# FINAL PROJECT

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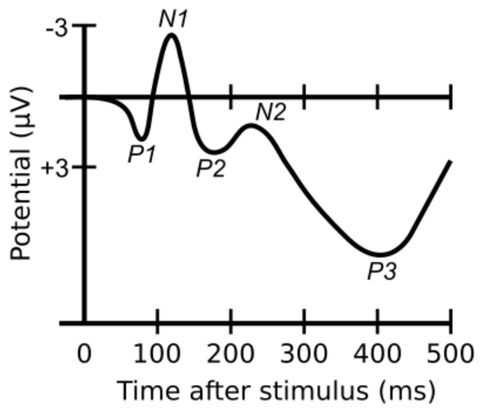
## Introduction

The purpose of this project is to identify the key differences in the brain signals when presented with misleading and consistent stimuli. 25 participants were presented with stimuli that were consistent, misleading and indifferent while strapped to an EEG machine. The stimulus was presented for eight trials, and the peak values for neural components: p2, fn400, p3, and n2 were aggregated and stored. Along with the area under the curve for respective time series (150-275 ms, 150-350 ms, 250-400 ms, 300-500 ms). The following paper analyzes this data and draws conclusions based on the data.

## Data Description



Based on this study there were nine datasets investigated. Four of these datasets represented four different neural ERP components of interest (FN400, P2, P3, N2). Each ERP component can be represented as a different portion of an EEG scan. These peaks can often be associated with different brain responses to stimuli. DIfferent ERP components manifest in different time intervals (P2: 150–275 ms, FN400: 300-500ms, P3: 250-400ms, N2: 150-350m). In addition to this, the five other datasets measured the area under the curve between each time interval. Each of these data points were measured by 32 electrode sites placed across the participants' scalp. The four peak datasets contained the peak voltage and latency (time from start) of the 32 electrodes at peak brain activity.

The grain on the dataset is represented by the peak values and/or AUC (area under curve) values for a participant in the study. Each dataset contains 24 entries for each participant who was studied in this experiment.

## Data Preprocessing

Among the nine datasets csv files, two datasets (ALLTRIALS150275.txt and Peaks_P3) were formatted radically different from the others.

*ALLTRIALS150275*

Unlike the other csv datasets, this dataset used tabs as a delimiter. Unfortunately, the size of the delimiters varied (space between first column and second was 6 spaces, the space between second and third was 3 spaces, spaces between data points was 12). To make matters worse, some column names also had a single space between. The data also lacked new line symbols. This provided a unique challenge. To clean the data, I first manually removed any unnecessary spaces between the few column names that had a space. Next, I utilized a regex[1] string to first identify spaces of variable length within the dataset and replace them with a comma. Next, I utilized a regex to add a new line symbol every 94th column (this step required some experimentation, 94 was the number of features for each of the alltrials datasets). In hindsight, I would of deleted the headers and replace them with the column names of another AllTrails dataset since they shared column headers.

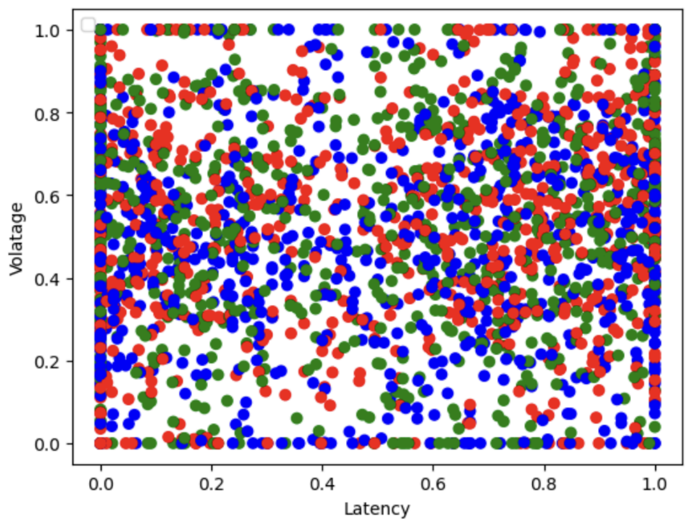
*PEAKS_P3*
The peaks file was another unique challenge. There were several headers that did not have commas. This resulted in column headers that merged together and several data values without any column. This was slightly difficult to solve programmatically so I cleaned it manually (though you could do it with another regex). I solved this issue by looking for all the entries that ended with -V, and -L and manually added a comma to each entry that was missing a comma. Again in hindsight, it would have been much easier to replace the headers of this dataset with a clean one instead.

**Data Exploration**
This dataset was unlike anything I had ever explored. For each participant there were over 90 columns. Each cell contained either a latency or voltage value that corresponded to an electrode and stimulus type. The compactness of the data made it extremely difficult to comprehend trends or correlations. As a result I needed to separate and reformat every dataset into something more machine (and human) readable. A further explanation of the refactoring steps I performed will be provided below. The measures of spread for the final dataset is shown below:

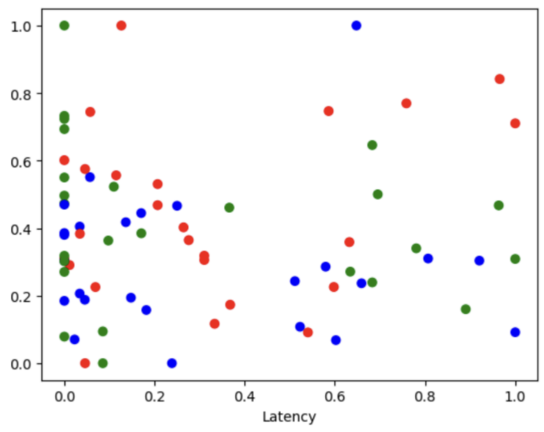
| | Electrode | Target | L | V | fn400 | n2 | p2 | p3 | AUC |
|---|---|---|---|---|---|---|---|---|---|
| **count** | 9000.000000 | 9000.000000 | 9000.000000 | 9000.000000 | 9000.000000 | 9000.000000 | 9000.000000 | 9000.000000 | 9000.000000 |
| **mean** | 14.500000 | 1.000000 | 0.500784 | 0.489205 | 0.250000 | 0.250000 | 0.250000 | 0.250000 | 0.502283 |
| **std** | 8.655922 | 0.816542 | 0.355223 | 0.263417 | 0.433037 | 0.433037 | 0.433037 | 0.433037 | 0.258893 |
| **min** | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| **25%** | 7.000000 | 0.000000 | 0.159338 | 0.295272 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.316809 |
| **50%** | 14.500000 | 1.000000 | 0.506667 | 0.487045 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.505285 |
| **75%** | 22.000000 | 2.000000 | 0.840662 | 0.680742 | 0.250000 | 0.250000 | 0.250000 | 0.250000 | 0.687512 |
| **max** | 29.000000 | 2.000000 | 1.000000 | 1.000000 | 1.000000 | 1.000000 | 1.000000 | 1.000000 | 1.000000 |

**Data Visualization**
Once the data was refactored, it was much easier to visualize. Below is a visualization of fn400. (Red = Consistent, Blue = Control, Green = Misleading). From the beginning, it was abundantly clear that there existed no simple relationship between the stimuli and Latency/Voltage).

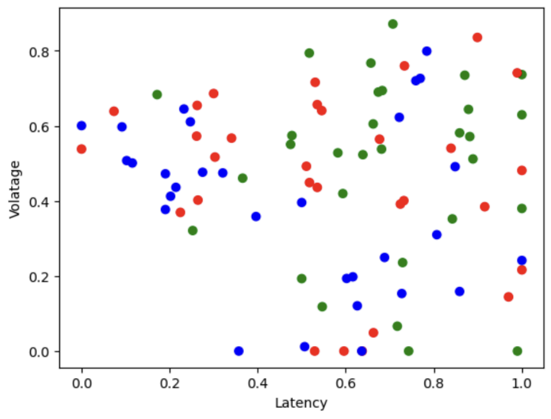
[1] Every Regex Expression along with other components used in this assignment was generated using Generative AI



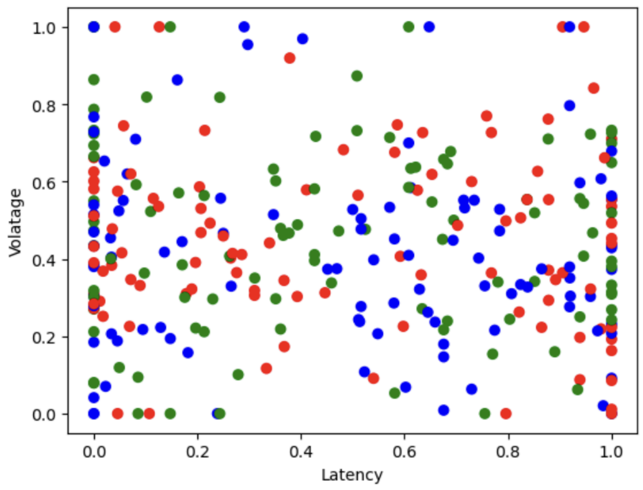
In order to simplify the visualization I also limited the stimulus to one electrode:



And also limited it to one subject:



Finally I tried to perform the same calculation across all neural components filtered by electrode and/or participant but this also proved to be largely incomprehensible. Below is a picture of a scatter plot across all participant and neural components but limited to one electrode.



**Feature Generation and Transformation**

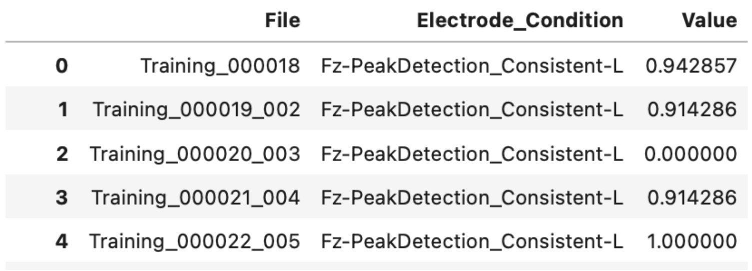
The peaks and alltrials datasets went through two separate workflows separately before they ultimately merged together. We will discuss each one in detail.

*Peaks*
Data Pipeline:

1) *Scale the data* - That way the voltage values would not be considered more potent than the latency (even though V values were much larger). The file value was removed and reapplied after this step

Once the data was scaled we needed to separate column names into a more granular format. That way they could be separate features in the dataset and utilized by an ML model

2) *Melt the Data* - I melted the data into a three column dataset. The file value was utilized as an index, and every other column was reduced to a row and corresponding value.

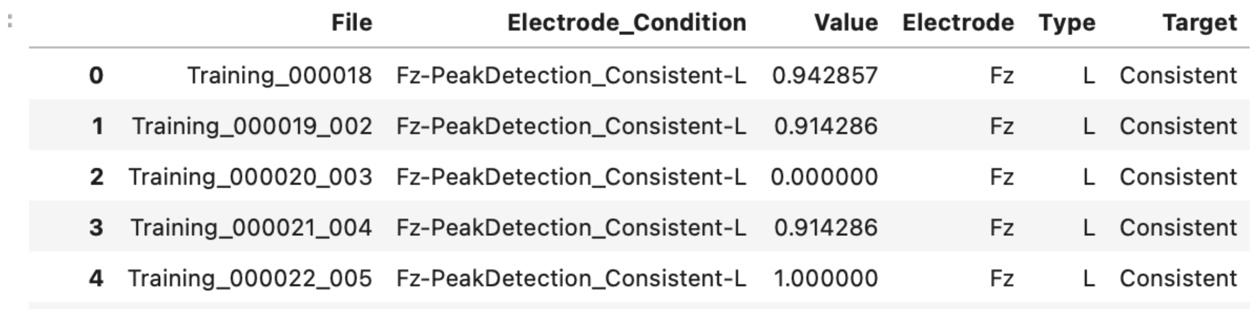


| | File | Electrode_Condition | Value |
|---|---|---|---|
| **0** | Training_000018 | Fz-PeakDetection_Consistent-L | 0.942857 |
| **1** | Training_000019_002 | Fz-PeakDetection_Consistent-L | 0.914286 |
| **2** | Training_000020_003 | Fz-PeakDetection_Consistent-L | 0.000000 |
| **3** | Training_000021_004 | Fz-PeakDetection_Consistent-L | 0.914286 |
| **4** | Training_000022_005 | Fz-PeakDetection_Consistent-L | 1.000000 |

Since the Electrode_Condition had so much information packed into a single column (Electrode, Target, Latency/Voltage), I needed to break it down into three separate features.

3) *Use Regex to Parse through the Column Name.* Specifically I looked for everything before the first dash to separate the electrode name, and everything between Underscore for the target value, and finally everything after a dash that resembled L or V. (Some peaks file headers varied in syntax so the regex was modified)

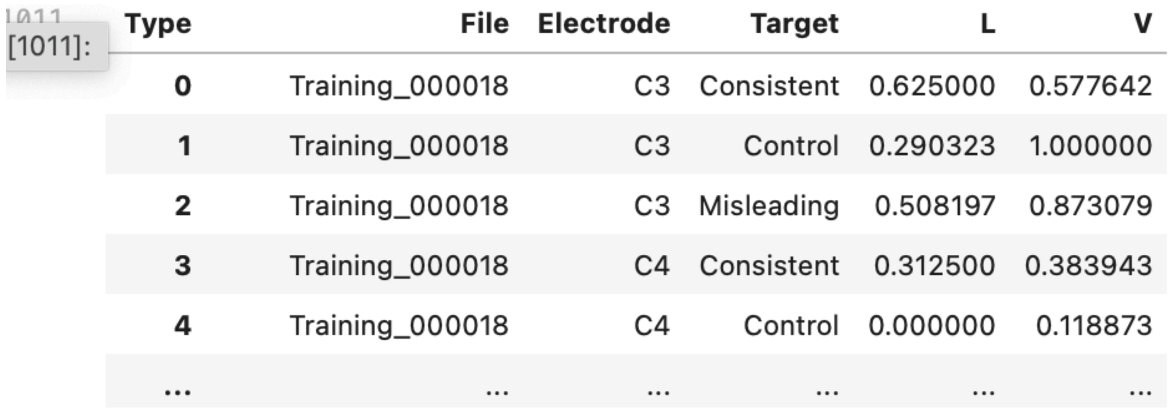
This separated the data into three more columns.



|   | File | Electrode_Condition | Value | Electrode | Type | Target |
|---|---|---|---|---|---|---|
| **0** | Training_000018 | Fz-PeakDetection_Consistent-L | 0.942857 | Fz | L | Consistent |
| **1** | Training_000019_002 | Fz-PeakDetection_Consistent-L | 0.914286 | Fz | L | Consistent |
| **2** | Training_000020_003 | Fz-PeakDetection_Consistent-L | 0.000000 | Fz | L | Consistent |
| **3** | Training_000021_004 | Fz-PeakDetection_Consistent-L | 0.914286 | Fz | L | Consistent |
| **4** | Training_000022_005 | Fz-PeakDetection_Consistent-L | 1.000000 | Fz | L | Consistent |

However I was unhappy with confusion required in having a Type column in which values oscillated from Latency and Voltage, which could easily confuse the model since values no longer represent one scale or type of value. This required me to generate a pivot table

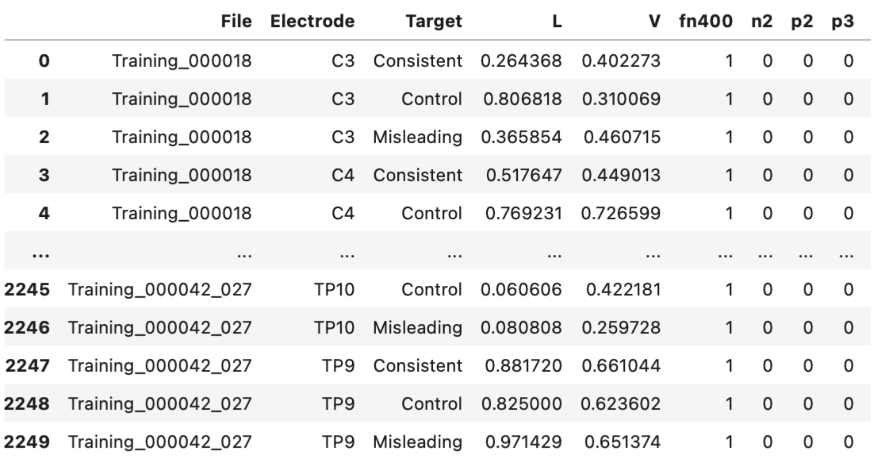
4) *Pivot the data.* The data was pivoted with a three column index (File, Electrode, and Target) causing the type column to become features (latency and voltage). Pivot tables by nature aggregate values, in order to prevent this, I needed to utilize three columns in my index, that way every value was unique and there was nothing to be averaged.



[1011]:

| Type | File | Electrode | Target | L | V |
|---|---|---|---|---|---|
| **0** | Training_000018 | C3 | Consistent | 0.625000 | 0.577642 |
| **1** | Training_000018 | C3 | Control | 0.290323 | 1.000000 |
| **2** | Training_000018 | C3 | Misleading | 0.508197 | 0.873079 |
| **3** | Training_000018 | C4 | Consistent | 0.312500 | 0.383943 |
| **4** | Training_000018 | C4 | Control | 0.000000 | 0.118873 |
| **...** | ... | ... | ... | ... | ... |

A similar pipeline was conducted for each of the peaks datasets. Next I wanted to merge these datasets, but wanted to keep their respective neural components. So I added a one-hot encoded neural component to display which component was being addressed.

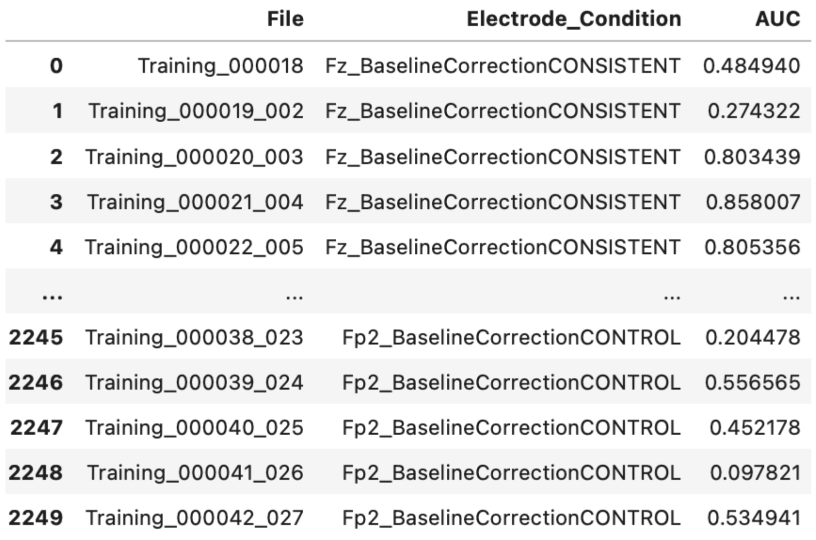


| | File | Electrode | Target | L | V | fn400 | n2 | p2 | p3 |
|---|---|---|---|---|---|---|---|---|---|
| **0** | Training_000018 | C3 | Consistent | 0.264368 | 0.402273 | 1 | 0 | 0 | 0 |
| **1** | Training_000018 | C3 | Control | 0.806818 | 0.310069 | 1 | 0 | 0 | 0 |
| **2** | Training_000018 | C3 | Misleading | 0.365854 | 0.460715 | 1 | 0 | 0 | 0 |
| **3** | Training_000018 | C4 | Consistent | 0.517647 | 0.449013 | 1 | 0 | 0 | 0 |
| **4** | Training_000018 | C4 | Control | 0.769231 | 0.726599 | 1 | 0 | 0 | 0 |
| **...** | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| **2245** | Training_000042_027 | TP10 | Control | 0.060606 | 0.422181 | 1 | 0 | 0 | 0 |
| **2246** | Training_000042_027 | TP10 | Misleading | 0.080808 | 0.259728 | 1 | 0 | 0 | 0 |
| **2247** | Training_000042_027 | TP9 | Consistent | 0.881720 | 0.661044 | 1 | 0 | 0 | 0 |
| **2248** | Training_000042_027 | TP9 | Control | 0.825000 | 0.623602 | 1 | 0 | 0 | 0 |
| **2249** | Training_000042_027 | TP9 | Misleading | 0.971429 | 0.651374 | 1 | 0 | 0 | 0 |

*All Trails*

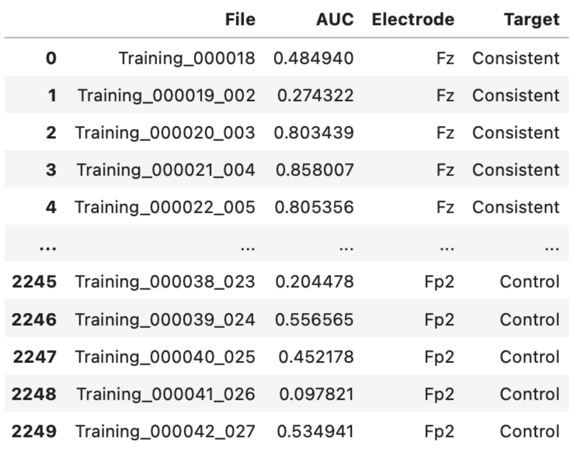
The alltrials dataset was simpler in the fact that each electrode had only value (area under the curve). Pipeline:

1) Dropped Fnp1 Columns from Analysis
2) Scale the Data. The file value was briefly excluded and the rest of the dataset was scaled.
3) Melt the Data. Once again one column contained too much information, so the data was melted into a two column format



| | File | Electrode_Condition | AUC |
|---|---|---|---|
| **0** | Training_000018 | Fz_BaselineCorrectionCONSISTENT | 0.484940 |
| **1** | Training_000019_002 | Fz_BaselineCorrectionCONSISTENT | 0.274322 |
| **2** | Training_000020_003 | Fz_BaselineCorrectionCONSISTENT | 0.803439 |
| **3** | Training_000021_004 | Fz_BaselineCorrectionCONSISTENT | 0.858007 |
| **4** | Training_000022_005 | Fz_BaselineCorrectionCONSISTENT | 0.805356 |
| **...** | ... | ... | ... |
| **2245** | Training_000038_023 | Fp2_BaselineCorrectionCONTROL | 0.204478 |
| **2246** | Training_000039_024 | Fp2_BaselineCorrectionCONTROL | 0.556565 |
| **2247** | Training_000040_025 | Fp2_BaselineCorrectionCONTROL | 0.452178 |
| **2248** | Training_000041_026 | Fp2_BaselineCorrectionCONTROL | 0.097821 |
| **2249** | Training_000042_027 | Fp2_BaselineCorrectionCONTROL | 0.534941 |

4) Use Regex to separate Electrode_Condition into separate features.

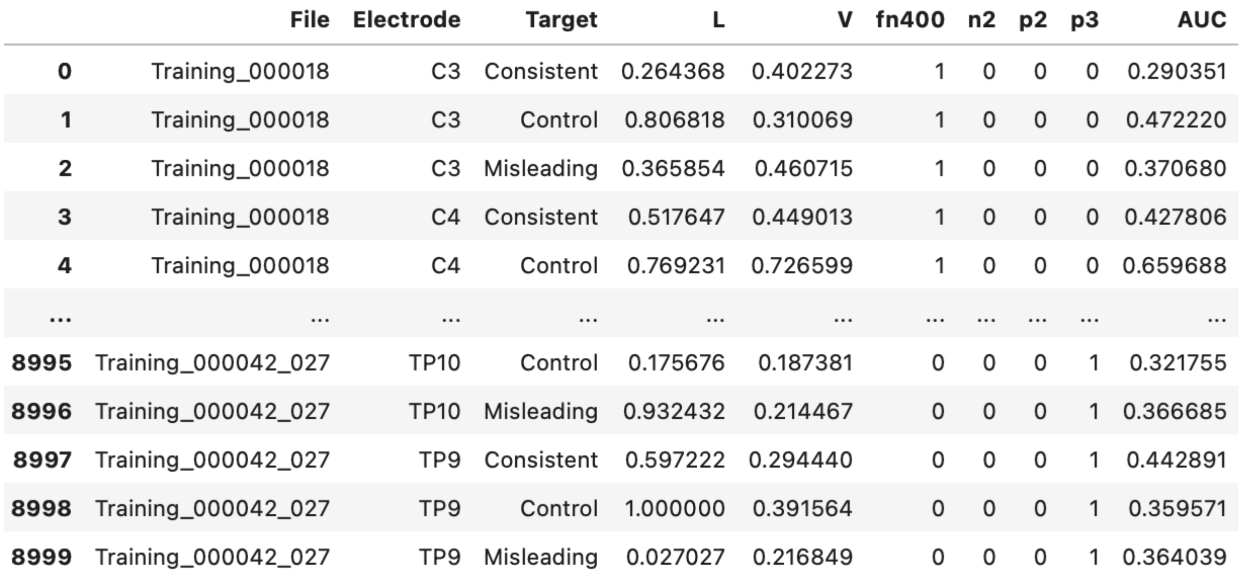


| | File | AUC | Electrode | Target |
|---|---|---|---|---|
| **0** | Training_000018 | 0.484940 | Fz | Consistent |
| **1** | Training_000019_002 | 0.274322 | Fz | Consistent |
| **2** | Training_000020_003 | 0.803439 | Fz | Consistent |
| **3** | Training_000021_004 | 0.858007 | Fz | Consistent |
| **4** | Training_000022_005 | 0.805356 | Fz | Consistent |
| **...** | ... | ... | ... | ... |
| **2245** | Training_000038_023 | 0.204478 | Fp2 | Control |
| **2246** | Training_000039_024 | 0.556565 | Fp2 | Control |
| **2247** | Training_000040_025 | 0.452178 | Fp2 | Control |
| **2248** | Training_000041_026 | 0.097821 | Fp2 | Control |
| **2249** | Training_000042_027 | 0.534941 | Fp2 | Control |

Since there was only one type of value, a pivot was not required.

Once all these steps were completed. I joined the alltrials dataset with peak files. This was possible because each neural component was associated with a specific time frame. (P2: 150–275 ms, FN400: 300-500ms, P3: 250-400ms, N2: 150-350m).

1) *Inner Join.* Since each dataset had the same patient, electrode, and target values I utilized an inner join (on these common features) so that the peaks dataset would have an extra column for the area under the curve (AUC)
2) Finally I concatenated all these datasets into one large dataset to be fed into the machine learning model.



| | File | Electrode | Target | L | V | fn400 | n2 | p2 | p3 | AUC |
|---|---|---|---|---|---|---|---|---|---|---|
| **0** | Training_000018 | C3 | Consistent | 0.264368 | 0.402273 | 1 | 0 | 0 | 0 | 0.290351 |
| **1** | Training_000018 | C3 | Control | 0.806818 | 0.310069 | 1 | 0 | 0 | 0 | 0.472220 |
| **2** | Training_000018 | C3 | Misleading | 0.365854 | 0.460715 | 1 | 0 | 0 | 0 | 0.370680 |
| **3** | Training_000018 | C4 | Consistent | 0.517647 | 0.449013 | 1 | 0 | 0 | 0 | 0.427806 |
| **4** | Training_000018 | C4 | Control | 0.769231 | 0.726599 | 1 | 0 | 0 | 0 | 0.659688 |
| **...** | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... |
| **8995** | Training_000042_027 | TP10 | Control | 0.175676 | 0.187381 | 0 | 0 | 0 | 1 | 0.321755 |
| **8996** | Training_000042_027 | TP10 | Misleading | 0.932432 | 0.214467 | 0 | 0 | 0 | 1 | 0.366685 |
| **8997** | Training_000042_027 | TP9 | Consistent | 0.597222 | 0.294440 | 0 | 0 | 0 | 1 | 0.442891 |
| **8998** | Training_000042_027 | TP9 | Control | 1.000000 | 0.391564 | 0 | 0 | 0 | 1 | 0.359571 |
| **8999** | Training_000042_027 | TP9 | Misleading | 0.027027 | 0.216849 | 0 | 0 | 0 | 1 | 0.364039 |

*Concluding Notes on Processing*

It was already extremely clear that the high dimensionality of this dataset was going to make the process extremely difficult. I had some experimental methods that I did not attempt but would have if given more time. One of these was to utilize PCA to reduce the number of dimensions in the model. Nevertheless, I chose against using this method in the end, because of the higher interdependence each feature has with the other.

**Machine Learning Model**

Once the dataset was completely merged and cleared, I prepared it for the machine learning model. Primarily I label encoded both the target value and the electrode value. I also removed File value to make the data more generalizable.

I considered dummy_encoding for the electrodes, but ultimately decided against it. This is because there are 32 electrodes. Adding 31 new column to the dataset could help stop the model from over emphasizing one model over another but it would exacerbate the curse of dimensionality that this dataset was facing.

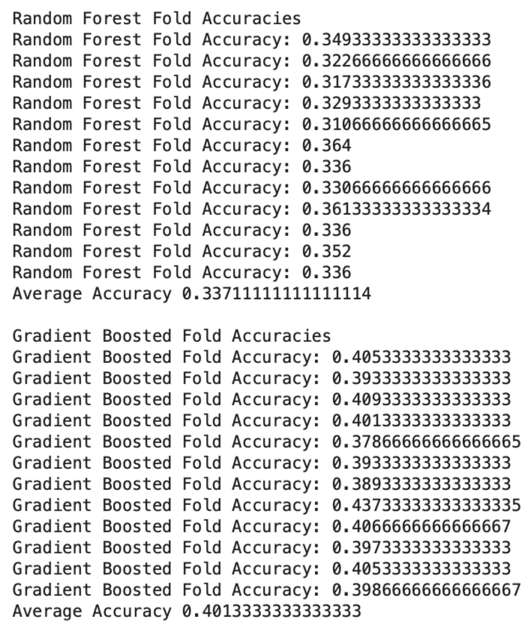
Given more time for processing, the most ideal method is to dummy encode the electrodes and perform PCA to reduce its dimensionality.

Once the data was encoded, I split the data into 60% Training and 40% Test (I also tried a 70-30 split and got better results). I trained two machine learning models (both of which are ideal for complex relationships) a Random Forest Classifier and a Gradient Boosted Classifier. Unfortunately, I was left with undesirable results, both models provided an accuracy between 35 and 39%. With three classes (Consistent, Control, and Misleading) this is only slightly better than complete guessing (33%).

**Cross Validation**

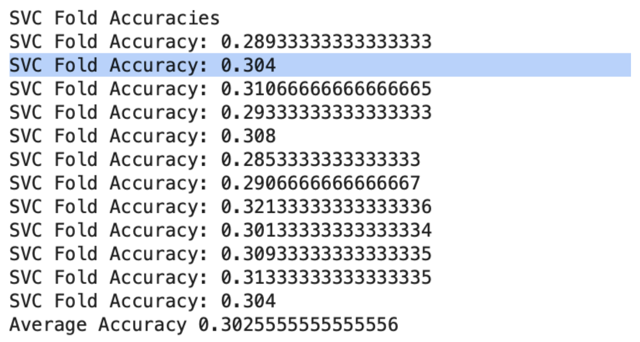
I've also added a cross validation step. This enabled me to identify the best model between random forest, svc, and gradient boosted. This step was tricky because I needed to scale each training set separately to prevent data leakage. Since I had an exceptionally large dataset, I performed a 12 fold cross validation.

Kfold validation works by separating the data into k folds and using one fold for validation while the other folds are used for training. This process is repeated k times where each k fold is rotated into the validation set. Doing so clearly demonstrated that the Gradient Boosted Classifier performed best on this dataset. In fact it had an average accuracy of 40%.



```
Random Forest Fold Accuracies
Random Forest Fold Accuracy: 0.34933333333333333
Random Forest Fold Accuracy: 0.32266666666666666
Random Forest Fold Accuracy: 0.31733333333333336
Random Forest Fold Accuracy: 0.3293333333333333
Random Forest Fold Accuracy: 0.31066666666666665
Random Forest Fold Accuracy: 0.364
Random Forest Fold Accuracy: 0.336
Random Forest Fold Accuracy: 0.33066666666666666
Random Forest Fold Accuracy: 0.36133333333333334
Random Forest Fold Accuracy: 0.336
Random Forest Fold Accuracy: 0.352
Random Forest Fold Accuracy: 0.336
Average Accuracy 0.33711111111111114

Gradient Boosted Fold Accuracies
Gradient Boosted Fold Accuracy: 0.4053333333333333
Gradient Boosted Fold Accuracy: 0.3933333333333333
Gradient Boosted Fold Accuracy: 0.4093333333333333
Gradient Boosted Fold Accuracy: 0.4013333333333333
Gradient Boosted Fold Accuracy: 0.37866666666666665
Gradient Boosted Fold Accuracy: 0.3933333333333333
Gradient Boosted Fold Accuracy: 0.3893333333333333
Gradient Boosted Fold Accuracy: 0.43733333333333335
Gradient Boosted Fold Accuracy: 0.4066666666666667
Gradient Boosted Fold Accuracy: 0.3973333333333333
Gradient Boosted Fold Accuracy: 0.4053333333333333
Gradient Boosted Fold Accuracy: 0.39866666666666667
Average Accuracy 0.4013333333333333
```



```
SVC Fold Accuracies
SVC Fold Accuracy: 0.28933333333333333
SVC Fold Accuracy: 0.304
SVC Fold Accuracy: 0.31066666666666665
SVC Fold Accuracy: 0.29333333333333333
SVC Fold Accuracy: 0.308
SVC Fold Accuracy: 0.2853333333333333
SVC Fold Accuracy: 0.2906666666666667
SVC Fold Accuracy: 0.32133333333333336
SVC Fold Accuracy: 0.30133333333333334
SVC Fold Accuracy: 0.30933333333333335
SVC Fold Accuracy: 0.31333333333333335
SVC Fold Accuracy: 0.304
Average Accuracy 0.3025555555555556
```

**Further Development**

Since the boosted classifier worked best, I also tried the AdaBoost Classifier, an extremely popular boosting algorithm. This algorithm performs better than random forest but did not show as strongly as GSB.

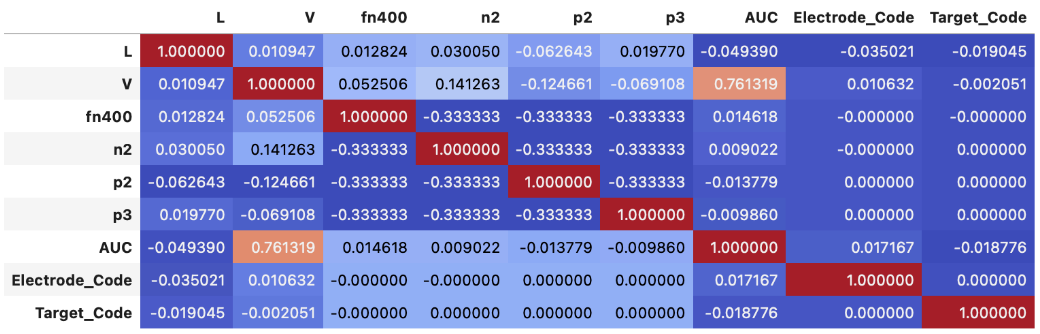
Furthermore, I tried creating two ensemble models. One that was a simple voting classifier (ending portion of bagging) and the other being stacking.

For the voting classifier I put AdaBoost, Gradient and Random Forest together and utilized a hard max aggregation technique (majority voting), this performed better than random forest or adaboost on their own but did not perform *necessarily* better than gradient boosting

Since Gradient Boosting worked well, I also attempted a stacking model since these traditionally use gradient descent in training. My stacking method used a neural network as the meta model, and adaboost + gradient boosting for the stacked models. This method was not very fruitful however and provided an accuracy of 35%

**Conclusion**

From this study, it is evident that brain EEG data is extremely complex. I was able to identify no simple relationships between any of the values, nor was I able to create a model that would accurately distinguish between normal and misleading brain stimuli. In hindsight, one of the largest issues I felt was the amount of dimensionality in this data. To mitigate this, I experimented removing features but got no higher accuracy. In the future I might employ PCA to reduce the dimensionality. I performed a correlation matrix to identify any relationships between variables



| | L | V | fn400 | n2 | p2 | p3 | AUC | Electrode_Code | Target_Code |
|---|---|---|---|---|---|---|---|---|---|
| **L** | 1.000000 | 0.010947 | 0.012824 | 0.030050 | -0.062643 | 0.019770 | -0.049390 | -0.035021 | -0.019045 |
| **V** | 0.010947 | 1.000000 | 0.052506 | 0.141263 | -0.124661 | -0.069108 | 0.761319 | 0.010632 | -0.002051 |
| **fn400** | 0.012824 | 0.052506 | 1.000000 | -0.333333 | -0.333333 | -0.333333 | 0.014618 | -0.000000 | -0.000000 |
| **n2** | 0.030050 | 0.141263 | -0.333333 | 1.000000 | -0.333333 | -0.333333 | 0.009022 | -0.000000 | 0.000000 |
| **p2** | -0.062643 | -0.124661 | -0.333333 | -0.333333 | 1.000000 | -0.333333 | -0.013779 | 0.000000 | 0.000000 |
| **p3** | 0.019770 | -0.069108 | -0.333333 | -0.333333 | -0.333333 | 1.000000 | -0.009860 | 0.000000 | 0.000000 |
| **AUC** | -0.049390 | 0.761319 | 0.014618 | 0.009022 | -0.013779 | -0.009860 | 1.000000 | 0.017167 | -0.018776 |
| **Electrode_Code** | -0.035021 | 0.010632 | -0.000000 | -0.000000 | 0.000000 | 0.000000 | 0.017167 | 1.000000 | 0.000000 |
| **Target_Code** | -0.019045 | -0.002051 | -0.000000 | 0.000000 | 0.000000 | 0.000000 | -0.018776 | 0.000000 | 1.000000 |

The only clear relationship existed between Voltage and AUC which of course was expected. All in all, I found this project extremely fun and intriguing, but was slightly disappointed with its result. Further analysis needs to be done to identify if any differences exist between brain activity when faced with misleading stimuli compared to normal stimuli.

## Works Cited

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"What is P2, FN400, P3 and N2 in ECG data?" prompt. ChatGPT, 13 Feb. version, OpenAI, 19 Dec. 2023, chat.openai.com.