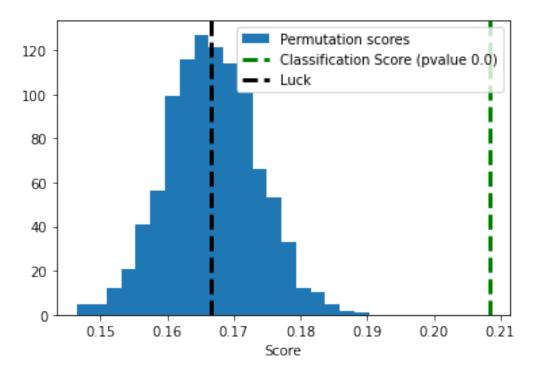
```
import os
import random
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import sklearn.metrics as sm
from sklearn import sym
from sklearn.model selection import GroupKFold
from sklearn.pipeline import make pipeline
from sklearn.preprocessing import StandardScaler
from sklearn.model selection import permutation test score
from google.colab import drive
drive.mount("/content/drive", force remount=True)
os.chdir('/content/drive/MyDrive/Colab Notebooks/PSY3100')
Mounted at /content/drive
Making it easy to iterate
def group permutation(area, n permutations = 1000, n features = None,
seed = None):
  numSubi = 10
  scores = []
  permutations = []
  for subj in range(numSubj):
    # construct file name
    filename = 'fMRI Scenes/S%02d %s.csv' % (subj + 1, area.upper())
    print('Processing Subj %d out of %d: %s' % (subj+1, numSubj,
filename))
    allData = pd.read csv(filename, sep=r',', skipinitialspace = True,
index col='type')
    # only use lineDrawings data
    lineData = allData.loc['lineDrawings']
    labels = lineData['category'].to numpy()
    runIdx = lineData['run'].to numpy()
    if n features is None:
      samples = lineData.iloc[:, 2:].to numpy()
      samples = lineData.iloc[:, 2:n features].to numpy()
    # set up cross validation classification
    numSplits = len(np.unique(runIdx))
    CVfolds = GroupKFold(n splits=numSplits)
```

```
# defining the model (using the same one Prof. Dirk used)
    clf = make pipeline(StandardScaler(), svm.SVC(kernel='linear'))
    # run permutation analysis
    random.seed(seed)
    score, permutation_scores, _ = permutation_test_score(clf,
samples, labels, groups=runIdx, scoring='accuracy', cv = CVfolds,
n permutations=n permutations, n jobs=-1)
    scores.append(score)
    permutations.append(permutation scores)
  return np.mean(score), np.mean(permutations, axis=0), scores,
permutations
def plot results(mean score, mean perm):
  chance = 1/6
  pvalue = (mean_score < mean_perm).sum() / len(mean_perm)</pre>
  plt.hist(mean perm, 20, label='Permutation scores')
  ylim = plt.ylim()
  (pvalue %s)' % pvalue)
  plt.vlines(chance, ylim[0], ylim[1], linestyle='--',
           color='k', linewidth=3, label='Luck')
  plt.ylim(ylim)
  plt.legend()
  plt.xlabel('Score')
  plt.show()
PPA (using the first 20 features)
%%time
mean score, mean perm, scores, perms = group permutation('ppa', 1000,
n features=20, seed=1)
print('\nMean score: %.3f | std: %.3f' % (mean score, np.std(scores)))
plot results(mean score, mean perm)
Processing Subj 1 out of 10: fMRI Scenes/S01 PPA.csv
Processing Subj 2 out of 10: fMRI Scenes/S02 PPA.csv
Processing Subj 3 out of 10: fMRI Scenes/S03 PPA.csv
Processing Subj 4 out of 10: fMRI_Scenes/S04_PPA.csv
Processing Subj 5 out of 10: fMRI Scenes/S05 PPA.csv
Processing Subj 6 out of 10: fMRI Scenes/S06 PPA.csv
Processing Subj 7 out of 10: fMRI_Scenes/S07_PPA.csv
Processing Subj 8 out of 10: fMRI Scenes/S08 PPA.csv
Processing Subj 9 out of 10: fMRI Scenes/S09 PPA.csv
```

Processing Subj 10 out of 10: fMRI_Scenes/S10_PPA.csv

Mean score: 0.208 | std: 0.033



CPU times: user 1min 4s, sys: 3.26 s, total: 1min 7s

Wall time: 43min 25s

V1 (using the first 20 features)

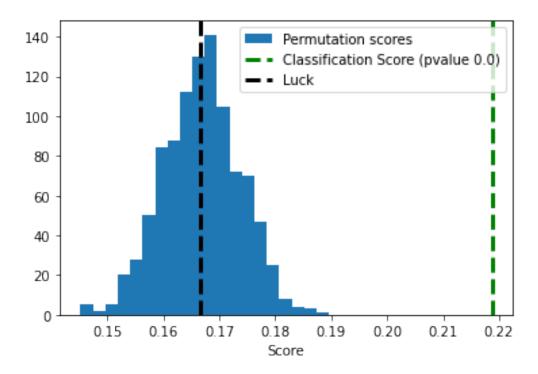
Runtime significanty higher because of the number of permutations (43 min 25s).

P-value was zero, meaning that none of the permutations exceeded the performance on the original labels.

```
%%time
mean_score, mean_perm, scores, perms = group_permutation('v1', 1000,
n_features=20, seed=1)
print('\nMean score: %.3f | std: %.3f' % (mean_score, np.std(scores)))
plot_results(mean_score, mean_perm)

Processing Subj 1 out of 10: fMRI_Scenes/S01_V1.csv
Processing Subj 2 out of 10: fMRI_Scenes/S02_V1.csv
Processing Subj 3 out of 10: fMRI_Scenes/S03_V1.csv
Processing Subj 4 out of 10: fMRI_Scenes/S04_V1.csv
Processing Subj 5 out of 10: fMRI_Scenes/S05_V1.csv
Processing Subj 6 out of 10: fMRI_Scenes/S06_V1.csv
Processing Subj 7 out of 10: fMRI_Scenes/S07_V1.csv
Processing Subj 8 out of 10: fMRI_Scenes/S08_V1.csv
Processing Subj 9 out of 10: fMRI_Scenes/S09_V1.csv
Processing Subj 10 out of 10: fMRI_Scenes/S09_V1.csv
```

Mean score: 0.219 | std: 0.027



CPU times: user 1min, sys: 2.73 s, total: 1min 3s

Wall time: 43min 17s

Runtime significanty higher because of the number of permutations (43min 17s).

P-value was zero, meaning that none of the permutations exceeded the performance on the original labels.