

# 10701 Project Final Report

## American Epilepsy Society Seizure Prediction Challenge

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## 1 Introduction

### 1.1 Background and Motivation

Epilepsy afflicts nearly 1% of the world's population, and is characterized by the occurrence of spontaneous seizures. For many patients, anticonvulsant medications can be given at sufficiently high doses to prevent seizures, but patients frequently suffer side effects. For 20-40% of patients with epilepsy, medications are not effective; and even after surgical removal of epilepsy-causing brain tissue, many patients continue to experience spontaneous seizures. Despite the fact that seizures occur infrequently, patients with epilepsy experience persistent anxiety due to the possibility of a seizure occurring.

Seizure forecasting systems thus have the potential to help patients with epilepsy lead more normal lives. In order for EEG-based seizure forecasting systems to work effectively, computational algorithms must reliably identify periods of increased probability of seizure occurrence. If these seizure-permissive brain states can be identified, devices designed to warn patients of impending seizures would be possible. Patients could avoid potentially dangerous activities like driving or swimming, and medications could be administered only when needed to prevent impending seizures, reducing overall side effects.

### 1.2 The Problem

Our project is based on a kaggle competition wherein the task is to distinguish between ten minute long data clips covering an hour prior to a seizure, and ten minute iEEG clips of interictal activity. The goal of the competition is to demonstrate the existence and accurate classification of the preictal brain state in dogs and humans with naturally occurring epilepsy.

### 1.3 Metrics

We have developed a K-fold cross-validation framework which we use to measure the performance of classifiers. The performance metrics that we consider are preictal recall, preictal precision, overall accuracy, error percentage and F-Measure. Since we want high recall on preictal segments, we use a weighted version of F-Measure as a metric. The rationale behind this is that for our use-case, it is important for us to not have false negatives (a patient should always be alerted before a seizure).

### 1.4 Goals

The minimum goal is to achieve good recall because that would mean that we are able to predict preictal states correctly and hence provide relief to epilepsy-afflicted patients. Specifically, we want to beat the bonehead model and attain high performance according to the metrics mentioned in the preceding section.

From the perspective of learning, we aim to apply various learning/classification algorithms suited to our problem, and study their pros and cons, and why some of them work well and others don't, based on our understanding of the data.

## 2 Dataset

Intracranial EEG was recorded from dogs with naturally occurring epilepsy using an ambulatory monitoring system. Datasets from patients with epilepsy undergoing intracranial EEG monitoring to identify a region of brain that can be resected to prevent future seizures are also included in the contest. These are available at <https://www.kaggle.com/c/seizure-prediction/data>.

- **Training Data Set :** This is organized into one hour sequences of ten-minute iEEG clips labeled 'Preictal' for pre-seizure data segments, or 'Interictal' for non-seizure data segments. The interictal activity data, in the case of canines, is recorded at least a week before and after a seizure. For human training data, the interictal training data

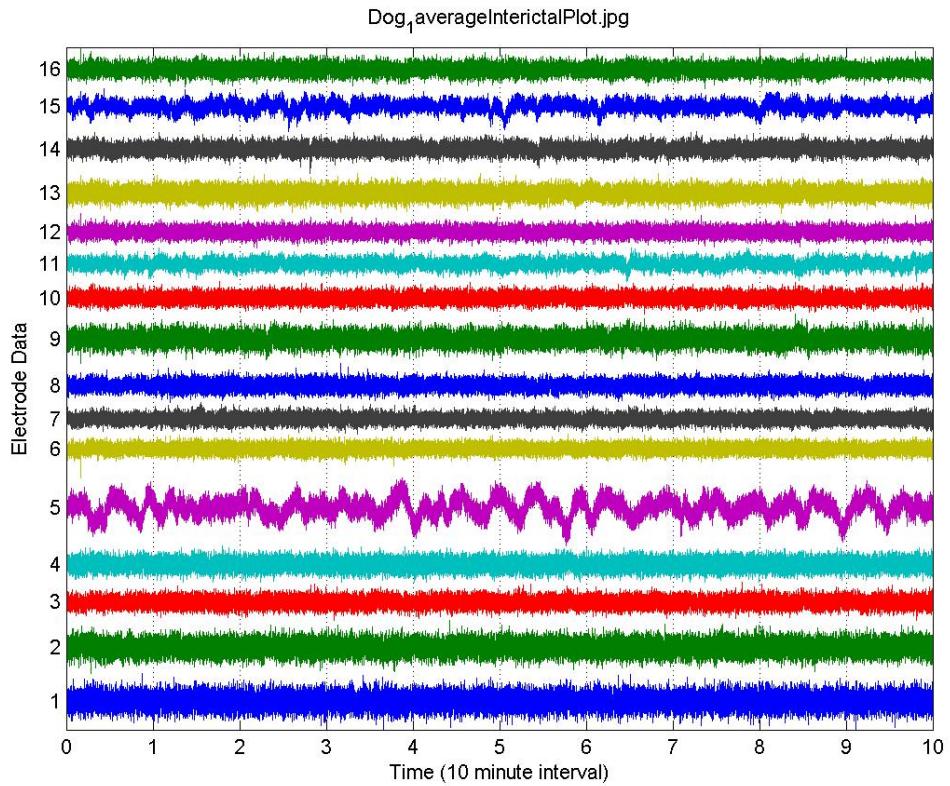


Figure 1: Plot of electrode-wise average EEG signal activity for a 10-minute segment. x-axis represents time in minutes

is recorded at least 4 hours before and after a seizure. The preictal activity data is recorded one hour prior to a seizure with a 5 minute offset.

- **Test Data Set :** For each subject (5 dogs and 2 patients), it consists of 10 minute iEEG clips which are provided in random order.

## 2.1 Preliminary Analysis

The first step taken was to plot the EEG sample values for the various subjects/electrodes and see if we could derive information out of them. An example of such a plot is shown in Figure 1.

Plots for interictal and preictal data segments were made in an attempt to see if there were any major differences that we could spot. Although, we weren't able to derive too much information from these plots (other than the existence of outlier data segments), it did serve as a motivation to try Fourier methods (described later on).

## 2.2 Extracting Basic Features

We calculated basic statistics like the mean/variance of each data segment over all subjects. This data is used to construct the feature vectors in our bonehead model.

The general trend that we observed was that the variance of the preictal data was lesser than that of the interictal data. This is illustrated in the following heatmap:

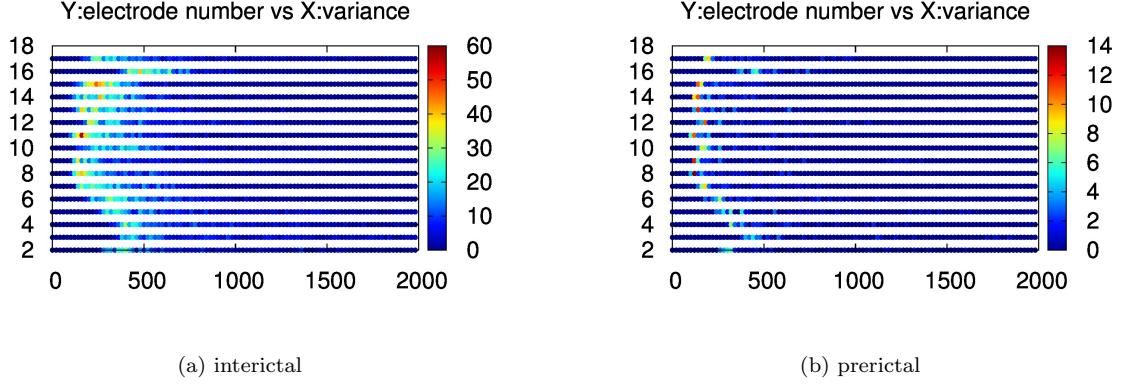


Figure 2: Heat maps showing the distribution of variance for every electrode for Dog 2

### 2.2.1 Trying To Find A Correlation

Another statistic that we calculated was the covariance matrix of data segments. Following that, we calculated the correlation coefficient matrix for each data segment and tried to see if that would give us any information about correlation between electrodes. To observe this, we used heatmaps (Figure 3) for interictal data and preictal data.

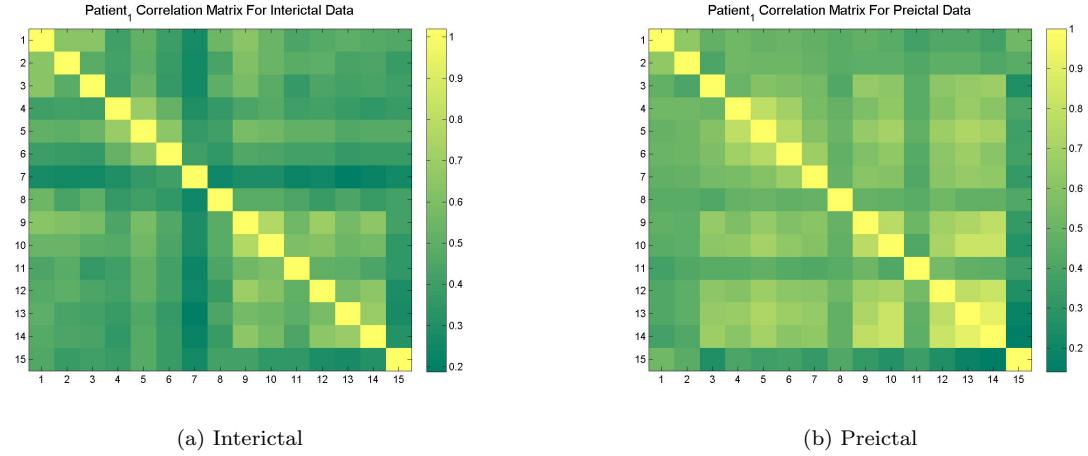


Figure 3: Correlation Coefficient Matrix for the two states

In the heatmap plots, a box with a more intense color (according to the color scale) corresponds to a pair of electrodes that have a high correlation coefficient (which is why the boxes in the diagonal have the most intense colors). Observe how the plot changes when we move from interictal to preictal. It becomes 'brighter'. This means that there is more correlation between pairs of electrodes in the preictal state when compared to the interictal state. This difference gives us motivation to look for bivariate features which will be able to distinguish between preictal and interictal states better than a normal univariate feature. This assumption is supported in a study that has been carried out in [1].

Using these simple features, we built a Naive Bayes classifier (which we call the Bonehead Model). The results are shown in Table 2. To improve on the results obtained, we ventured into extracting features that are more data-driven and hence can be expected to help build better classifiers. We also explored another avenue, namely treating the problem as a 7-class one instead of binary classification. These are explained in the following section.

## 3 Proposed Methods and Features

### 3.1 7-Class classification

The training data is labeled with sequence numbers which identify the 10-minute interval within an hour. One of the approaches that we tried was separating the preictal class into 6 classes corresponding to the 6 sequence types. The rationale underlying this model was that one would expect the “preictalness” of a preictal segment to increase markedly with time in the hour before the seizure unlike the “interictalness” of an interictal segment. We conducted several analyses of the test data in an attempt to find evidence to support this intuition. Figure 4 demonstrates the results of two of our experiments:

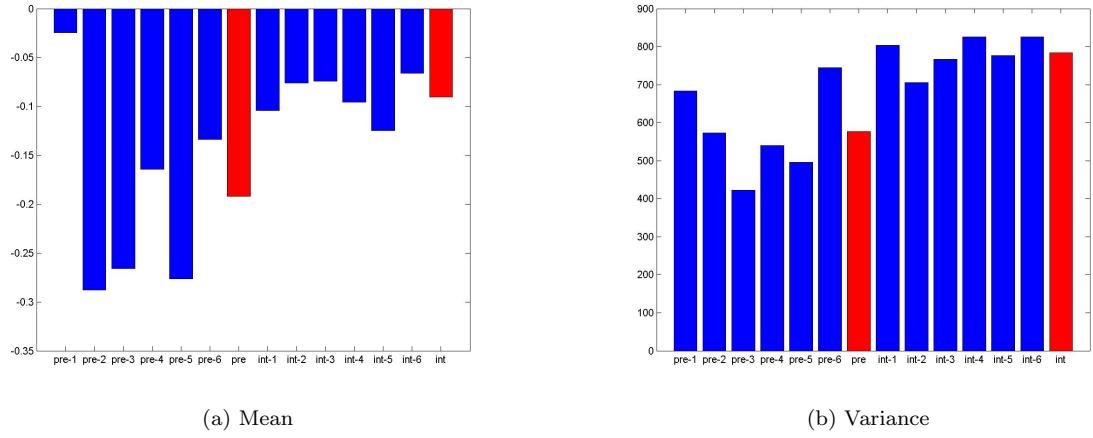


Figure 4: Segment-specific (averaged) mean and variance for Dog 2 and Electrode 4

This analysis showed us the general trend of interictal variances being higher than preictal variances. We also observed that in general, the 6 interictal means for a given subject-electrode pair were clustered together as compared to the preictal means. However we did not observe any clear trend across all subjects which could help us differentiate between the 6 preictal classes.

In contrast, the Fourier analysis presented in the following section showed clear patterns which could be used to differentiate between preictal and interictal data. Hence, we focus on binary classification with Fourier Analysis.

## 3.2 Fourier Analysis

As observed from the EEG graphs in 2.1, the signals from each electrode in a segment are quite periodic. Hence, we can apply Fourier Analysis on these signals to obtain amplitude spectrum over a range of frequencies. Below, we summarize our experiments relating to this:

### 3.2.1 Principal Frequencies

We calculated the principal frequencies, i.e., the ones with maximum amplitude in the Fourier spectrum, for each electrode in each segment. Then, we took the mean over all electrode-wise principal frequencies for a subject, and were able to get good separation between preictal and interictal segments. As an example, for Dog 1, we obtain the mean principal frequencies for the 16 electrodes as shown in Figure 5

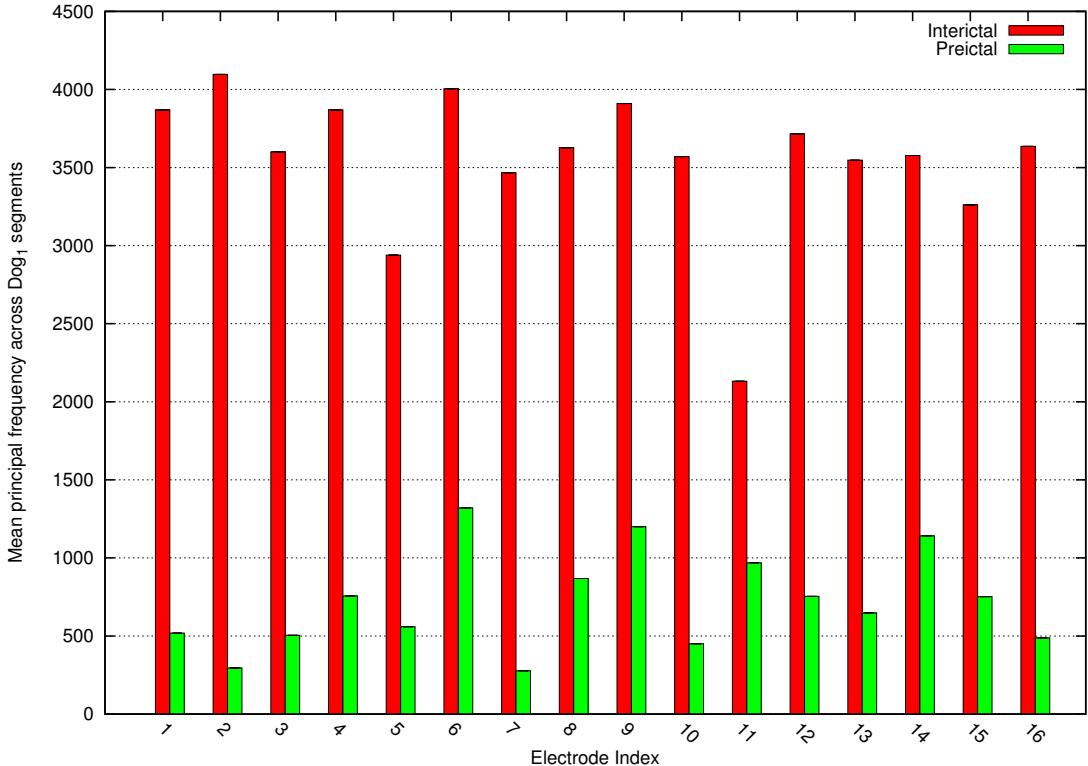


Figure 5: Electrode-wise Mean Principal Frequency for Dog1 Interictal and Preictal segments

On taking a closer look at the individual principal frequencies, we observe that there are some huge outliers, in the range of  $10^5$  to  $10^6$ , while the smaller values are all clustered in ranges of around 0-200 Hz, for both preictal as well as interictal segments. This is the reason why the mean principal frequencies for interictal segments reach values upto 4 kHz.

### 3.2.2 Outlier Detection

To deal with the above-mentioned issue of outliers, we filtered the electrode-wise principal frequencies and retained only those segments where the frequencies were less than 10 times the average values for their respective electrodes. On doing so, we observed that the principal frequencies for both interictal as well as preictal data had clustered in the range 0-100 Hz. This is depicted via the sample heatmaps in figure 6. Hence, just the set of principal frequencies doesn't seem to be a good distinguishing feature. We have, in a way, aggregated a 10-minute signal into one value, which leads to loss of information.

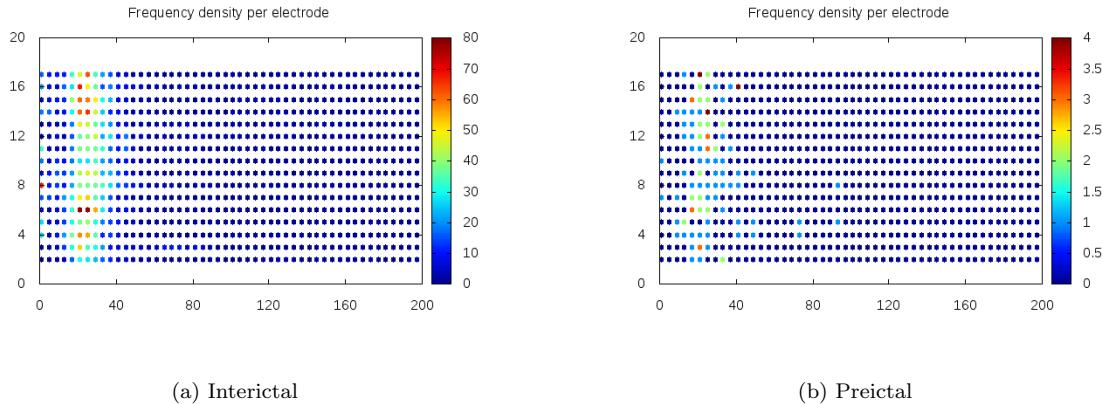


Figure 6: Heatmaps showing distribution of electrode-wise principal frequency for Dog1 data. x-axis represents frequency in Hertz. y-axis is marked with electrode indices

### 3.2.3 Fourier Spectra

Next we looked at the spectrum of amplitudes obtained from a Fourier decomposition on each electrode's signals. Here, we observe marked differences among preictal and interictal spectra for some particular electrodes. A few representative examples can be seen in figures 7 and 8. For both cases shown here, the interictal plots are more peaked towards frequencies close to 0. Thus, we can use the vector of amplitudes across a range of frequencies, say 0-200 Hz as a feature for distinguishing between pre- and inter-ictal segments.

We take the vector of amplitudes obtained on Fourier decomposition of each electrode's signal and use it as a feature vector to train models. In [1], the use of patient-specific machine learning-based classifiers (support vector machines, logistic regression or convolutional neural networks) has been mentioned.

As the size of such a feature vector can become very large (number of electrodes \* number of frequencies), we use a low band pass filter. This is meaningful because we can observe from the fourier spectra that the amplitudes past a certain frequency (around 100 Hz) are almost 0. We do not expect sinusoidal waves of high frequency to show up in neural activity anyway.

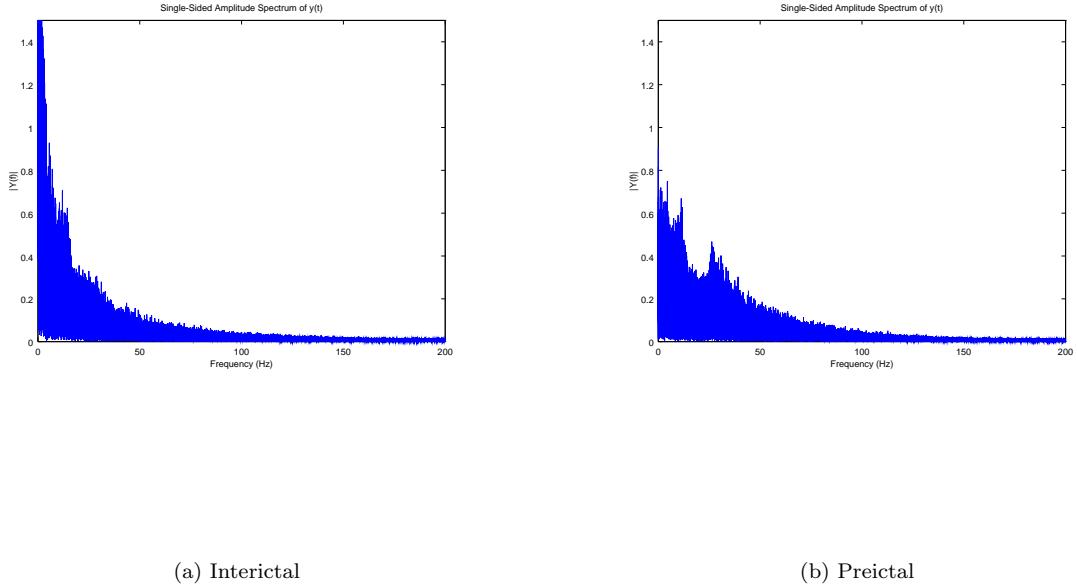


Figure 7: Fourier spectra for the 5<sup>th</sup> electrode in Dog1 data.

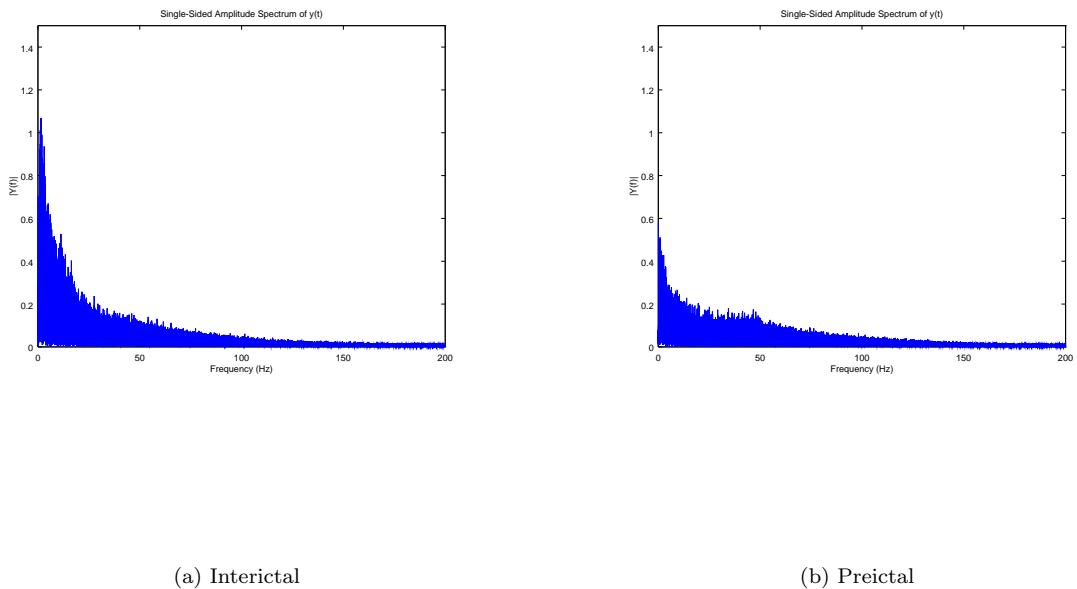


Figure 8: Fourier spectra for the 10<sup>th</sup> electrode in Dog2 data.

### 3.2.4 Using bivariate features

After filtering outliers, we plotted correlation heatmaps among electrode-pairs, looking at their principal frequencies, and obtained good distinction between the two classes of data. We therefore used such correlation matrices as bivariate features for our models. This is also supported by [1]. In figure 9, we can see that there is more correlation among the electrodes in preictal segments, which is to be expected during a seizure.

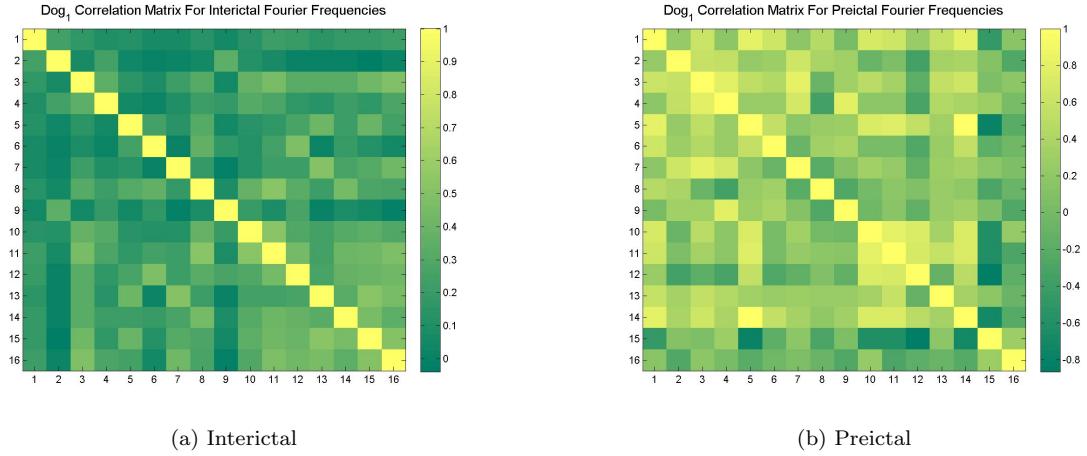


Figure 9: Correlation heatmap among principal frequencies for different electrodes in Dog1 data

## 4 Experiments

#### 4.1 Types Of Features Used

The classifiers that we tried out used combinations of the features listed below.

NOTE: Letters in bracket denote code used in Figures 10 and 11.

1. **Means** (M) of the sample values of each electrode.
  2. **Variances** (V) of the sample values of each electrode.
  3. **Correlation Coefficients** (CC) for each pair of electrodes. This is essentially the lower (or upper) triangle portion of the correlation coefficient matrix of a data clip.
  4. **Fourier Frequency Vectors** (TF): The top few principal frequencies of the Fourier amplitude spectrum for an electrode's readings.
  5. **Frequency Vector Similarities** (TFS): For each pair of electrodes, the similarity between their 'top frequencies' vectors is calculated. This is done by observing the number of common frequencies (with a tolerance) in the two vectors.
  6. **Fourier Amplitude Vectors** (FA): We apply a low band pass filter and restrict ourselves to the amplitudes of the first few frequencies. For the dogs, the sampling frequency is 399Hz, so, we pick the Fourier amplitudes for the first 100 frequencies. The corresponding numbers for patients are 5000Hz and 1000 amplitudes.
  7. **Fourier Amplitude Vector Similarity**: To compare how similar two electrodes are based on their amplitude vectors, we have two approaches:
    - **Cosine Similarity** (ACS): For each pair of electrodes, the similarity between the two amplitude vectors is calculated using the cosine similarity measure.
    - **Euclidean Distance** (AED): For each pair of electrodes, the distance(and in a way, similarity) between the two amplitude vectors is calculated using the euclidean distance measure.

## 4.2 Testing Framework

For testing purposes, we're using a K-Fold cross-validation approach. For each subject, the M training segments of interictal data and N segments of preictal data are divided into partitions of size  $\frac{M}{K}, \frac{N}{K}$  respectively. Thus, we will have K subsamples that contain equal number of interictal and preictal training segments.

One of the subsamples is chosen for validation purposes while the rest are used to train the classifier. This is repeated for all K subsamples and we note down the average metric score. For this project, we're setting K=3 so that we have a decent number of preictal data segments for testing.

The basic metric that could be used for evaluation is the average number of classification errors (or error percentage) of the classifier.

For our project, an important point to consider is that it is crucial for us to be able to predict the occurrence of a seizure given a preictal data segment (so that the patient may make preparations). False negatives (classifying a preictal segment as interictal) should be penalized more when compared to false positives(classifying an interictal segment as preictal). Thus, it is important for us to have a higher recall than precision. For that purpose we will be using the f-Measure metric (with higher weight on recall) =  $\frac{3PR}{2P+R}$  as a part of our evaluation.

For our evaluation, we define,

$$\text{Precision} = \frac{\text{Number of Accurate Preictal Predictions}}{\text{Number of Preictal Predictions}}$$

$$\text{Recall} = \frac{\text{Number of Accurate Preictal Predictions}}{\text{Number of Preictal Segments in the Test Set}}$$

$$\text{Error Percentage} = \frac{\text{Number of Misclassifications made} * 100}{\text{Number of Testing Data Segments}}$$

Our experimental set up is as shown below:

| Subject   | Interictal data : Preictal data | # Training data | # Testing data |
|-----------|---------------------------------|-----------------|----------------|
| Dog 1     | 480 : 24                        | 336             | 168            |
| Dog 2     | 500 : 42                        | 361             | 181            |
| Dog 3     | 1440 : 72                       | 1008            | 504            |
| Dog 4     | 804 : 97                        | 601             | 300            |
| Dog 5     | 450 : 30                        | 320             | 160            |
| Patient 1 | 50 : 18                         | 45              | 23             |
| Patient 2 | 42 : 18                         | 40              | 20             |

Table 1: Data Used By The Models, during cross-validation

In Table 1, the second column refers to the number of interictal data segments we have vs the number of preictal data segments. Columns 3 & 4 refer to the number of training and testing segments we will be using for our 3 fold cross validation framework.

It has to be noted that we build subject specific models (in terms of parameters). The underlying algorithm and feature extraction would remain same but while predicting for a given subject, we only consider the relevant training data. We do not intend on building a ‘one size fits all’ classifier. The merits of using patient specific classifiers have been studied in [3].

### 4.3 Bonehead Model

For this model, we are considering the mean sample values for each electrode as the set of features for a data segment. For example, given a data segment of a subject with M electrodes, we would represent it with a 1 x M vector with each value representing the average data value for each electrode.

These data points are then fed to a Naive Bayes learner which generates a Gaussian Naive Bayes classifier.

The results of this classifier can be seen in Table 2.

| Subject   | Test on Fold 1 |           |        |           | Test on Fold 2 |           |        |           | Test on Fold 3 |           |        |           | MeanError |
|-----------|----------------|-----------|--------|-----------|----------------|-----------|--------|-----------|----------------|-----------|--------|-----------|-----------|
|           | Errors         | Precision | Recall | f-Measure | Errors         | Precision | Recall | f-Measure | Errors         | Precision | Recall | f-Measure |           |
| Dog 1     | 7.74%          | 0.27      | 0.38   | 0.33      | 12.5%          | 0.16      | 0.38   | 0.26      | 10.12%         | 0.15      | 0.25   | 0.21      | 10.12%    |
| Dog 2     | 10.5%          | 0.42      | 1.0    | 0.69      | 15.47%         | 0.28      | 0.64   | 0.45      | 9.39%          | 0.45      | 1.0    | 0.71      | 11.78%    |
| Dog 3     | 5.75%          | 0.0       | 0.0    | 0         | 4.56%          | 1.0       | 0.04   | 0.06      | 5.95%          | 0.0       | 0.0    | 0         | 5.42%     |
| Dog 4     | 10.33%         | 1.0       | 0.03   | 0.05      | 11.0%          | 0.0       | 0.0    | 0         | 11.33%         | 0.0       | 0.0    | 0         | 10.89%    |
| Dog 5     | 8.75%          | 0.36      | 0.5    | 0.44      | 8.13%          | 0.33      | 0.3    | 0.31      | 16.88%         | 0.16      | 0.4    | 0.27      | 11.25%    |
| Patient 1 | 34.78%         | 0.25      | 0.17   | 0.19      | 26.09%         | 0.0       | 0.0    | 0         | 21.74%         | 0.67      | 0.33   | 0.4       | 27.52%    |
| Patient 2 | 30.0%          | 0.5       | 0.17   | 0.21      | 50.0%          | 0.17      | 0.17   | 0.17      | 35.0%          | 0.0       | 0.0    | 0         | 38.35%    |

Table 2: Performance of the bonehead model.

### 4.4 Regression Trees

The bonehead model tries fitting all segments of a type using the same global parameters, which might not be a good idea if there actually are variations within a class. So, we tried the regression tree model which allows us to fit simple models to small partitions of the training data and hence, take into account local variations.

We used the following combinations of features:

- Variances and Correlation Coefficients (Table 3):** This is our base set of features which we use for all the models that follow. We observe that this model beats the bonehead model with ease in terms of accuracy of prediction and recall. This is expected given that we’re using more discriminating features.
- Variances, Correlation Coefficients, Top Fourier Frequencies (Table 4):** We’re including the top principal frequencies of each electrode’s Fourier Spectrum. The performance of this model seems to be poor which can be attributed to the fact that the frequency values themselves aren’t features that can differentiate between interictal and preictal samples (as seen in Figure 6).

3. **Variances, Correlation Coefficients, Similarity between frequency vectors (Table 5):** To solve the problems of the previous model, we try looking at how each pair of electrodes correlates with each other with respect to their top principal frequencies. This is a bivariate feature and seems to be improving the accuracy of the classifier.
4. **Variances, Correlation Coefficients, Amplitude Vectors (Table 6):** Adding the amplitude vectors to the base set of features improves the performance which suggests that the amplitude vectors are good features.
5. **Variances, Correlation Coefficients, Cosine Similarity between Amplitude Vectors (Table 7):** Here we try introducing more bivariate features by including the cosine similarities between all pairs of amplitude vectors. This model outperforms the previous one which lends support to the claim that bivariate features are better features.
6. **Variances, Correlation Coefficients, Euclidean Distance between Amplitude Vectors (Table 8):** This is similar to the previous model. Here, we're using the Euclidean distance between two amplitude vectors as a measure of similarity/dissimilarity between two electrodes.

## 4.5 Ensemble Methods(Adaboost)

Carrying on from trees, we used Ensemble methods (Adaboost) with decision stumps as the weak learner. The motivation for this is that boosting lets us learn complex decision boundaries by training a series of weak learners.

Again, we used multiple combinations here too:

1. **Variances, Correlation Coefficients and Fourier Frequencies Similarity (Table 14):** Using Adaboost as the classifier for these features gives better results when compared to the same features being used with an SVM or a Regression Tree.
2. **Variances, Correlation Coefficients and Amplitude Vectors (Table 15):** Similar to the previous case, using Adaboost with these features results in a better result than when SVM or a Regression Tree was used.
3. **Variances, Correlation Coefficients and Cosine Similarity between Amplitude Vectors (Table 16):** The introduction of cosine similarity between amplitude vectors as bivariate features improves the recall for some subjects and remains same/goes down for the others. Except for Patient-1, the mean error is lower than linear SVM. For all subjects, the mean error is lower than that for regression tree with same set of features.
4. **Variances, Correlation Coefficients and Euclidean Distance between Amplitude Vectors (Table 17):** Similar to the previous case, using Euclidean distance to measure the similarity/dissimilarity of two amplitude vectors results in an improvement for some subjects only.

## 4.6 SVM

Next, we tried the SVM classifier primarily because of the power of the classifier and the ability to use the Kernel trick which allows us to map our features to a high dimensional space. For our experiments, we used the linear and RBF kernels.

### 4.6.1 Linear SVM

We used the following combinations of features:

1. **Variances, Correlation Coefficients, Top Fourier Frequencies (Table 9):** Here, we use the top principal frequencies of each electrode's Fourier spectrum as features. This model performs better than the bonehead model.
2. **Variances, Correlation Coefficients, similarities between top frequency vectors (Table 10):** In this model, we add bivariate features that measure the correlation between two electrodes on the basis of their frequency vectors. This results in a slightly better model when compared to the previous one.
3. **Variances, Correlation Coefficients, Amplitude Vectors (Table 11):** Using the amplitude vectors of each electrode as features results in a model that outperforms the previous two models. This is further indication that the amplitude vectors tell us more about the data than just the top principal frequency vectors.
4. **Variances, Correlation Coefficients, Cosine Similarity between Amplitude Vectors (Table 12):** This classifier yields high pre-ictal recall on all subjects. Only for Dog4 and Patient2, the mean error across folds is slightly high, indicating that a higher number of inter-ictal segments are being classified wrongly. This can be explained using our earlier observations that Fourier frequencies and amplitudes are more strongly correlated among electrodes for pre-ictal segments (Figure 9). So, for these two subjects in particular, inter-electrode similarity-score vectors for inter-ictal segments might be scattered around. Hence, a linear decision boundary tends to mis-classify some inter-ictal vectors.
5. **Variances, Correlation Coefficients, Euclidean Distance between Amplitude Vectors (Table 13):** Similar observations and conclusions as above. This is essentially because the similarity and distance are inversely related to each other.

In general, we observe that a linear SVM outperforms the regression tree classifier in terms of pre-ictal recall, especially when we provide the amplitude-similarity features. In terms of overall cross-validation error, its performance is equivalent to that of Adaboost.

### 4.6.2 RBF Kernel SVM

Our experiments with the RBF Kernel SVM were of a different nature from those with the other classifiers. Initially we tried various combinations of parameters but none of them resulted in significant recall. This can be seen in figure 10.

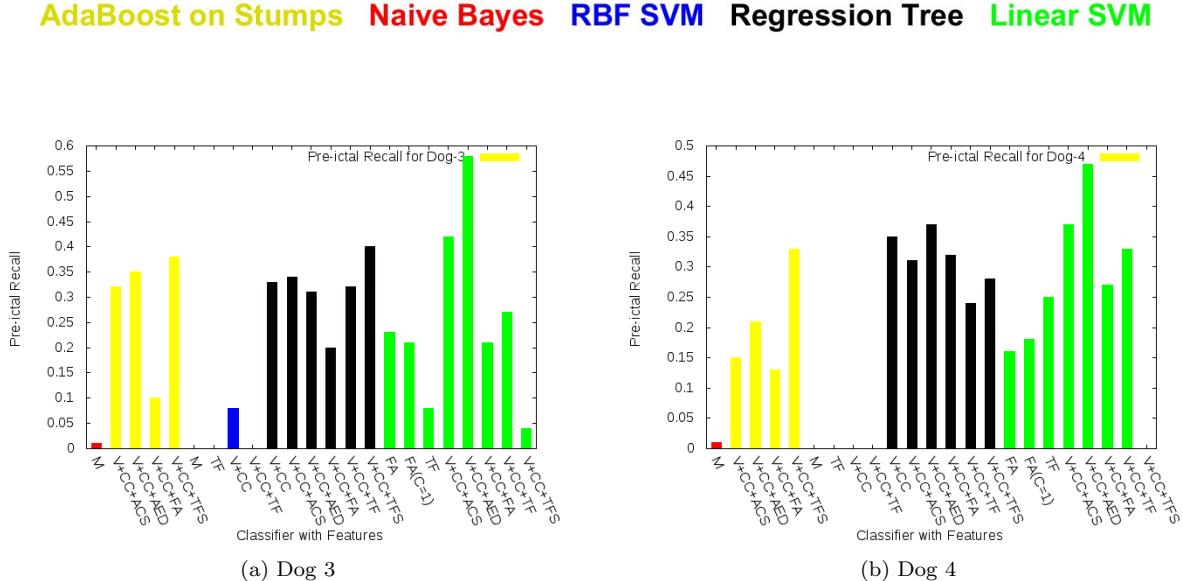


Figure 10: Pre-ictal Recall Comparison amongst different classifier-feature combinations for two of the subjects. The x-axis labels indicate the set of features used, the codes being the ones mentioned in section 4.1. Note the 3 empty columns (zero recall) for Dog-3, and 4 empty ones for Dog-4. These correspond to RBF SVM

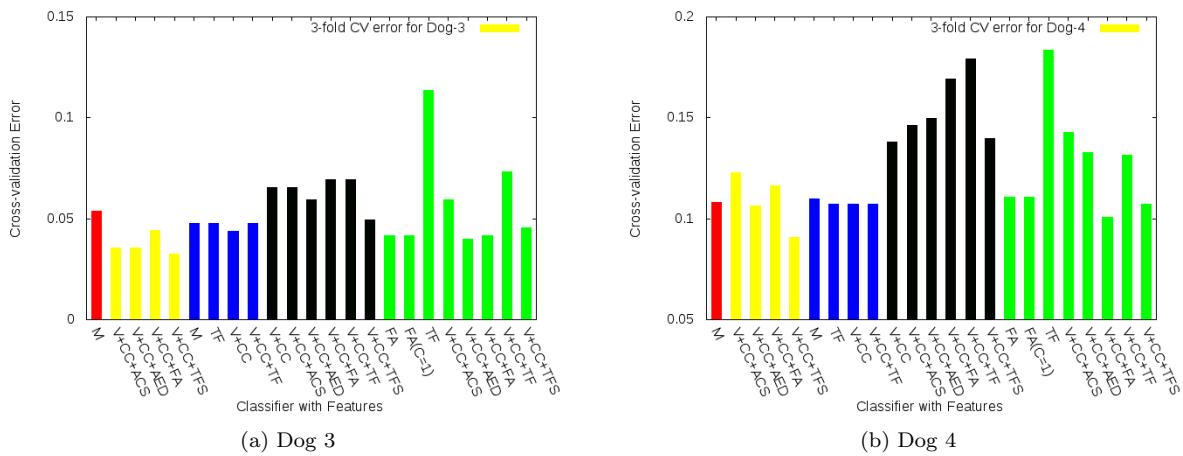


Figure 11: Overall error comparison amongst different classifier-feature combinations for two of the subjects. The x-axis labels indicate the set of features used, the codes being the ones mentioned in section 4.1

To address this issue, we fixed a set of features and tuned the values of the SVM penalty parameter  $C$  and the RBF bandwidth parameter  $\sigma$  using cross-validation. The set of features used was **Variances, Correlation Coefficients and Cosine Similarity between Amplitude Vectors**.

We separated 20% of the test data from the rest and tuned the parameters  $C$  and  $\sigma$  using cross-validation to maximize certain metrics, namely pre-ictal recall and the F-measure described in section 4.2. We then tested those combinations of  $C$  and  $\sigma$  which gave the best results on the test data separated out initially and recorded the results. We tried out three different tuning mechanisms, the results of each of which are described in the three subsections which follow.

#### 4.5.2.1 Maximizing Recall

The parameters were tuned so as to maximize the average pre-ictal recall over the three folds of cross-validation. Results showed a high recall and good accuracy. The results for Dog 4 are shown below:

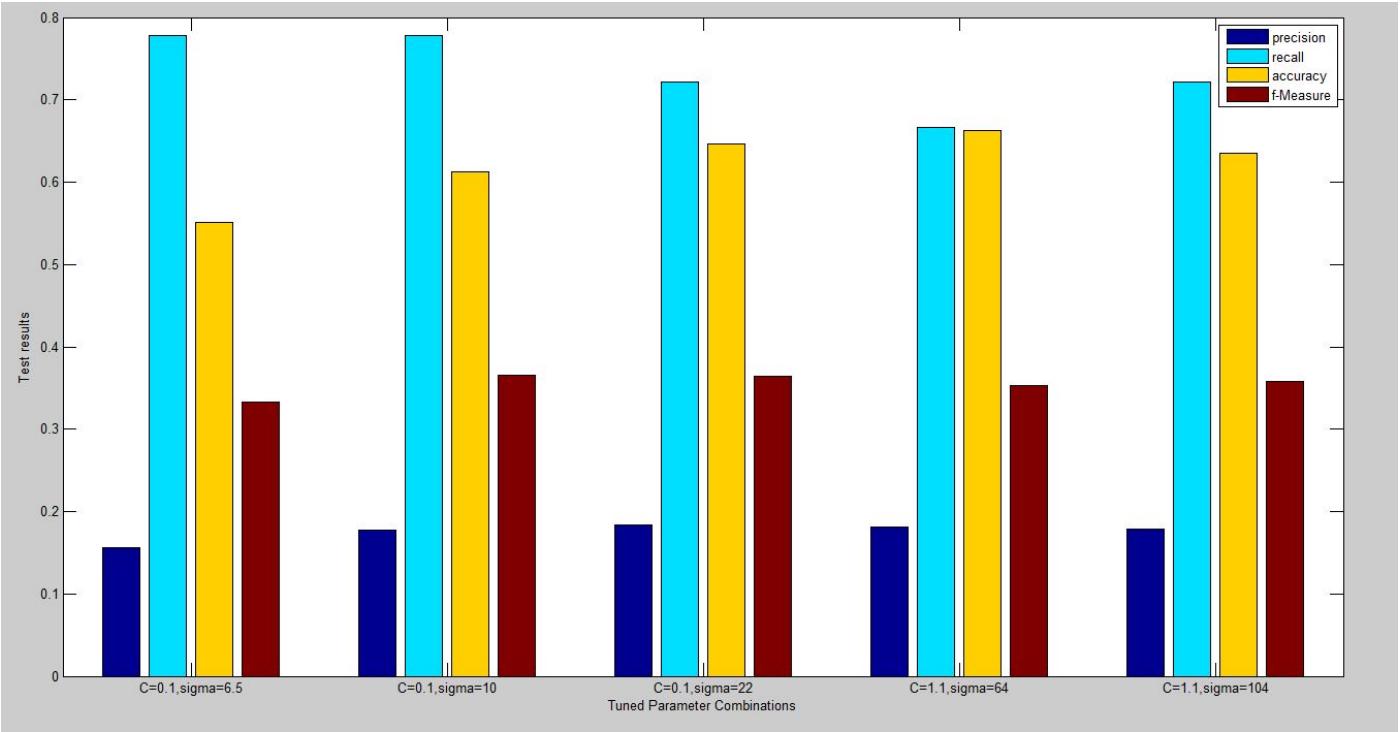


Figure 12: Testing results for Dog 4 when parameters are tuned by maximizing average cross-validation recall.

#### 4.5.2.2 Maximizing F-measure

The parameters were tuned so as to maximize the average F-measure over the three folds of cross-validation. The results for Patient 2 are shown below:

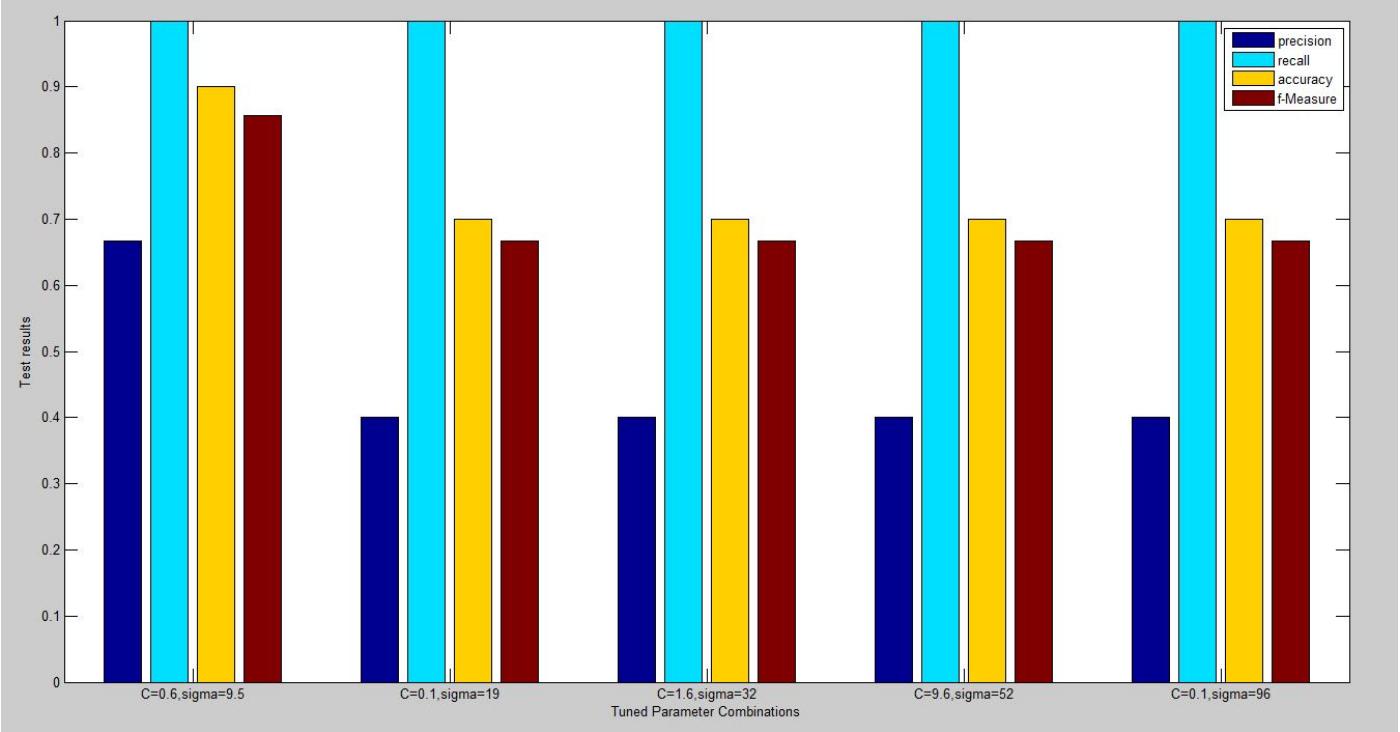


Figure 13: Testing results for Patient 2 when parameters are tuned by maximizing average cross-validation F-measure.

#### 4.5.2.3 Maximizing Recall subject to an Accuracy Threshold

In some cases we observed that tuning to maximize pre-ictal recall resulted in low overall accuracy and low precision. The classifier was simply attaining a high recall by predicting most labels as preictal, clearly an undesirable trait. This can be seen in the following figure which shows the results of tuning to maximize recall for Dog 3:

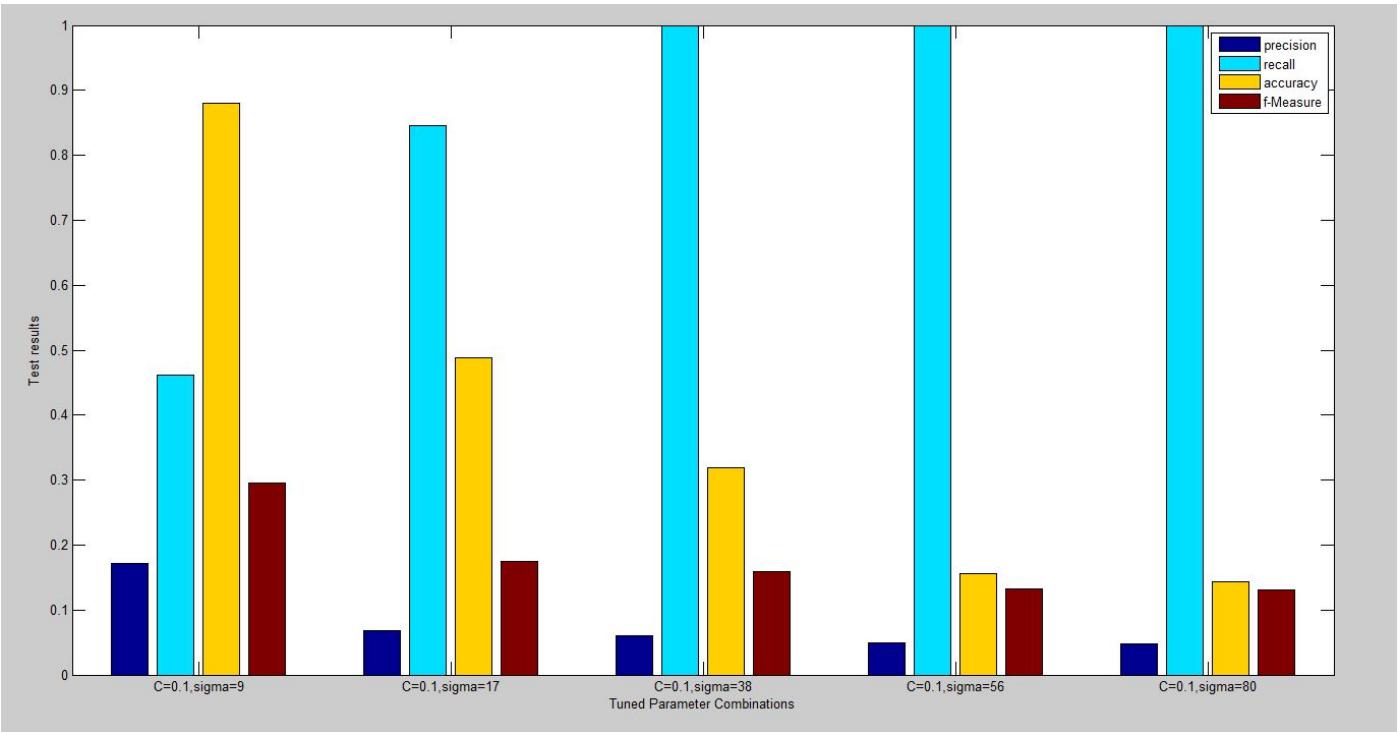


Figure 14: Testing results for Dog 3 when parameters are tuned by maximizing average cross-validation pre-ictal recall.

To resolve this issue, the parameters were tuned so as to maximize the average recall over the three folds of cross-validation subject to a threshold on the average accuracy. The threshold we used for this purpose was 0.6. A marked increase in the accuracy and the F-measure was observed. The results for Dog 3 are shown below:

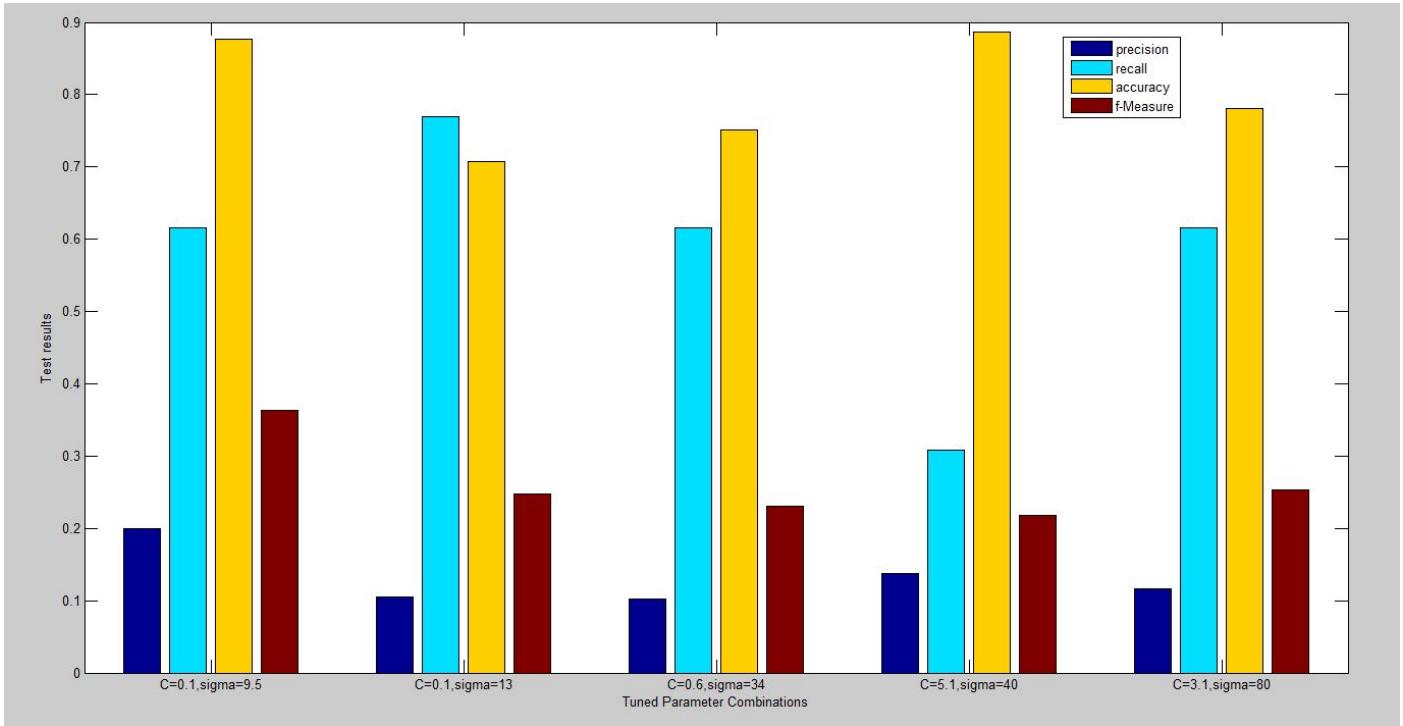


Figure 15: Testing results for Dog 3 when parameters are tuned by maximizing average cross-validation recall after imposing a threshold on the average cross-validation accuracy.

#### 4.5.2.4 RBF Kernel SVM Summary

Tuning the parameters in the RBF kernel SVM resulted in classifiers with high accuracy and high recall. The low pre-ictal precision is not necessarily a bad trait considering the fact that there is much more interictal data than preictal data. The best results (ones with high recall and high accuracy) for each subject obtained by tuning the parameters of the RBF kernel SVM classifiers are shown below:

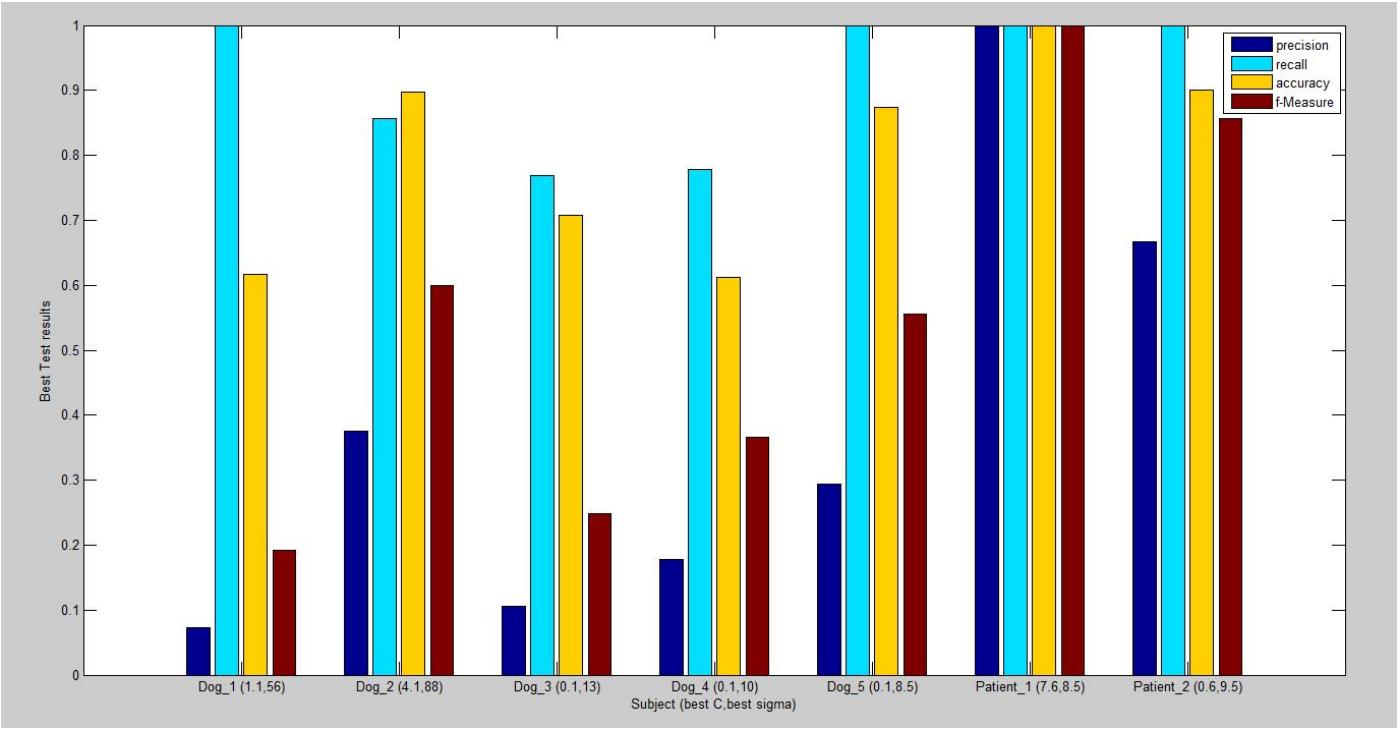


Figure 16: Best classifiers for each of the 7 subjects.

## 5 Conclusions

1. Mean of signal is not a good discriminating feature. Variance, when combined with other features (Fourier and bivariate) helps.
2. When compared to univariate features, bivariate features seem to do a better job at distinguishing between preictal and interictal samples.
3. In terms of the classifiers used, we observed that boosting gives the lowest error for a given set of features.
4. Regression trees, boosting on stumps and linear SVMs give good pre-ictal recall on use of bivariate amplitude features such as cosine similarity and euclidean distance.
5. RBF kernels can easily overfit, owing to the high complexity of the class. Tuning using cross-validation and then testing on a separate dataset yields good results though, suggesting that we aren't overfitting in this case.
6. Using just the top principal frequencies of the fourier spectrum of EEG data as features doesn't seem to help much. On the other hand, applying a low band pass filter and using the amplitudes (and their correlations) of the relevant frequencies appears to be a better choice of features which gives improved results.

## 6 Future Work

1. Applying techniques like PCA (Principal Component Analysis) or ICA (Independent Component Analysis) for decorrelation of data.
2. Exploring the possibility of using wavelets such as Haar for Discrete Wavelet Transformation of the signals. This would be able to capture local patterns/spikes more effectively than the Fourier transform.
3. Exploring the usage of non parametric methods like k-NN.

## References

- [1] Piotr Mirowski, Deepak Madhavan, Yann LeCun, Ruben Kuzniecky (2008) *Classification of Patterns of EEG Synchronization for Seizure Prediction* IEEE Workshop on Machine Learning for Signal Processing.
- [2] Klaus Lehnertz, Ralph G. Andrzejak, Jochen Arnhold, Thomas Kreuz (2001) *Nonlinear EEG Analysis in Epilepsy: Its Possible Use for Interictal Focus Localization, Seizure Anticipation, and Prevention* Journal of Clinical Neurophysiology.
- [3] Yun Park, Lan Luo, Keshab K. Parhi, and Theoden Netoff(2011) *Seizure prediction with spectral power of EEG using cost-sensitive support vector machines*

# Appendix

## Classifier Results

The following tables are the results obtained upon using each classifier and a combination of features on the dataset:

| Subject   | Test on Fold 1 |           |        |           | Test on Fold 2 |           |        |           | Test on Fold 3 |           |        |           | MeanError |
|-----------|----------------|-----------|--------|-----------|----------------|-----------|--------|-----------|----------------|-----------|--------|-----------|-----------|
|           | Errors         | Precision | Recall | f-Measure | Errors         | Precision | Recall | f-Measure | Errors         | Precision | Recall | f-Measure |           |
| Dog 1     | 11.90%         | 0.12      | 0.25   | 0.19      | 6.55%          | 0.20      | 0.12   | 0.14      | 5.95%          | 0.25      | 0.12   | 0.15      | 8.13%     |
| Dog 2     | 6.08%          | 0.59      | 0.71   | 0.67      | 9.94%          | 0.33      | 0.29   | 0.30      | 4.97%          | 0.69      | 0.64   | 0.66      | 7.00%     |
| Dog 3     | 6.75%          | 0.31      | 0.33   | 0.32      | 6.35%          | 0.33      | 0.33   | 0.33      | 6.55%          | 0.32      | 0.33   | 0.33      | 6.55%     |
| Dog 4     | 14.33%         | 0.32      | 0.28   | 0.29      | 15.00%         | 0.32      | 0.37   | 0.35      | 12.33%         | 0.42      | 0.40   | 0.41      | 13.89%    |
| Dog 5     | 7.50%          | 0.43      | 0.60   | 0.53      | 4.38%          | 0.64      | 0.70   | 0.68      | 6.25%          | 0.50      | 0.60   | 0.56      | 6.04%     |
| Patient 1 | 22.73%         | 0.56      | 0.83   | 0.71      | 27.27%         | 0.50      | 0.33   | 0.38      | 22.73%         | 0.55      | 1.00   | 0.78      | 24.24%    |
| Patient 2 | 25.00%         | 0.60      | 0.50   | 0.53      | 45.00%         | 0.00      | 0.00   | nan       | 45.00%         | 0.29      | 0.33   | 0.32      | 38.33%    |

Table 3: **Regression Tree** using Variances and Correlation Coefficients as Features

| Subject   | Test on Fold 1 |           |        |           | Test on Fold 2 |           |        |           | Test on Fold 3 |           |        |           | MeanError |
|-----------|----------------|-----------|--------|-----------|----------------|-----------|--------|-----------|----------------|-----------|--------|-----------|-----------|
|           | Errors         | Precision | Recall | f-Measure | Errors         | Precision | Recall | f-Measure | Errors         | Precision | Recall | f-Measure |           |
| Dog 1     | 13.69%         | 0.06      | 0.12   | 0.09      | 13.69%         | 0.06      | 0.12   | 0.09      | 10.12%         | 0.09      | 0.12   | 0.11      | 12.50%    |
| Dog 2     | 7.73%          | 0.50      | 0.36   | 0.39      | 8.84%          | 0.45      | 0.71   | 0.60      | 8.29%          | 0.33      | 0.07   | 0.10      | 8.29%     |
| Dog 3     | 7.74%          | 0.26      | 0.33   | 0.30      | 5.36%          | 0.40      | 0.25   | 0.29      | 7.74%          | 0.27      | 0.38   | 0.33      | 6.94%     |
| Dog 4     | 16.67%         | 0.20      | 0.19   | 0.19      | 17.00%         | 0.25      | 0.28   | 0.27      | 20.33%         | 0.18      | 0.25   | 0.22      | 18.00%    |
| Dog 5     | 11.25%         | 0.10      | 0.10   | 0.10      | 10.00%         | 0.29      | 0.40   | 0.35      | 11.25%         | 0.21      | 0.30   | 0.26      | 10.83%    |
| Patient 1 | 17.39%         | 0.67      | 0.67   | 0.67      | 34.78%         | 0.25      | 0.17   | 0.19      | 43.48%         | 0.00      | 0.00   | nan       | 31.88%    |
| Patient 2 | 30.00%         | 0.50      | 0.17   | 0.21      | 45.00%         | 0.40      | 1.00   | 0.67      | 45.00%         | 0.29      | 0.33   | 0.32      | 40.00%    |

Table 4: **Regression Tree** using Variances, Correlation Coefficients and Top Fourier Frequencies

| Subject   | Test on Fold 1 |           |        |           | Test on Fold 2 |           |        |           | Test on Fold 3 |           |        |           | MeanError |
|-----------|----------------|-----------|--------|-----------|----------------|-----------|--------|-----------|----------------|-----------|--------|-----------|-----------|
|           | Errors         | Precision | Recall | f-Measure | Errors         | Precision | Recall | f-Measure | Errors         | Precision | Recall | f-Measure |           |
| Dog 1     | 8.33%          | 0.25      | 0.38   | 0.32      | 4.76%          | 0.50      | 0.25   | 0.30      | 10.71%         | 0.08      | 0.12   | 0.11      | 7.94%     |
| Dog 2     | 10.56%         | 0.35      | 0.43   | 0.40      | 7.22%          | 0.55      | 0.43   | 0.46      | 7.78%          | 0.50      | 0.50   | 0.50      | 8.52%     |
| Dog 3     | 4.76%          | 0.50      | 0.38   | 0.41      | 5.36%          | 0.43      | 0.42   | 0.42      | 4.96%          | 0.47      | 0.38   | 0.40      | 5.03%     |
| Dog 4     | 15.95%         | 0.21      | 0.19   | 0.19      | 11.96%         | 0.41      | 0.28   | 0.31      | 14.62%         | 0.34      | 0.37   | 0.36      | 14.17%    |
| Dog 5     | 8.75%          | 0.17      | 0.10   | 0.12      | 3.75%          | 0.75      | 0.60   | 0.64      | 6.88%          | 0.45      | 0.50   | 0.48      | 6.46%     |
| Patient 1 | 27.27%         | 0.50      | 0.50   | 0.50      | 13.64%         | 0.67      | 1.00   | 0.86      | 31.82%         | 0.43      | 0.50   | 0.47      | 24.24%    |
| Patient 2 | 30.00%         | 0.50      | 0.17   | 0.21      | 20.00%         | 0.62      | 0.83   | 0.75      | 15.00%         | 0.71      | 0.83   | 0.79      | 21.67%    |

Table 5: **Regression Tree** using Variances, Correlation Coefficients and Frequency Similarity

| Subject   | Test on Fold 1 |           |        |           | Test on Fold 2 |           |        |           | Test on Fold 3 |           |        |           | MeanError |
|-----------|----------------|-----------|--------|-----------|----------------|-----------|--------|-----------|----------------|-----------|--------|-----------|-----------|
|           | Errors         | Precision | Recall | f-Measure | Errors         | Precision | Recall | f-Measure | Errors         | Precision | Recall | f-Measure |           |
| Dog 1     | 11.31%         | 0.08      | 0.12   | 0.10      | 10.71%         | 0.08      | 0.12   | 0.11      | 7.14%          | 0.00      | 0.00   | nan       | 9.72%     |
| Dog 2     | 2.76%          | 0.85      | 0.79   | 0.80      | 11.05%         | 0.38      | 0.64   | 0.52      | 7.73%          | 0.50      | 0.43   | 0.45      | 7.18%     |
| Dog 3     | 7.14%          | 0.20      | 0.17   | 0.18      | 7.14%          | 0.20      | 0.17   | 0.18      | 6.75%          | 0.27      | 0.25   | 0.26      | 7.01%     |
| Dog 4     | 14.95%         | 0.32      | 0.37   | 0.35      | 17.61%         | 0.23      | 0.28   | 0.26      | 18.60%         | 0.23      | 0.31   | 0.28      | 17.05%    |
| Dog 5     | 12.50%         | 0.08      | 0.10   | 0.09      | 9.38%          | 0.31      | 0.40   | 0.36      | 11.88%         | 0.20      | 0.30   | 0.26      | 11.25%    |
| Patient 1 | 56.52%         | 0.23      | 0.50   | 0.36      | 17.39%         | 0.67      | 0.67   | 0.67      | 17.39%         | 0.62      | 0.83   | 0.75      | 30.43%    |
| Patient 2 | 45.00%         | 0.33      | 0.50   | 0.43      | 35.00%         | 0.40      | 0.33   | 0.35      | 45.00%         | 0.29      | 0.33   | 0.32      | 41.67%    |

Table 6: **Regression Tree** using Variances, Correlation Coefficients and Amplitude Vectors

| Subject   | Test on Fold 1 |           |        |           | Test on Fold 2 |           |        |           | Test on Fold 3 |           |        |           | MeanError |
|-----------|----------------|-----------|--------|-----------|----------------|-----------|--------|-----------|----------------|-----------|--------|-----------|-----------|
|           | Errors         | Precision | Recall | f-Measure | Errors         | Precision | Recall | f-Measure | Errors         | Precision | Recall | f-Measure |           |
| Dog 1     | 10.71%         | 0.14      | 0.25   | 0.20      | 5.95%          | 0.00      | 0.00   | nan       | 5.95%          | 0.25      | 0.12   | 0.15      | 7.54%     |
| Dog 2     | 6.63%          | 0.57      | 0.57   | 0.57      | 5.52%          | 0.62      | 0.71   | 0.68      | 6.08%          | 0.62      | 0.57   | 0.59      | 6.08%     |
| Dog 3     | 7.54%          | 0.28      | 0.38   | 0.34      | 6.75%          | 0.22      | 0.17   | 0.18      | 5.36%          | 0.44      | 0.46   | 0.45      | 6.55%     |
| Dog 4     | 13.29%         | 0.37      | 0.34   | 0.35      | 17.94%         | 0.21      | 0.25   | 0.23      | 13.62%         | 0.37      | 0.34   | 0.35      | 14.95%    |
| Dog 5     | 10.00%         | 0.31      | 0.50   | 0.42      | 6.88%          | 0.33      | 0.10   | 0.13      | 10.62%         | 0.27      | 0.40   | 0.34      | 9.17%     |
| Patient 1 | 26.09%         | 0.50      | 0.50   | 0.50      | 26.09%         | 0.50      | 0.17   | 0.21      | 13.04%         | 1.00      | 0.50   | 0.60      | 21.74%    |
| Patient 2 | 35.00%         | 0.40      | 0.33   | 0.35      | 30.00%         | 0.50      | 0.33   | 0.38      | 40.00%         | 0.33      | 0.33   | 0.33      | 35.00%    |

Table 7: **Regression Tree** using variances, Correlation Coefficients and Cosine Similarity between Amplitude vectors

| Subject   | Test on Fold 1 |           |        |           | Test on Fold 2 |           |        |           | Test on Fold 3 |           |        |           | MeanError |
|-----------|----------------|-----------|--------|-----------|----------------|-----------|--------|-----------|----------------|-----------|--------|-----------|-----------|
|           | Errors         | Precision | Recall | f-Measure | Errors         | Precision | Recall | f-Measure | Errors         | Precision | Recall | f-Measure |           |
| Dog 1     | 11.90%         | 0.00      | 0.00   | nan       | 5.95%          | 0.38      | 0.38   | 0.38      | 7.14%          | 0.17      | 0.12   | 0.14      | 8.33%     |
| Dog 2     | 6.67%          | 0.60      | 0.43   | 0.47      | 3.89%          | 0.82      | 0.64   | 0.69      | 5.56%          | 0.67      | 0.57   | 0.60      | 5.37%     |
| Dog 3     | 4.56%          | 0.53      | 0.38   | 0.42      | 6.75%          | 0.32      | 0.38   | 0.36      | 6.55%          | 0.24      | 0.17   | 0.18      | 5.95%     |
| Dog 4     | 17.00%         | 0.23      | 0.25   | 0.24      | 17.33%         | 0.23      | 0.25   | 0.24      | 11.33%         | 0.47      | 0.59   | 0.54      | 15.22%    |
| Dog 5     | 6.25%          | 0.50      | 0.30   | 0.35      | 10.62%         | 0.18      | 0.20   | 0.19      | 5.62%          | 0.55      | 0.60   | 0.58      | 7.50%     |
| Patient 1 | 17.39%         | 0.62      | 0.83   | 0.75      | 8.70%          | 0.83      | 0.83   | 0.83      | 26.09%         | 0.50      | 0.50   | 0.50      | 17.39%    |
| Patient 2 | 25.00%         | 0.56      | 0.83   | 0.71      | 30.00%         | 0.50      | 0.67   | 0.60      | 40.00%         | 0.25      | 0.17   | 0.19      | 31.67%    |

Table 8: **Regression Tree** using Variances, Correlation Coefficients and Euclidean Distance between Amplitude Vectors

| Subject   | Test on Fold 1 |           |        |           | Test on Fold 2 |           |        |           | Test on Fold 3 |           |        |           | MeanError |
|-----------|----------------|-----------|--------|-----------|----------------|-----------|--------|-----------|----------------|-----------|--------|-----------|-----------|
|           | Errors         | Precision | Recall | f-Measure | Errors         | Precision | Recall | f-Measure | Errors         | Precision | Recall | f-Measure |           |
| Dog 1     | 4.76%          | 0.50      | 0.12   | 0.17      | 5.36%          | 0.33      | 0.12   | 0.16      | 5.36%          | 0.00      | 0.00   | nan       | 5.16%     |
| Dog 2     | 9.39%          | 0.29      | 0.14   | 0.17      | 9.39%          | 0.20      | 0.07   | 0.09      | 7.18%          | 0.56      | 0.36   | 0.41      | 8.66%     |
| Dog 3     | 6.94%          | 0.21      | 0.17   | 0.18      | 7.94%          | 0.25      | 0.33   | 0.30      | 6.94%          | 0.24      | 0.21   | 0.22      | 7.28%     |
| Dog 4     | 13.29%         | 0.38      | 0.37   | 0.37      | 14.95%         | 0.24      | 0.19   | 0.20      | 13.29%         | 0.35      | 0.25   | 0.27      | 13.84%    |
| Dog 5     | 4.38%          | 0.71      | 0.50   | 0.56      | 5.00%          | 1.00      | 0.20   | 0.27      | 6.25%          | 0.50      | 0.20   | 0.25      | 5.21%     |
| Patient 1 | 13.04%         | 1.00      | 0.50   | 0.60      | 8.70%          | 1.00      | 0.67   | 0.75      | 8.70%          | 1.00      | 0.67   | 0.75      | 10.14%    |
| Patient 2 | 25.00%         | 1.00      | 0.17   | 0.23      | 35.00%         | 0.44      | 0.67   | 0.57      | 30.00%         | 0.00      | 0.00   | nan       | 30.00%    |

Table 9: **Linear SVM** on Variances, Correlation Coefficients and Top Fourier Frequencies.

| Subject   | Test on Fold 1 |           |        |           | Test on Fold 2 |           |        |           | Test on Fold 3 |           |        |           | MeanError |
|-----------|----------------|-----------|--------|-----------|----------------|-----------|--------|-----------|----------------|-----------|--------|-----------|-----------|
|           | Errors         | Precision | Recall | f-Measure | Errors         | Precision | Recall | f-Measure | Errors         | Precision | Recall | f-Measure |           |
| Dog 1     | 5.95%          | 0.25      | 0.12   | 0.15      | 5.95%          | 0.33      | 0.25   | 0.27      | 5.95%          | 0.33      | 0.25   | 0.27      | 5.95%     |
| Dog 2     | 8.84%          | 0.44      | 0.50   | 0.48      | 7.73%          | 0.50      | 0.50   | 0.50      | 5.52%          | 0.67      | 0.57   | 0.60      | 7.37%     |
| Dog 3     | 6.35%          | 0.38      | 0.50   | 0.45      | 7.14%          | 0.30      | 0.38   | 0.35      | 6.94%          | 0.24      | 0.21   | 0.22      | 6.81%     |
| Dog 4     | 15.95%         | 0.28      | 0.31   | 0.30      | 18.27%         | 0.28      | 0.46   | 0.38      | 15.95%         | 0.29      | 0.31   | 0.30      | 16.72%    |
| Dog 5     | 1.88%          | 1.00      | 0.70   | 0.78      | 7.50%          | 0.33      | 0.20   | 0.23      | 5.62%          | 0.57      | 0.40   | 0.44      | 5.00%     |
| Patient 1 | 4.35%          | 1.00      | 0.83   | 0.88      | 8.70%          | 0.83      | 0.83   | 0.83      | 8.70%          | 1.00      | 0.67   | 0.75      | 7.25%     |
| Patient 2 | 35.00%         | 0.33      | 0.17   | 0.20      | 25.00%         | 0.67      | 0.33   | 0.40      | 20.00%         | 0.67      | 0.67   | 0.67      | 26.67%    |

Table 10: **Linear SVM** on Variances, Correlation Coefficients and Similarities between the top frequency vectors.

| Subject   | Test on Fold 1 |           |        |           | Test on Fold 2 |           |        |           | Test on Fold 3 |           |        |           | MeanError |
|-----------|----------------|-----------|--------|-----------|----------------|-----------|--------|-----------|----------------|-----------|--------|-----------|-----------|
|           | Errors         | Precision | Recall | f-Measure | Errors         | Precision | Recall | f-Measure | Errors         | Precision | Recall | f-Measure |           |
| Dog 1     | 4.76%          | 0.00      | 0.00   | nan       | 4.76%          | 0.00      | 0.00   | nan       | 5.95%          | 0.00      | 0.00   | nan       | 5.16%     |
| Dog 2     | 6.63%          | 1.00      | 0.14   | 0.20      | 7.73%          | 0.00      | 0.00   | nan       | 7.18%          | 1.00      | 0.07   | 0.10      | 7.18%     |
| Dog 3     | 4.37%          | 0.67      | 0.17   | 0.22      | 3.97%          | 0.70      | 0.29   | 0.36      | 4.17%          | 0.80      | 0.17   | 0.23      | 4.17%     |
| Dog 4     | 9.33%          | 0.62      | 0.31   | 0.37      | 10.00%         | 0.60      | 0.28   | 0.34      | 11.00%         | 0.47      | 0.22   | 0.26      | 10.11%    |
| Dog 5     | 5.62%          | 1.00      | 0.10   | 0.14      | 5.00%          | 1.00      | 0.20   | 0.27      | 4.38%          | 0.80      | 0.40   | 0.48      | 5.00%     |
| Patient 1 | 13.04%         | 1.00      | 0.50   | 0.60      | 4.35%          | 1.00      | 0.83   | 0.88      | 0.00%          | 1.00      | 1.00   | 1.00      | 5.80%     |
| Patient 2 | 30.00%         | 0.50      | 0.17   | 0.21      | 25.00%         | 0.67      | 0.33   | 0.40      | 20.00%         | 0.75      | 0.50   | 0.56      | 25.00%    |

Table 11: **Linear SVM** on Variance, Correlation Coefficients and Amplitude Vectors

| Subject   | Test on Fold 1 |           |        |           | Test on Fold 2 |           |        |           | Test on Fold 3 |           |        |           | MeanError |
|-----------|----------------|-----------|--------|-----------|----------------|-----------|--------|-----------|----------------|-----------|--------|-----------|-----------|
|           | Errors         | Precision | Recall | f-Measure | Errors         | Precision | Recall | f-Measure | Errors         | Precision | Recall | f-Measure |           |
| Dog 1     | 5.36%          | 0.44      | 0.50   | 0.48      | 6.55%          | 0.29      | 0.25   | 0.26      | 4.17%          | 0.60      | 0.38   | 0.43      | 5.36%     |
| Dog 2     | 4.44%          | 0.71      | 0.71   | 0.71      | 5.00%          | 0.69      | 0.64   | 0.66      | 4.44%          | 0.69      | 0.79   | 0.75      | 4.63%     |
| Dog 3     | 6.35%          | 0.32      | 0.29   | 0.30      | 5.95%          | 0.38      | 0.42   | 0.41      | 5.75%          | 0.42      | 0.54   | 0.49      | 6.02%     |
| Dog 4     | 15.95%         | 0.28      | 0.31   | 0.30      | 12.62%         | 0.41      | 0.40   | 0.40      | 14.62%         | 0.35      | 0.40   | 0.38      | 14.40%    |
| Dog 5     | 5.00%          | 0.60      | 0.60   | 0.60      | 1.88%          | 1.00      | 0.70   | 0.78      | 3.75%          | 0.83      | 0.50   | 0.58      | 3.54%     |
| Patient 1 | 4.55%          | 1.00      | 0.83   | 0.88      | 9.09%          | 1.00      | 0.67   | 0.75      | 0.00%          | 1.00      | 1.00   | 1.00      | 4.55%     |
| Patient 2 | 40.00%         | 0.38      | 0.50   | 0.45      | 20.00%         | 1.00      | 0.33   | 0.43      | 30.00%         | 0.50      | 0.33   | 0.38      | 30.00%    |

Table 12: **Linear SVM** on Variances, Correlation Coefficients and Cosine Similarity between Amplitude Vectors.

| Subject   | Test on Fold 1 |           |        |           | Test on Fold 2 |           |        |           | Test on Fold 3 |           |        |           | MeanError |
|-----------|----------------|-----------|--------|-----------|----------------|-----------|--------|-----------|----------------|-----------|--------|-----------|-----------|
|           | Errors         | Precision | Recall | f-Measure | Errors         | Precision | Recall | f-Measure | Errors         | Precision | Recall | f-Measure |           |
| Dog 1     | 7.74%          | 0.33      | 0.62   | 0.48      | 6.55%          | 0.33      | 0.38   | 0.36      | 4.17%          | 0.67      | 0.25   | 0.32      | 6.15%     |
| Dog 2     | 3.89%          | 0.77      | 0.71   | 0.73      | 3.33%          | 0.83      | 0.71   | 0.75      | 0.00%          | 1.00      | 1.00   | 1.00      | 2.41%     |
| Dog 3     | 3.77%          | 0.59      | 0.71   | 0.66      | 4.17%          | 0.56      | 0.58   | 0.58      | 4.37%          | 0.54      | 0.54   | 0.54      | 4.10%     |
| Dog 4     | 15.00%         | 0.33      | 0.40   | 0.38      | 13.33%         | 0.39      | 0.40   | 0.40      | 11.67%         | 0.47      | 0.62   | 0.56      | 13.33%    |
| Dog 5     | 3.12%          | 0.73      | 0.80   | 0.77      | 3.12%          | 0.86      | 0.60   | 0.67      | 2.50%          | 0.75      | 0.90   | 0.84      | 2.92%     |
| Patient 1 | 13.04%         | 1.00      | 0.50   | 0.60      | 8.70%          | 0.83      | 0.83   | 0.83      | 4.35%          | 0.86      | 1.00   | 0.95      | 8.70%     |
| Patient 2 | 40.00%         | 0.38      | 0.50   | 0.45      | 45.00%         | 0.29      | 0.33   | 0.32      | 35.00%         | 0.43      | 0.50   | 0.47      | 40.00%    |

Table 13: **Linear SVM** on Variances, Correlation Coefficients and Euclidean Distance between Amplitude Vectors.

| Subject   | Test on Fold 1 |           |        |           | Test on Fold 2 |           |        |           | Test on Fold 3 |           |        |           | MeanError |
|-----------|----------------|-----------|--------|-----------|----------------|-----------|--------|-----------|----------------|-----------|--------|-----------|-----------|
|           | Errors         | Precision | Recall | f-Measure | Errors         | Precision | Recall | f-Measure | Errors         | Precision | Recall | f-Measure |           |
| Dog 1     | 4.76%          | 0.00      | 0.00   | nan       | 4.17%          | 0.67      | 0.25   | 0.32      | 5.95%          | 0.25      | 0.12   | 0.15      | 4.96%     |
| Dog 2     | 0.55%          | 1.00      | 0.93   | 0.95      | 3.31%          | 0.90      | 0.64   | 0.71      | 3.31%          | 0.83      | 0.71   | 0.75      | 2.39%     |
| Dog 3     | 3.37%          | 0.89      | 0.33   | 0.42      | 2.78%          | 0.86      | 0.50   | 0.58      | 3.57%          | 0.80      | 0.33   | 0.41      | 3.24%     |
| Dog 4     | 10.30%         | 0.53      | 0.25   | 0.30      | 7.31%          | 0.81      | 0.40   | 0.48      | 9.63%          | 0.61      | 0.34   | 0.40      | 9.08%     |
| Dog 5     | 2.50%          | 1.00      | 0.60   | 0.69      | 5.00%          | 0.62      | 0.50   | 0.54      | 4.38%          | 0.71      | 0.50   | 0.56      | 3.96%     |
| Patient 1 | 4.35%          | 1.00      | 0.83   | 0.88      | 17.39%         | 1.00      | 0.33   | 0.43      | 13.04%         | 0.80      | 0.67   | 0.71      | 11.59%    |
| Patient 2 | 40.00%         | 0.33      | 0.33   | 0.33      | 40.00%         | 0.00      | 0.00   | nan       | 15.00%         | 1.00      | 0.50   | 0.60      | 31.67%    |

Table 14: **Adaboost** with Variance, Correlation Coefficients and Frequency Similarities.

| Subject   | Test on Fold 1 |           |        |           | Test on Fold 2 |           |        |           | Test on Fold 3 |           |        |           | MeanError |
|-----------|----------------|-----------|--------|-----------|----------------|-----------|--------|-----------|----------------|-----------|--------|-----------|-----------|
|           | Errors         | Precision | Recall | f-Measure | Errors         | Precision | Recall | f-Measure | Errors         | Precision | Recall | f-Measure |           |
| Dog 1     | 4.76%          | 0.00      | 0.00   | nan       | 4.76%          | 0.00      | 0.00   | nan       | 4.76%          | 0.00      | 0.00   | nan       | 4.76%     |
| Dog 2     | 5.52%          | 0.70      | 0.50   | 0.55      | 4.42%          | 1.00      | 0.43   | 0.53      | 4.97%          | 0.78      | 0.50   | 0.57      | 4.97%     |
| Dog 3     | 4.17%          | 0.80      | 0.17   | 0.23      | 4.56%          | 1.00      | 0.04   | 0.06      | 4.56%          | 0.67      | 0.08   | 0.12      | 4.43%     |
| Dog 4     | 9.97%          | 0.60      | 0.19   | 0.24      | 11.63%         | 0.33      | 0.09   | 0.12      | 13.29%         | 0.23      | 0.09   | 0.12      | 11.63%    |
| Dog 5     | 5.00%          | 1.00      | 0.20   | 0.27      | 4.38%          | 1.00      | 0.30   | 0.39      | 5.62%          | 1.00      | 0.10   | 0.14      | 5.00%     |
| Patient 1 | 30.43%         | 0.44      | 0.67   | 0.57      | 17.39%         | 0.75      | 0.50   | 0.56      | 34.78%         | 0.25      | 0.17   | 0.19      | 27.54%    |
| Patient 2 | 25.00%         | 0.67      | 0.33   | 0.40      | 15.00%         | 0.80      | 0.67   | 0.71      | 35.00%         | 0.00      | 0.00   | nan       | 25.00%    |

Table 15: **Adaboost** with Variance, Correlation Coefficients and Amplitudes.

| Subject   | Test on Fold 1 |           |        |           | Test on Fold 2 |           |        |           | Test on Fold 3 |           |        |           | MeanError |
|-----------|----------------|-----------|--------|-----------|----------------|-----------|--------|-----------|----------------|-----------|--------|-----------|-----------|
|           | Errors         | Precision | Recall | f-Measure | Errors         | Precision | Recall | f-Measure | Errors         | Precision | Recall | f-Measure |           |
| Dog 1     | 5.36%          | 0.00      | 0.00   | nan       | 4.76%          | 0.00      | 0.00   | nan       | 4.17%          | 1.00      | 0.12   | 0.18      | 4.76%     |
| Dog 2     | 3.87%          | 0.82      | 0.64   | 0.69      | 3.31%          | 0.75      | 0.86   | 0.82      | 4.42%          | 0.88      | 0.50   | 0.58      | 3.87%     |
| Dog 3     | 4.17%          | 0.62      | 0.33   | 0.39      | 3.17%          | 0.90      | 0.38   | 0.47      | 3.57%          | 1.00      | 0.25   | 0.33      | 3.64%     |
| Dog 4     | 14.33%         | 0.18      | 0.09   | 0.11      | 11.33%         | 0.45      | 0.15   | 0.20      | 11.67%         | 0.40      | 0.19   | 0.23      | 12.44%    |
| Dog 5     | 3.12%          | 0.78      | 0.70   | 0.72      | 5.00%          | 0.67      | 0.40   | 0.46      | 3.75%          | 1.00      | 0.40   | 0.50      | 3.96%     |
| Patient 1 | 4.35%          | 1.00      | 0.83   | 0.88      | 17.39%         | 0.75      | 0.50   | 0.56      | 13.04%         | 0.80      | 0.67   | 0.71      | 11.59%    |
| Patient 2 | 25.00%         | 0.57      | 0.67   | 0.63      | 30.00%         | 0.50      | 0.33   | 0.38      | 25.00%         | 0.60      | 0.50   | 0.53      | 26.67%    |

Table 16: **Adaboost** with Variance, Correlation Coefficients and Cosine Similarities between Amplitude Vectors

| Subject   | Test on Fold 1 |           |        |           | Test on Fold 2 |           |        |           | Test on Fold 3 |           |        |           | MeanError |
|-----------|----------------|-----------|--------|-----------|----------------|-----------|--------|-----------|----------------|-----------|--------|-----------|-----------|
|           | Errors         | Precision | Recall | f-Measure | Errors         | Precision | Recall | f-Measure | Errors         | Precision | Recall | f-Measure |           |
| Dog 1     | 4.17%          | 0.67      | 0.25   | 0.32      | 4.76%          | 0.00      | 0.00   | nan       | 4.76%          | 0.50      | 0.12   | 0.17      | 4.56%     |
| Dog 2     | 3.33%          | 0.75      | 0.86   | 0.82      | 3.33%          | 0.90      | 0.64   | 0.71      | 3.33%          | 0.83      | 0.71   | 0.75      | 3.33%     |
| Dog 3     | 2.78%          | 0.86      | 0.50   | 0.58      | 4.37%          | 0.62      | 0.21   | 0.27      | 3.57%          | 0.80      | 0.33   | 0.41      | 3.57%     |
| Dog 4     | 10.96%         | 0.46      | 0.19   | 0.23      | 9.30%          | 0.70      | 0.22   | 0.28      | 11.63%         | 0.44      | 0.22   | 0.26      | 10.63%    |
| Dog 5     | 3.75%          | 1.00      | 0.40   | 0.50      | 1.25%          | 0.90      | 0.90   | 0.90      | 3.12%          | 0.86      | 0.60   | 0.67      | 2.71%     |
| Patient 1 | 4.55%          | 1.00      | 0.83   | 0.88      | 18.18%         | 0.67      | 0.67   | 0.67      | 18.18%         | 1.00      | 0.33   | 0.43      | 13.64%    |
| Patient 2 | 25.00%         | 0.67      | 0.33   | 0.40      | 40.00%         | 0.38      | 0.50   | 0.45      | 35.00%         | 0.43      | 0.50   | 0.47      | 33.33%    |

Table 17: **Adaboost** with Variance, Correlation Coefficients and Euclidean Distances between Amplitude Vectors