # Mean
34
       sd_cv = np.std(cv_score) # Standard Deviation
       CI_low, CI_high=sms.DescrStatsW(cv_score).tconfint_mean() # 95 % Confidence
35
   intervals
       Classification = Classification.append({"Sample": sample_index, "Score":
36
   mean_cv, "SD": sd_cv, "CI_low": CI_low, "CI_high": CI_high}, ignore_index = True) #
   Append to dataframe
37
38 # Create a preliminary plot
39 plt.plot(Classification["Sample"], Classification["Score"])
40 plt.show()
41
42 # Save results csv file
43 Classification.to_csv('linearSVM.csv')
45 # Loop through each sample and perform cross-validation (GaussianNB)
46 n samples = data.shape[2]
47 index=np.arange(0)
48 Classification = pd.DataFrame(columns = ["Sample", "Score", "SD", "CI low",
   "CI_high"], index = index)
49
50 for sample_index in range(n_samples):
51
       temp = data[:, :, sample_index]
52
       clf = GaussianNB()
53
       clf = make pipeline(StandardScaler(copy=False), clf)
54
       cv_score = cross_val_score(clf, temp, labels, cv=10)
55
       mean_cv = np.mean(cv_score)
```

```
56
        sd_cv = np.std(cv_score)
 57
        CI low, CI_high=sms.DescrStatsW(cv_score).tconfint_mean()
        Classification = Classification.append({"Sample": sample_index, "Score":
    mean_cv, "SD": sd_cv, "CI_low": CI_low, "CI_high": CI_high}, ignore_index = True)
 59
 60 # Make preliminary plot
 61 plt.plot(Classification["Sample"], Classification["Score"])
 62 plt.show()
 63
 64 # Save results csv file
65 Classification.to csv('GaussianNB.csv')
66
 67 # Loop through each sample and perform cross-validation (K-nearest neighbour )
 68 n samples = data.shape[2]
 69 index=np.arange(0)
70 Classification = pd.DataFrame(columns = ["Sample", "Score", "SD", "CI_low",
    "CI_high"], index = index)
71
 72 for sample index in range(n samples):
73
        temp = data[:, :, sample_index]
74
        clf = KNeighborsClassifier(3)
 75
        clf = make pipeline(StandardScaler(copy=False), clf)
 76
        cv_score = cross_val_score(clf, temp, labels, cv=10)
 77
        mean_cv = np.mean(cv_score)
 78
        sd_cv = np.std(cv_score)
 79
        CI_low, CI_high=sms.DescrStatsW(cv_score).tconfint_mean()
        Classification = Classification.append({"Sample": sample_index, "Score":
 80
    mean_cv, "SD": sd_cv, "CI_low": CI_low, "CI_high": CI_high}, ignore_index = True)
 81
 82 # Make preliminary plots
83 plt.plot(Classification["Sample"], Classification["Score"])
 84 plt.show()
86 # Save results as csv file
87 Classification.to_csv('Knearest(3).csv')
88
89 """
90 MEG analysis - Plots
92 @author: Martin, Christoffer, Line and Simon (Study Group 6) (Adapted script from
    Lau)
93 """
94
95 # Import relevant libraries
96 from os.path import join ## connects strings into filepaths
97 import mne
98 import matplotlib.pyplot as plt # for plotting control
99 import numpy as np
100
101 # Set data path
102 data_path = 'C:\\Users\\Simon\\Documents\\MEG_numpy\\ME'
103
104 # Choose what subjects to analyse
105 subjects = [
                              'Group1',
106 #
107 #
                              'Group2', # noisy: change rejection parameters
                              'Group3',
108 #
                              'Group4',
109 #
                              'Group5',
110 #
                              'Group6',
111
                              'Group7'
112 #
```

```
113
                         ]
114
115 # Specify filename
116 filename = 'Session_70_Hz-ave.fif'
117
118 # Close all exisiting figures
119 plt.close('all')
120
121 # Loop over choosen subjects
122 for subject in subjects:
        # Read in the evokeds
        evokeds = mne.read evokeds(join(data path, subject, filename))
124
125
        for evoked in evokeds: # loop through evokeds
            # Pick the two stimulus classes ("img_pos" and "img_neg")
126
            if evoked.comment == 'img_pos' or evoked.comment == 'img_neg':
127
128
                # Create butterfly plots
                evoked.plot(window_title=subject + '_' + evoked.comment)
129
130
                evoked.plot(spatial_colors=True, gfp=True, picks='meg')
                # Create topomaps
131
132
                evoked.plot_topomap(times='peaks', ch_type='mag', time_unit='s')
133
134
135 # Plot Global Field Power
conditions = ["img_pos", "img_neg"] # Specify condition
137 evoked_dict = dict() # Create empty dictionary
138 for condition in conditions: # Loop through conditions
139
        evoked_dict[condition.replace(" ", "/")] = mne.read_evokeds(
140
            join(data path, subject, filename), baseline=(None, 0), proj=True,
    condition=condition) # Read in evokeds and append to dictionary
141 print(evoked_dict) # Print to check
143 colors = dict(img_pos="Crimson", img_neg="CornFlowerBlue") # Choose colours for each
    condition
144
145 # Create the plot based on the evoked dictionary
146 mne.viz.plot compare evokeds(evoked dict, colors=colors, split legend=True)
```

```
1 | """
 2 MEG analysis - Classification performance plots
4 @author: Martin, Christoffer, Line and Simon (Study Group 6)
5
6
7 #---- Libraries -----
8 library(ggplot2)
10 #---- Paths ----
11 #Set working directory
12 setwd("C:\\Users\\Martin\\Documents\\UNI\\7th semester\\Advanced Neuro\\exam\\meg")
13
14 #Paths to data
15 NB path = "GaussianNB.csv"
16 SVC_path = "SVCC1.csv"
17 KN path = "KNearest(3).csv"
18
19 #---- Load data ----
20 #Naive bayes classifier
21 NB_data = read.csv(NB_path) #Read file
22 NB_data$Sample = NB_data$Sample-500 #move stimulus presentation to 0
23 NB_data[NB_data$Score == max(NB_data$Score),] #Find sample with max accuracy
24
25 #Linear support vector machine
26 SVC_data = read.csv(SVC_path) #Read file
27 SVC data$Sample = SVC data$Sample-500 #move stimulus presentation to 0
28 SVC_data[SVC_data$Score == max(SVC_data$Score),] #Find sample with max accuracy
29
30 #Knearest neighbours, 3
31 #Linear support vector machine
32 KN_data = read.csv(KN_path) #Read file
33 KN_data$Sample = KN_data$Sample-500 #move stimulus presentation to 0
34 KN data[KN data$Score == max(KN data$Score),] #Find sample with max accuracy
35
36
37 #---- Plot data -----
38 #Naive bayes
39 ggplot(NB_data, aes(x = Sample, y = Score))+
    scale_x_continuous(breaks=seq(-500,1000,100))+ #Fix x axis interval and increment
41
    ylim(0.25, 1)+ #Y-axis limits
42
    geom_ribbon(aes(ymin = CI_low, ymax = CI_high), fill = "grey", alpha = 0.5)+ #CI
43
    geom vline(xintercept = 0, color = "red")+ #Vertical line at x = 0
44
    geom line()+ #Line between scores
    geom_hline(yintercept = 0.5, linetype = "dashed", color = "black")+ #Dashed line
45
  at chance level
46
    labs(title ="Accuracy of Naive Bayes Classifier Over Time", #Labels
47
          x = "Time after stimulus in ms",
          y = "Accuracy")+
48
49
    theme_minimal() #Theme
50
51 #Linear support vector machine
52 ggplot(SVC data, aes(x = Sample, y = Score))+
53
    scale_x_continuous(breaks=seq(-500,1000,100))+ #Fix x axis interval and increment
54
    ylim(0.25, 1) + #Y-axis limits
     geom_ribbon(aes(ymin = CI_low, ymax = CI_high), fill = "grey", alpha = 0.5)+ #CI
55
     geom_vline(xintercept = 0, color = "red")+ \#Vertical\ line\ at\ x=0
56
57
    geom_line()+ #Line between scores
58
    geom hline(yintercept = 0.5, linetype = "dashed", color = "black")+ #Dashed line
  at chance level
59
    labs(title ="Accuracy of Linear Support Vector Machine Over Time", #Labels
```

```
60
          x = "Time after stimulus in ms",
         y = "Accuracy")+
61
62
    theme_minimal() #Theme
63
64 #K nearest neighbours, k=3
65 ggplot(KN_data, aes(x = Sample, y = Score))+
    scale_x_continuous(breaks=seq(-500,1000,100))+ #Fix x axis interval and increment
67
    ylim(0.25, 1)+ #Y-axis limits
    geom_ribbon(aes(ymin = CI_low, ymax = CI_high), fill = "grey", alpha = 0.5)+ #CI
68
69
    geom_vline(xintercept = 0, color = "red")+ #Vertical line at x = 0
70
    geom_line()+ #Line between scores
    geom_hline(yintercept = 0.5, linetype = "dashed", color = "black")+ #Dashed line
  at chance level
   labs(title ="Accuracy of K Nearest Neighbour Classifier (K = 3) Over Time",
73
         x = "Time after stimulus in ms",
         y = "Accuracy")+
74
75
    theme_minimal() #Theme
```

$fMRI\,Analysis-Code$

Study Group 6

```
0.00
 1
  fMRI analysis - Classification algorithms
 3
 4 @author: Martin, Christoffer, Line and Simon (Study Group 6)
 5
 6
 7
  %matplotlib inline
 8
 9 #Adding data paths
10
11 #The fMRI data
12 fmri_filename='/Users/christoffer/Documents/CogSci/MA/Neuro/fMRI/subject064_r
   esults/beta4D.nii'
13
14 #Normalized Structural file
15 anat_filename='/Users/christoffer/Documents/CogSci/MA/Neuro/spm12/canonical/s
   ingle_subj_T1.nii'
16
17 #A whole brain mask
18 mask wb filename='/Users/christoffer/Documents/CogSci/MA/Neuro/fMRI/subject06
   4_results/mask.nii'
19
20 #The classification labels
21 class filename='/Users/christoffer/Documents/CogSci/MA/Neuro/fMRI/scripts/cla
   ss labels faces.txt'
22
23
24
25
26 # Making training and test split
27
28 import pandas as pd
29 import numpy as np
30 #from nilearn import datasets
31 from nilearn.image import new_img_like, load_img, index_img, clean_img
32 from sklearn.model_selection import train_test_split
33
34 # Reshaping data--
35 from nilearn.image import index_img, concat_imgs
36
37 #load fMRI data
38 fmri_img = load_img(fmri_filename)
39 #Print dimensions of data to get overview
40 print(fmri_img.shape)
41
42
43 #fmri_img=clean_img(fmri_img_raw, sessions=None, detrend=True,
   standardize=True, confounds=None, low_pass=None, high_pass=1/128, t_r=2,
   ensure_finite=False, mask_img=None)
44
45 #load csv-file with class labels
46 conditions = pd.read_csv(class_filename, sep=",")
47 conditions = conditions['labels']
48 #Print dimensions of data
49 print(conditions.shape)
50
51 #Make an index for spliting fMRI data with same size as class labels
52 idx=np.arange(conditions.shape[0])
53 # create training and testing vars on the basis of class labels
```

```
54 #the function train_test_split outputs 4 values --> we need to make sure the
   names of the outputs are correct
55 idx1,idx2, conditions1, conditions2 = train_test_split(idx,conditions,
   test size=0.2)
56 print(idx1, idx2)
57
58 # Reshaping data----
59 from nilearn.image import index_img
60 fmri img1 = index img(fmri img, idx1)
61 fmri_img2 = index_img(fmri_img, idx2)
62 #Check data sizes
63 print(fmri_img1.shape)
64 print(fmri_img2.shape)
65
66
67
68 # SEARCHLIGHT
69 import pandas as pd
70 import numpy as np
71 from nilearn.image import new_img_like, load_img
72 from nilearn.plotting import plot_stat_map, plot_img, show
73 from nilearn import decoding
74 from nilearn.decoding import SearchLight
75 from sklearn import naive_bayes, model_selection #import GaussianNB
76 from sklearn.naive_bayes import GaussianNB
77
79
80 #Load the whole brain mask
81 mask_img = load_img(mask_wb_filename)
82 process mask = mask img.get data().astype(np.int)
83 process_mask_img = new_img_like(mask_img, process_mask)
84
85 #Plot the searchlight scores on an anatomical background
86|plot_img(process_mask_img, bg_img=anat_filename, #bg_img=mean_fmri,
            title="Mask", display_mode="x",cut_coords=
87
   [28, 32, 36, 40, 44, 48, 52, 56, 60, 64, 68, 72],
            vmin=.40, cmap='jet', threshold=0.9, black_bg=True)
88
90
91 # USING NB
92 # The radius is the one of the Searchlight sphere that will scan the volume
93 searchlight = SearchLight(
94
       mask_img,
95
       estimator=GaussianNB(),
96
       process_mask_img=process_mask_img,
97
       radius=5, n_jobs=1,
98
       verbose=1, cv=8)
99 searchlight.fit(fmri_img1, conditions1) #Run function on training data
   (fmri_img1) for condition 1.
100
101 #USING SVM
102 # The radius is the one of the Searchlight sphere that will scan the volume
103 searchlight = SearchLight(
104
       mask_img,
       process_mask_img=process_mask_img,
105
106
       radius=5, n_jobs=1,
107
       verbose=1, cv=8)
108 searchlight.fit(fmri_img1, conditions1) #Run function on training data
   (fmri_img1) for condition 1.
```

```
109
110 #USING k-NN
111 from sklearn import neighbors, datasets
112 searchlight = SearchLight(
113
        mask img,
114
        estimator=neighbors.KNeighborsClassifier(3),
115
        process_mask_img=process_mask_img,
116
        radius=5, n_jobs=1,
117
        verbose=1, cv=8)
118 searchlight.fit(fmri img1, conditions1) #Run function on training data
    (fmri_img1) for condition 1.
119
120
121 # 500 BEST VOXELS
122 print(searchlight.scores .size)
123 #Find the percentile that makes the cutoff for the 500 best voxels
124 perc=100*(1-500.0/searchlight.scores_.size)
125 #Print percentile
126 print(perc)
127 #Find the cutoff
128 cut=np.percentile(searchlight.scores_,perc)
129 #Print cutoff
130 print(cut)
131
132 #Make a mask using cutoff
133
134 #Load the whole brain mask
135 mask_img2 = load_img(mask_wb_filename)
136
137
138 # MAKE GLASS BRAIN PLOT
139 # .astype() makes a copy.
140 process_mask2 = mask_img2.get_data().astype(np.int)
141 process_mask2[searchlight.scores_<=cut] = 0
142 process_mask2_img = new_img_like(mask_img2, process_mask2)
143
144 rom nilearn import image
145 from nilearn.plotting import plot_stat_map, plot_img, show
146 from nilearn import plotting
147 %matplotlib inline
148 #Create an image of the searchlight scores
149 searchlight_img = new_img_like(anat_filename, searchlight.scores_)
150 print(searchlight img.shape)
151
152 #Ploting all voxels
153 plotting.plot_glass_brain(searchlight_img)
154
155 #Plotting 500 best voxels
156 plotting.plot_glass_brain(searchlight_img, threshold=cut)
157
158
159
160
161 #CLASSIFICATION
162 #using NB
163 from nilearn.input_data import NiftiMasker
164 masker = NiftiMasker(mask_img=process_mask2_img, standardize=False)
165
166 # We use masker to retrieve a 2D array ready
167 # for machine learning with scikit-learn
```

```
168 fmri_masked = masker.fit_transform(fmri_img2)
169 #Print size of matrix (images x voxels)
170 print(fmri_masked.shape)
171
172 from sklearn naive bayes import GaussianNB
173 from sklearn.model_selection import cross_val_score
174 cv_score = cross_val_score(GaussianNB(), fmri_masked, conditions2, cv=4)
175 print(cv_score)
176 print('Mean prediction score:')
177 print(np.mean(cv score))
178
179 #Using SVM
180 from nilearn.input_data import NiftiMasker
181 masker = NiftiMasker(mask_img=process_mask2_img, standardize=False)
183 # We use masker to retrieve a 2D array ready
184 # for machine learning with scikit-learn
185 fmri_masked = masker.fit_transform(fmri_img2)
186 #Print size of matrix (images x voxels)
187 print(fmri_masked.shape)
188
189 from sklearn.naive_bayes import GaussianNB
190 from sklearn.model_selection import cross_val_score
191 from sklearn import svm
192 cv_score = cross_val_score(svm.SVC(kernel='linear', C=1), fmri_masked,
   conditions2, cv=4)
193 print(cv_score)
194 print('Mean prediction score:')
195 print(np.mean(cv_score))
196
197 #Using k-NN
198 from nilearn.input_data import NiftiMasker
199 masker = NiftiMasker(mask_img=process_mask2_img, standardize=False)
200
201 # We use masker to retrieve a 2D array ready
202 # for machine learning with scikit-learn
203 fmri_masked = masker.fit_transform(fmri_img2)
204 #Print size of matrix (images x voxels)
205 print(fmri_masked.shape)
206
207 from sklearn.naive_bayes import GaussianNB
208 from sklearn.model_selection import cross_val_score
209 cv_score = cross_val_score(neighbors.KNeighborsClassifier(3), fmri_masked,
   conditions2, cv=4)
210 print(cv_score)
211 print('Mean prediction score:')
212 print(np.mean(cv score))
213
214 #PERMUTATION TESTS
215 #using NB
216 from sklearn.model_selection import permutation_test_score
217 score, permutation_scores, pvalue= permutation_test_score(
218
       GaussianNB(), fmri_masked, conditions2, cv=4, n_permutations=100,
219
        n_jobs=1, random_state=0, verbose=0, scoring=None)
220 print("Classification Accuracy: %s (pvalue : %s)" % (score, pvalue))
221
222 #using SVM
223 from sklearn.model_selection import permutation_test_score
224 score, permutation_scores, pvalue= permutation_test_score(
```

```
svm.SVC(kernel='linear', C=1), fmri_masked, conditions2, cv=4,
225
   n_permutations=100,
226
       n_jobs=1, random_state=0, verbose=0, scoring=None)
227 print("Classification Accuracy: %s (pvalue : %s)" % (score, pvalue))
228
229 #using k-NN
230 from sklearn.model_selection import permutation_test_score
231 score, permutation_scores, pvalue= permutation_test_score(
       neighbors.KNeighborsClassifier(3), fmri_masked, conditions2, cv=4,
   n permutations=100,
233
       n_jobs=1, random_state=0, verbose=0, scoring=None)
234 print("Classification Accuracy: %s (pvalue : %s)" % (score, pvalue))
235
236
237
238 #Plot permutation histogram
239 import numpy as np
240 import matplotlib.pyplot as plt
241 #How many classes
242 n classes = np.unique(conditions2).size
243
244 plt.hist(permutation_scores, 20, label='Permutation scores',
245
             edgecolor='black')
246 ylim = plt.ylim()
247 plt.plot(2 * [score], ylim, '--g', linewidth=3,
248
             label='Classification Score'
             ' (pvalue %s)' % pvalue)
249
250 plt.plot(2 * [1. / n_classes], ylim, '--k', linewidth=3, label='Chance
   level')
251
252 plt.ylim(ylim)
253 plt.legend()
254 plt.xlabel('Score')
255 plt.show()
```