Importing Packages & Set Up Data Layout

Preprocessing Information for the Given Data.

A high-pass filter with a 30 Hz cut-off frequency and a power line notch filter (50 Hz) were used. All recordings are artifact-free EEG segments of 60 seconds duration. At the stage of data preprocessing, the Independent Component Analysis (ICA) was used to eliminate the artifacts (eyes, muscle, and cardiac overlapping of the cardiac pulsation). The arithmetic task was the serial subtraction of two numbers. Each trial started with the communication orally 4-digit (minuend) and 2-digit (subtrahend) numbers (e.g. 3141 and 42).

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In [1]: # Let's load some packages we need (pip install mne)
              import mne
              import mne.viz
              from mne.datasets import eegbci
              from mne.io import concatenate raws, read raw edf
              from mne.channels import make standard montage
              import numpy as np
              import scipy as sp
              import matplotlib.pyplot as plt
              # ! pip install mne
              # Read raw data files where each file contains a run
              files = ['../../datasets/HW2Datasets/Subject06_1.edf', '../../datasets/HW2Datasets/Subject06_2.edf', '../../datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Datasets/HW2Dataset
              # Read the raw EDF files into an array
              raws = [read_raw_edf(f, preload=True) for f in files]
              # Loop through the array and make the following changes to the raw files
               for raw in raws:
                      # Rename the raw channels
                      raw.rename_channels({'EEG F3':'F3', 'EEG F4':'F4',
                                                                 'EEG Fp1':'Fp1', 'EEG Fp2':'Fp2', 'EEG F7':'F7', 'EEG F8':'F8', 'EEG T3':'T3', 'EEG T4':'T4', 'EEG C3':'C3', 'EEG C4':'C4',
                                                                 'EEG T5':'T5', 'EEG T6':'T6', 'EEG P3':'P3', 'EEG P4':'P4',
                                                                 'EEG 01':'01', 'EEG 02':'02', 'EEG Fz':'Fz', 'EEG 'EEG Pz':'Pz', 'EEG A2-A1':'A2', 'ECG ECG':'ECG'})
                                                                                                                                               'EEG Cz':'Cz',
                     # Set channel types
                      raw.set_channel_types({'ECG':'ecg'})
                      # Define the channel locations
                      raw.set_montage(mne.channels.make_standard_montage('standard_1020'))
                      # Print Raw Channel Names for double checking
                      print(raw.ch_names)
               # Rename the raws with more insightfull names
              subject6 background = raws[0] # Subject 6 background raw
              subject6 task = raws[1] # Subject 6 task raw
              subject7_background = raws[2] # Subject 7 background raw
              subject7_task = raws[3] # Subject 7 task raw
              # Function to segment data into non-overlapping windows of length 300 samples
              def segment_data(raw, window_size=300):
                      data = raw.get_data() # Get the raw data
                      n channels, n samples = data.shape # get dimensions
                      print("Data Shape Before:", n_channels, n_samples) # display dimensions for understanding
                     n_windows = n_samples // window_size # Number of windows
                     # Reshape data into (n channels, n windows, window size)
                      segmented_data = data[:, :n_windows * window_size].reshape(n_channels, n_windows, window_size)
                      print("Data Shape After:", n_channels, n_windows, window_size) # display shape after reshaping
                      return segmented data # return the segmented data
              # Segment each raw file into windows
              subject6_background_segments = segment_data(subject6_background)
              subject6_task_segments = segment_data(subject6_task)
              subject7_background_segments = segment_data(subject7_background)
              subject7_task_segments = segment_data(subject7_task)
              # Create labels: 0 for background, 1 for task
              subject6 background labels = np.zeros(subject6 background segments.shape[1])
              subject6 task labels = np.ones(subject6 task segments.shape[1])
              subject7 background labels = np.zeros(subject7 background segments.shape[1])
              subject7 task labels = np.ones(subject7 task segments.shape[1])
```

```
# Concatenate data for both subjects
 X = np.concatenate([subject6 background segments, subject6 task segments,
                     subject7 background segments, subject7 task segments], axis=1)
 # Concatenate labels for both subjects
 y = np.concatenate([subject6 background labels, subject6 task labels,
                     subject7 background labels, subject7 task labels])
 # Reshape the data for model training (n_samples, n_features)
 X = X.reshape(X.shape[1], -1) # (n_windows, n_channels * window_size)
 # X shape will be (n channels, total windows * window size), and y will be the labels for each window
 print("Shape of segmented data:", X.shape) # See the dimensions of X
 print("Shape of labels:", y.shape) # See the dimensions of y
Extracting EDF parameters from /home/joshua/Desktop/MainFolder/OuClasses/2024 Fall/Neural-Data-Science/datasets/
HW2Datasets/Subject06_1.edf...
EDF file detected
Setting channel info structure...
Creating raw.info structure...
Reading 0 ... 90999 =
                          0.000 ... 181.998 secs...
Extracting EDF parameters from /home/joshua/Desktop/MainFolder/OuClasses/2024 Fall/Neural-Data-Science/datasets/
HW2Datasets/Subject06 2.edf...
EDF file detected
Setting channel info structure...
Creating raw.info structure...
Reading 0 ... 30999 = 0.000 ... 61.998 secs...
Extracting EDF parameters from /home/joshua/Desktop/MainFolder/OuClasses/2024 Fall/Neural-Data-Science/datasets/
HW2Datasets/Subject07 1.edf...
EDF file detected
Setting channel info structure...
Creating raw.info structure...
Reading 0 ... 90999 =
                          0.000 ...
                                      181.998 secs...
Extracting EDF parameters from /home/joshua/Desktop/MainFolder/OuClasses/2024 Fall/Neural-Data-Science/datasets/
HW2Datasets/Subject07_2.edf...
EDF file detected
Setting channel info structure...
Creating raw.info structure...
Reading 0 ... 30999 =
                           0.000 ...
                                        61.998 secs...
['Fp1', 'Fp2', 'F3', 'F4', 'F7', 'F8', 'T3', 'T4', 'C3', 'C4', 'T5', 'T6', 'P3', 'P4', '01', '02', 'Fz', 'Cz', '
Pz', 'A2', 'ECG']
['Fp1', 'Fp2', 'F3', 'F4', 'F7', 'F8', 'T3', 'T4', 'C3', 'C4', 'T5', 'T6', 'P3', 'P4', '01', '02', 'Fz', 'Cz', '
Pz', 'A2', 'ECG']
['Fp1', 'Fp2', 'F3', 'F4', 'F7', 'F8', 'T3', 'T4', 'C3', 'C4', 'T5', 'T6', 'P3', 'P4', '01', '02', 'Fz', 'Cz', '
['Fp1', 'Fp2', 'F3', 'F4', 'F7', 'F8', 'T3', 'T4', 'C3', 'C4', 'T5', 'T6', 'P3', 'P4', '01', '02', 'Fz', 'Cz', '
Pz', 'A2', 'ECG']
Data Shape Before: 21 91000
Data Shape After: 21 303 300
Data Shape Before: 21 31000
Data Shape After: 21 103 300
Data Shape Before: 21 91000
Data Shape After: 21 303 300
Data Shape Before: 21 31000
Data Shape After: 21 103 300
Shape of segmented data: (812, 6300)
Shape of labels: (812,)
```

Q2)

Repeat the analysis in (Q1) using the 5-fold cross validation technique. Compare the results with the previous case and provide detailed explanation of potential causes of these differences.

Previously...

```
In [2]: # Import ML Libraries
    from sklearn.model_selection import train_test_split
    from sklearn.linear_model import LogisticRegression
    from sklearn.metrics import accuracy_score, balanced_accuracy_score, f1_score

# Split the dataset into 50% train and 50% test set
    X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.5, random_state=42)
    print("Total Number of Train Values", len(y_train)) # See number of trained values
    print("Total Number of y=1 Train Values", sum(y_train)) # See number of y=1 values

# Initialize the Logistic Regression model
model = LogisticRegression(max_iter=1000)
```

```
# Fit the model
 model.fit(X train, y train)
 # Predict on the test set
 y pred = model.predict(X test)
 # Evaluate the model using accuracy
 accuracy = accuracy_score(y_test, y_pred)
 # Evaluate the model using balanced accuracy
 balanced_accuracy = balanced_accuracy_score(y_test, y_pred)
 # Evaluate the model using f1 score
 f1 = f1 score(y test, y pred)
 # Print accuracy
 print(f"Accuracy: {accuracy*100:.2f}%")
 # Print balanced accuracy
 print(f"Balanced Accuracy: {balanced accuracy*100:.2f}%")
 # Print fl score
 print(f"F1 Score: {f1*100:.2f}%")
Total Number of Train Values 406
Total Number of y=1 Train Values 100.0
Accuracy: 73.89%
Balanced Accuracy: 50.00%
F1 Score: 0.00%
```

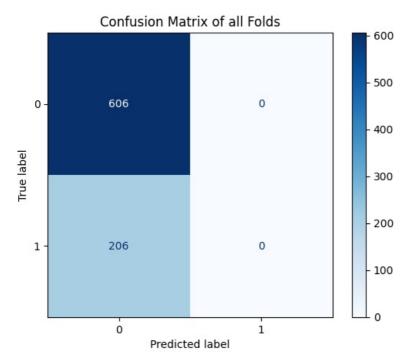
Last Question (Q1) I talked in detail why this model sucks & explained what each of the evaluation metrics mean.

This time we will do the same procedure as above, but using k-folds with k=5. This will allow us to have 5 different training and evaluating pools which could lead to different results.

```
In [3]: # Import library for k-folds
        from sklearn.model_selection import StratifiedKFold
        # Initialize the Logistic Regression model
        model = LogisticRegression(max_iter=1000)
        # Create k-folds where k=5
        skf = StratifiedKFold(n splits=5)
        folds = skf.split(X, y) # make different folds for X and y
        train idxs=[] # store training indexes
        test_idxs=[] # store test indexes
        total y test = [] # store all y test values
        total_y_pred = [] # store all y pred values
        # Loop through all folds
        for i, fold in enumerate(folds):
            train idx, test idx = fold # Grab indexes from fold
            train_idxs.append(train_idx) # append training indexes to the training list
            test idxs.append(test idx) # append testing indexes to the testing list
        # Loop through the 5 folds made previously
        for i in range(5):
           X train = X[train idxs[i][:]] # Load in the training X values from index i
            y_train = y[train_idxs[i][:]] # Load in the training y values from index i
            X test = X[test idxs[i][:]] # Load in the testing X values from index i
            y test = y[test idxs[i][:]] # Load in the testing y values from index i
            # Fit the model
            model.fit(X train, y train)
            # Predict on the test set
            y_pred = model.predict(X_test)
            # Extend total y test array
            total_y_test.extend(y_test)
            # Extend total y pred array
            total y pred.extend(y pred)
            # Print out the current fold we are itterating over
            print("Examining fold %i" % (i + 1))
            # Evaluate the model using accuracy
            accuracy = accuracy_score(y_test, y_pred)
            # Evaluate the model using balanced accuracy
```

```
balanced_accuracy = balanced_accuracy_score(y_test, y_pred)
             # Evaluate the model using f1 score
             f1 = f1_score(y_test, y_pred)
            # Print accuracy
            print(f"Accuracy: {accuracy*100:.2f}%")
             # Print balanced accuracy
             print(f"Balanced Accuracy: {balanced_accuracy*100:.2f}%")
             # Print fl score
             print(f"F1 Score: {f1*100:.2f}%\n")
       Examining fold 1
       Accuracy: 74.85%
       Balanced Accuracy: 50.00%
       F1 Score: 0.00%
       Examining fold 2
       Accuracy: 74.23%
       Balanced Accuracy: 50.00%
       F1 Score: 0.00%
       Examining fold 3
       Accuracy: 74.69%
       Balanced Accuracy: 50.00%
       F1 Score: 0.00%
       Examining fold 4
       Accuracy: 74.69%
       Balanced Accuracy: 50.00%
       F1 Score: 0.00%
       Examining fold 5
       Accuracy: 74.69%
       Balanced Accuracy: 50.00%
       F1 Score: 0.00%
In [6]: # Import library for confusion matrix
        from sklearn.metrics import confusion matrix, ConfusionMatrixDisplay
        # Generate the confusion matrix
        cm = confusion_matrix(total_y_test, total_y_pred)
        # Construct the matrix
        disp = ConfusionMatrixDisplay(confusion_matrix=cm, display_labels=[0, 1])
        disp.plot(cmap=plt.cm.Blues) # plot the matrix
        plt.title("Confusion Matrix of all Folds") # title matrix
        plt.show() # show matrix
        # Get the confusion matrix values
        tn, fp, fn, tp = cm.ravel()
        \label{eq:print}  \text{print}(f\text{"True Negatives (TN): } \{\text{tn}\}\text{"}) \text{ $\#$ Show the Number of True Negatives}
        print(f"False Positives (FP): {fp}") # Show the Number of False Positives
```

print(f"False Negatives (FN): {fn}") # Show the Number of False Negatives
print(f"True Positives (TP): {tp}") # Show the Number of True Positives



True Negatives (TN): 606 False Positives (FP): 0 False Negatives (FN): 206 True Positives (TP): 0

Here we can see that the F1 Score is still 0% and the Balanced Accuracy is still 50% which tells us that our model given different training data in terms of being divided into k-folds is not statisfactory enough change in order to make the model work as intended. That intended thing being that the model can accurately predict if brain signals are associated with a task as well as a background, not just background which the model is doing here just as it was doing before.

Also the Accuracy metric is changing throughout the folds sometimes and the reason for that is because the accuracy metric is more sensitive to little changes in the data (one more y=0 improves score) in comparision to the other metrics in this circumstance (in F1 Score & Balanced Accuracy, more y=0 will never improve this score because the other term is 0, removing the chances for any improvement).

Overall these metric results given with k-folds are almost the same as the results given in Q1. F1 Score is the same, Balanced Accuracy is the same, and Accuracy is 1% different given the fold itteration, but mostly the same too.

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