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).

```
In [4]: # 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])
 # 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...
FDF 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', '
Pz', 'A2', 'ECG']
['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: (21, 812, 300)
Shape of labels: (812,)
```

Q3)

Apply three different feature engineering methods of your choice (feature extraction, transformation, or selection), and repeat the analysis in (Q2). Discuss how your results differ and how you could improve your results.

The 3 feature engineering methods I have choosen for Q3 are SMOTE, stardard normalization, and FFT. The reason why i choose FFT is because you can gather more clearly defined features through FFT than raw data, this could improve all metrics further. In SMOTE it distributes the samples in an evenly distributed way where the ML model finds more complicated relationships that gives something better than a y=0 model (clear improvement in balanced accuracy and f1 score). Lastly, standard normalization should help all datapoints be located within the sigmoid function to allow for clear classification (improve all metrics).

```
In [5]: # 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

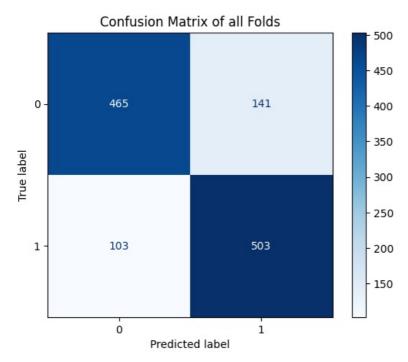
# Import library for k-folds
  from sklearn.model_selection import StratifiedKFold

# Import library for fast fourier transform
  from scipy.fft import fft
```

```
# Import library for equal data distribution
from imblearn.over_sampling import SMOTE
# Import library for normalization
from sklearn.preprocessing import StandardScaler
# Make FFT function
def apply fft(X, n fft=300):
    # X is of shape (n_samples, n_channels, n_points_per_window)
    X_{fft} = np.abs(fft(X, n=n_fft, axis=2)) # FFT along the last axis (window axis)
    return \ X_{fft}[:, :, :n_{fft}/2]  # Take only the positive frequencies (half of the spectrum)
# Apply FFT to the data (shape will still be (n samples, n channels, n features per channel))
X fft = apply fft(X)
# Reshape the data for model training (n samples, n features)
X reshaped = X fft.reshape(X fft.shape[1], -1) # (n windows, n channels * window size)
# Apply SMOTE after transformation
smote = SMOTE(random_state=42)
X_resampled, y_resampled = smote.fit_resample(X_reshaped, y)
# 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\_resampled, y\_resampled) # 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
accuracy_arr = []
balanced_accuracy_arr = []
f1 score arr = []
# Loop through the 5 folds made previously
for i in range(5):
    X_{train} = X_{resampled[train_idxs[i]]] # Load in the training X values from index i
    y train = y resampled[train idxs[i][:]] # Load in the training y values from index i
   X_{test} = X_{resampled[test_idxs[i][:]]} \# Load in the testing X values from index i
   y_test = y_resampled[test_idxs[i][:]] # Load in the testing y values from index i
   scaler = StandardScaler()
   X_train = scaler.fit_transform(X_train)
   X_test = scaler.fit_transform(X_test)
   # 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)
   accuracy_arr.append(accuracy) # Append accuracy to array
    # Evaluate the model using balanced accuracy
    balanced accuracy = balanced accuracy score(y test, y pred)
   balanced_accuracy_arr.append(balanced_accuracy) # Append balanced accuracy to array
    # Evaluate the model using f1 score
    f1 = f1 score(y test, y pred)
    fl_score_arr.append(f1) # Append f1 score to array
    # Print accuracy
```

```
print(f"Accuracy: {accuracy*100:.2f}%")
            # Print balanced accuracy
            print(f"Balanced Accuracy: {balanced_accuracy*100:.2f}%")
            # Print f1 score
            print(f"F1 Score: {f1*100:.2f}%\n")
        print(f"Average Accuracy Score: {np.sum(accuracy_arr)*100/5:.2f}%")
        print(f"Average Balanced Accuracy Score: {np.sum(balanced_accuracy_arr)*100/5:.2f}%")
        print(f"Average F1 Score: {np.sum(f1_score_arr)*100/5:.2f}%")
       Examining fold 1
       Accuracy: 70.37%
       Balanced Accuracy: 70.40%
       F1 Score: 72.31%
       Examining fold 2
       Accuracy: 76.95%
       Balanced Accuracy: 77.00%
       F1 Score: 74.07%
       Examining fold 3
       Accuracy: 86.78%
       Balanced Accuracy: 86.78%
       F1 Score: 87.69%
       Examining fold 4
       Accuracy: 85.54%
       Balanced Accuracy: 85.54%
       F1 Score: 86.59%
       Examining fold 5
       Accuracy: 79.75%
       Balanced Accuracy: 79.75%
       F1 Score: 80.63%
       Average Accuracy Score: 79.88%
       Average Balanced Accuracy Score: 79.89%
       Average F1 Score: 80.26%
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()
        print(f"True Negatives (TN): {tn}") # 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): 465 False Positives (FP): 141 False Negatives (FN): 103 True Positives (TP): 503

Unlike Q2, our Q3 results are **Drastically** better than both Q1 and Q2. Main reason is due to the feature engineering techniques added above being super beneficial to the data. I will not re-explain what they do here (as I have done that in a previous section), but I will talk about the changes of the results. The model this time around actually tries to make y=1 predictions sometimes, which is straight up better than what we had before (you can see this b/c the number of TP and FP are not 0).

When it comes to the metrics, the F1 score is on average 80.6% which is *way better* than the 0% we had before. This tells us the model is making correct decisions for both y=0 and y=1 cases. Our balanced accuracy is 79.89% which is 29.89 percentage points higher than what we had before (for the same reason as the F1 score increase basically). Surprisingly the Accuracy also increased to 79.88% which is higher than the before metric which was around 74% and this is because the model was predicting y=1 cases for the most part correctly, however it would still miss more y=0 cases than before which would decrease this metric to not reward the change made as much as the F1 score did for example.

I could potentially improve results by testing and added more feature engineering methods, like adding powerbands, or removing higher frequencies from FFT, PCA, and many many more. However Another clear way I can think of is now changing the model itself, that being either the hyperparameters of the model or the model class (logistic regression vs random forest for example). However change in model and getting the best out of that model could involve different feature engineering methods.

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