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PARKINSON'S DISEASE DETECTION USING HANDWRITING DATASETS.

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Abstract Neurodegenerative disease patients have been increasing in number over the years. Parkinson's is one of these diseases that has a severe impact on the patient's life. There is no specific test to detect this disease but to do various tests based on which the patient is then diagnosed. Handwriting of a Parkinson's patient is different from that of a normal patient and this could be used to detect the disease. There have been many attempts to detect Parkinson's disease using various datasets and different approaches. Deep learning has been the most popular approach that has been used extensively. Deep learning models being a "black-box" give accurate predictions but with no justification as to why the prediction has been made. Machine learning models that achieve the same results as the deep learning models will be beneficial in giving justifications for the predictions of the models. This work uses a few popular machine learning algorithms that are known to be explainable such as Logistic Regression, Support Vector Machines, Decision Trees, Random Forest and Naive Bayes Classifier to reach the same level of accuracy as those of deep learning models.
Keywords Logistic Regression, Support Vector Machines, Decision Trees, Random Forest, Naive Bayes Classifier, Machine Learning, Neurodegenerative Disease, Parkinson's Disease.

1. Introduction

Parkinson's disease is a neurodegenerative disease that is the second most common after Alzheimer's[1]. The chances of being affected by this disease increase as a person's age increases[2]. There have been a few studies that identified some gene patterns that could be found among those that were suffering from this disease, which increases the chance of inheriting the disease by 5-10%[3] but the most significant factor seems to be due to pollution in the environment[4]. The two most common reasons[5] for Parkinson's disease proving to be fatal are that the patients are more prone to falling, and bad falls can be fatal. The other reason is pneumonia, as the patients have problems swallowing hence increasing the chances for them being affected by pneumonia when they swallow wrong and the food enters the windpipe. The patient's suffering from this disease have low dopamine and hence have to take drugs that increase the dopamine levels in the brain or atleast mimic the action of dopamine in the brain. There are no particular tests that can detect the disease[6] but it is based on a total review of the signs and symptoms that they exhibit. SPECT scans or DAT scans help in making the diagnosis. The people affected by Parkinson's disease have tremors in their hands which makes the majority of the patients suffering from Parkinson's disease suffer from handwriting abnormalities. There has been a lot of research on handwriting which uses a biometric pen to collect the data and can also measure the tremors produced. The SPECT and DAT scans are also used to detect the disease and most of the research done used the PPMI dataset to do so. The PPMI dataset being larger than NewHandPD it has been able to produce models that have

significant accuracies. Explainability of machine learning algorithms is important so that a proper reasoning and justification is provided for the outputs that are received from the models especially for medical applications. The deep neural networks are known as "black-box" models owing to the fact that they give highly accurate results while not providing any justifications or reasons for their outputs. Machine learning algorithms that have the same level of accuracy as that of the deep neural networks are less computationally intensive and are explainable by being able to give reasons for the decisions.

2.1 Literature Review

In this paper [7], the model used for classifying as healthy or having Parkinson's is based on MRI PPMI Image data.They selected a particular type of images (3T T1) and trained using CNN with 35 layers. SMBO for hyperparameter selection. The model achieved 95% accuracy and 0.98 AUC curve. In paper[8] the model used to classify as HC and PD based on PPMI, ADNI, HCP image data.The UNET model produced 84.7%accuracy, and VGGNet produced 76% accuracy. In paper[9] the model used to classify as HC and PD based on PPMI survey data. The build model used several motor assessments and non-motor assessments. The paper achieved 98.6% accuracy using enhanced probabilistic neural networks. In another paper[10] it is used for PD and Control build using PPMI image data. The model was built using Image processing, LENET, and ALEXNET. The model produced 90% accuracy for binary classification of LD. In paper[11] LENET and ALEXNET were used for feature extraction on PPMI DaTscan images. Both the model produced 95% accuracy.In paper[12] they build model for classifying the severity of the Parkinson disease.They have built a deep neural network with 3 hidden layers with 50 neurons to predict UPDRS scores using Parkinson's Telemonitoring Voice Data from UCI Machine Learning Repository. In the paper for motor UPDRS the accuracy achieved is 82%, while 62% accuracy in the case of total UPDRS.The accuracy could have been better if more instances are used for training with more features. In paper[13] Parkison classification is done by predicting UPDRS scores of the patients using UCI voice dataset. It involves 3 phases. The model used used SOM for clustering the data, NIPAL for dimensionality reduction, ISVM for predicting the UPDRS scores.which is effective for incremental data. It achieved a MAE of 0.46 for total UPDRS and 0.49 for the motor UPDRS. In paper[14] the model used for classifying parkinson disease based on sleep behavior,smell detection and other biomarkers using PPMI dataset. They have used 8 supervised classification algorithms. Boosted logistic regression outperformed seven other models with an accuracy of 97.1% and AUC of 98.9. This study didn't include patients who are having premotor symptoms but are not diagnosed as PD due to lack of motor symptoms. In paper[15] it is used for classification of parkinson disease and also severity of disease. DT,LR,NB,RF algorithms are used for classification and k means clustering to find out the severity using UCI voice dataset. Initially DT has given 100% accuracy; this might be due to overfitting. After performing pruning the accuracy varied from 88% to 94%. In paper[16] for PD classification, PCA and a genetic algorithm feature selection techniques. SVM with rbf kernel function combined with GA feature selection performed well with an accuracy of 95.57%. In paper[17] NMS-MRI scans were used to detect PD. The model used CNN (ResNet50) to train the images. 83.6% training accuracy and 80% testing accuracy CNN-DL. In [12], Pedram Khatamino et al. introduced a dataset for a novel test called dynamic spiral test for PD detection. CNN model is used, which yielded an accuracy of 88%. In [13], authors have used two deep learning models

trained end to end on time series data namely CNN and CNN-BLSTM and achieved an accuracy of 97.6%. [14] R. Castrillon et al. reported an accuracy of around 81% and 97% when SVM, KNN, and MLP are used. In their paper [15], the authors used CNN to learn features from images produced by handwritten dynamics and achieved an accuracy of 95%. PaHaw Dataset was used for PD detection by A. Della Cioppa et al. [16]. Their study used Cartesian genetic programming that automatically detects Parkinson's disease and reported an accuracy of 76%. Further, in [17], the images of handwriting of PD patients are preprocessed, followed by training using CNN with 4-fold and 10-fold cross-validation techniques, which achieved an accuracy of 88%. In order to decrease the dimensionality of the preprocessed image data, Zhifei Xu et al. [18] used PCA. After training with a support vector machine using a linear kernel function, they reported an accuracy of 77%. Lucas Salvador Bernardo et al. [19] proposed a hybrid technique that combines CNN and SVM trained in different stages, the proposed technique achieved accuracy of 91.26%. In the study [20], authors trained two different CNNs for analyzing the drawing patterns of both spiral and wave sketches. In [21], Catherine Taleb et al. used a multi-class support vector machine to identify PD by predicting H&Y stage, UPDRS, and total UPDRS scores and yielded accuracies of 94%, 92%, and 88%, respectively. In this paper [22], principal component analysis is used to reduce the dimensionality of sensor signals. 6 random forest models are trained with k-fold cross validation, displaying an accuracy of 89.4%. In [23], Rohit Lamba et al. proposed a novel method for detecting Parkinson's disease patients using kinematic features extracted from handwritten drawings. Due to the data's extreme imbalance, the SMOTE technique is used, the information gain technique is used for feature selection, and the data is trained using the ensemble technique Adaboost, which achieved an accuracy of 96%. However, only the PD is predicted by this study; the disease's severity is not.

2.2 Proposed Work

Deep neural networks have been known to be "black box" models because they produce the correct output without giving any proper justification to why it has reached that particular conclusion . There have been multiple approaches to open this "black box" [24] but still supervised machine learning models like Logistic Regression, Decision Trees, Random Forest, Support Vector Machine, Naive Bayes are significantly more interpretable. The medical field being one that requires people to have reasons for a particular diagnosis it is important to have models that are able to be interpretable and their decisions being justifiable. Our proposal is to reach the similar level of accuracy of that of neural networks in detecting Parkinson's disease while using interpretable machine learning models. Hence, we chose the algorithms Logistic Regression, Decision Trees, Random Forest, Support Vector Machine, and Naive Bayes.

2.3 Implementation

The NewHandPD dataset has the data of three different handwriting images being meander, spiral and circular. We do a 60-40 (train-test) split of the data first. For each type of handwriting data in the three types of data, the workflow specified below is followed. After training the data with each model we then validate the models accuracy by validating with the testing dataset. The workflow for spiral data is shown in the image below, the same will be followed with meander and circular handwriting data.

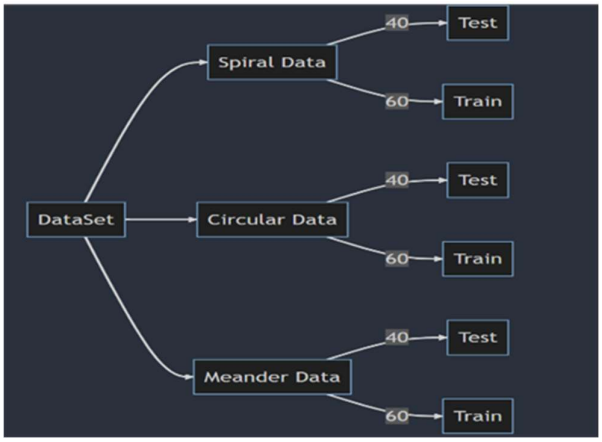

Figure 1. WorkFlow diagram of NewHandPD dataset.

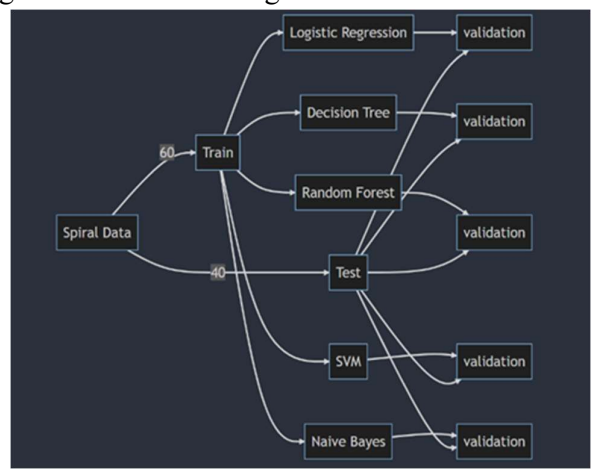

Figure 2. WorkFlow diagram of Spiral data.

Figure 3. Example of Spiral data in NewHandPD dataset.

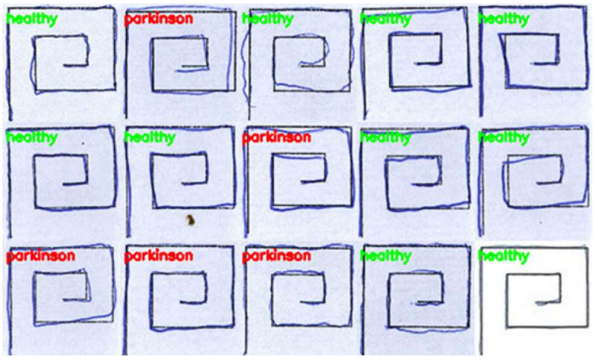

Figure 4. Example of Meander data in NewHandPD dataset.

2.3.1 Decision Trees

Decision Tree is a Supervised learning technique that can be used for both classification and Regression problems, but mostly it is preferred for solving Classification problems. It is a tree-structured classifier, where internal nodes represent the features of a dataset, branches represent the decision rules and each leaf node represents the outcome. To make a decision tree we need two formulas that are given below based on which the trees are made.

$$\text{Entropy}(S) = \sum_{i=1}^{c} P_i \log 2^{P_i} \quad \text{- Equation 1}$$

$$\text{Gain}(S, A) = \sum_{v \in V(A)} \frac{|S_v|}{|S|} \text{Entropy}(S_v) \quad \text{- Equation 2}$$

Using the Entropy the information gain for each attribute present in the dataset is calculated and the dataset is split according to the attribute that gives us the most information gain. This split will be done until we have homogenous classes in the leaf nodes or sometimes for all attributes or till you reach a specified depth of the tree.

2.3.2 Support Vector Machines

SVMs are popular supervised learning algorithms that have been in use since a long time and there has also been research on improving explainability of SVMs like [25, 26]. What is fundamentally done in the SVM is that it finds a decision boundary (hyperplane) which segregates the dataset into different classes to do further classification of new data points. The maximum margin hyperplane is chosen and is used as the decision boundary. Depending on the sample space a line could be used for 2 - dimensional space or in case of a 3 - dimensional space a plane and so on. There could be many hyperplanes that divide the classes in the dataset space out of all these possibilities the hyperplane that has the maximum distance from all classes is chosen as the optimal hyperplane. SVMs also uses kernels and what it basically does is, it converts a low dimensional space into a high dimensional space which is useful in cases when there aren't any linear boundaries possible to separate the sample space. The kernels functions increase the dimensionality of the dataset making it possible for a linear separation to be possible. It is very efficient for binary classification problems hence making us choose SVMs as one of the models.

2.3.3 Random Forest

The random forest algorithm is used for regression and for classification as well. In our case, we are using it for classification. Like the name suggests, the random forest includes many trees, i.e decision trees. The random forest classifiers take the decision by taking the votes of

decision trees that are trained on the subsets of the training data. Based on popular vote the final prediction is then predicted. To make these subsets of data it follows an ensemble technique called bagging which reduces the variance and decreases the chance of the model overfitting, it is used popularly for high variance models.

2.3.4 Naive Bayes

Naive Bayes' classifier works on Bayes' theorem. Let a sample, X = {x1, x2, x3,... xn} where the elements are attributes or features of the data. We then assume a hypothesis (H) that the given X belongs to any class, the probability is denoted as P(H/X). P(H) in this case is our prior probability, which is the chance of an event regardless of what the X is and P(H/X) is the posteriori probability which is the chance of an event given that X event has already occurred. Bayes' theorem states that the P(H/X) = {P(X/H)*P(H)}/P(X). The classifier also works on the similar principle that the highest probability each sample achieves towards a particular class will then be the class assigned to that sample. As the P(X) is constant for a particular sample we just have to calculate the P(X/Ci)*P(Ci) where Ci is a class for all classes and compare which one produces the highest probability. The name naive comes to the classifier as it "naively" assumes that there is conditional independence between the classes to reduce the computation complexity, giving us the formula given below.

$$P(\mathbf{X}|C_i) \approx \prod_{k=1}^{n} P(x_k|C_i). \quad \textbf{- Equation 3.}$$

The class that has the maximum probability for a given sample X is going to be the predicted class.

2.3.5 Logistic Regression

Logistic regression is one of the most widely used machine learning algorithms and performs well on classes that are easily separable. Logistic regression relies on the sigmoid function given by the equation. Let W be weights, x be the sample set and b be biases.

$$Z = W^T x + b \quad \textbf{- Equation 4}$$

$$\sigma(z) = \frac{1}{1 + e^{-z}} \quad \textbf{- Equation 5.}$$

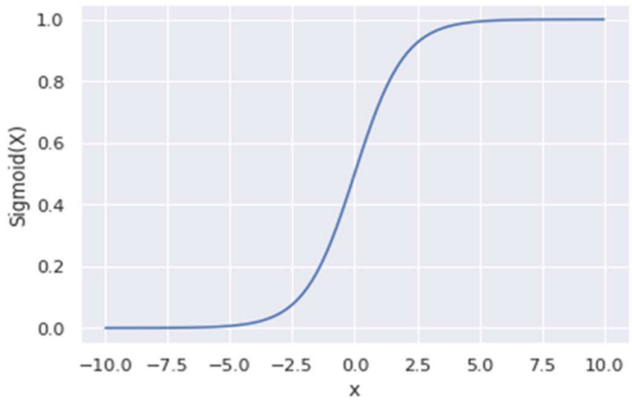

Figure 5. Sigmoid graph.

For the loss function in logistic regression, we use the log loss function to calculate the loss. Gradient descent algorithm is followed to reduce the loss and to find the best fit. After applying the sigmoid function there will be a threshold function.

$$= \sum_{i=1}^{n} \left[y^{(i)} \log\left(\sigma\left(z^{(i)}\right)\right) + \left(1 - y^{(i)}\right) \log\left(1 - \sigma\left(z^{(i)}\right)\right) \right] \quad \text{- Equation 6.}$$

$$\hat{y} = \begin{cases} 1 & \text{if } z \geq 0.0 \\ 0 & \text{otherwise} \end{cases} \quad \text{- Equation 7.}$$

Based on the threshold function the class is either 0 or 1. The logistic regression is not just for binary classification but can also be extended for multiple classes using multinomial logistic regression with the big difference being in the use of Softmax activation function.

2.4 Performance Analysis

The algorithms that we used in this were logistic regression, decision trees, random forest, support vector machine and naive bayes classifier and they were chosen due to the interpretability of their predictions. In the paper [27] they used the CNN architectures of ImageNet, CIFAR-10 and LeNet while the use OPF classifier as a baseline for comparison. They used two training splits of 50-50 and 25-75 (test- train) and fed them to the models achieving the best average overall accuracy for meander dataset was 87.14% and best average overall accuracy for spiral dataset was 83.77% using the OPF classifier.

The machine learning models that we chose achieved the below results as shown in the Table 1,2,3 and the Figures 1,2,3.

Table 1. Metrics for Spiral data.

Model	Accuracy	Sensitivity	Specificity
Logistic Regression	0.893939	0.85	0.9615384615384616
Decision Trees	0.772727	0.7435897435897436	0.7777777777777778
Random Forest	0.924242	0.7954545454545454	1.0
Support Vector Machine	0.909091	0.8918918918918919	0.9310344827586207
Naive Bayes	0.681818	0.6590909090909091	0.7272727272727273

Table 2. Metrics for Circular data.

Model	Accuracy	Sensitivity	Specificity
Logistic Regression	0.647059	0.7142857142857143	0.6
Decision Trees	0.529412	0.5833333333333334	0.6
Random Forest	0.588235	0.6	0.5714285714285714
Support Vector Machine	0.647059	0.8	0.5833333333333334
Naive Bayes	0.588235	1	0.47058823529411764

Table 3. Metrics for Meander data.

Model	Accuracy	Sensitivity	Specificity
Logistic Regression	0.893939	0.9117647058823529	0.875
Decision Trees	0.696970	0.7142857142857143	0.6428571428571429
Random Forest	0.893939	0.8823529411764706	0.84375
Support Vector Machine	0.878788	0.8857142857142857	0.8709677419354839
Naive Bayes	0.651515	1	0.4696969696969697

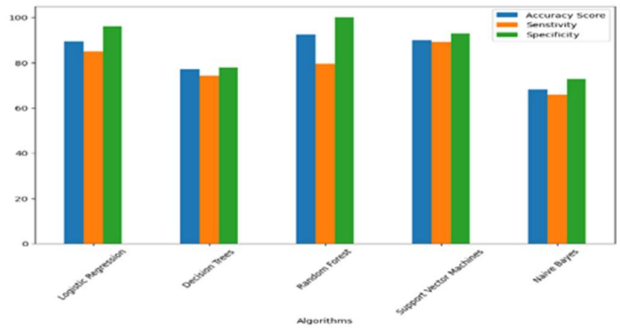

Figure 6. Results of Spiral data.

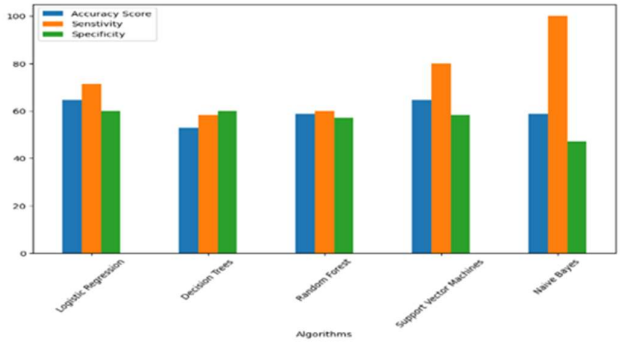

Figure 7. Results of Circle data.

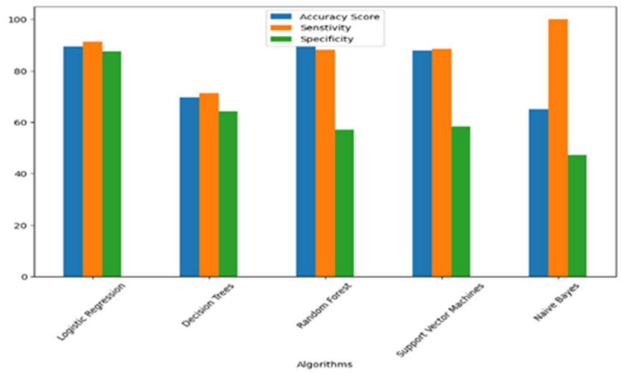

Figure 8. Results of Meander data.

2.5 Conclusion

This paper tries to detect the Parkinson's disease of a person based on their handwriting to aid in the process of detecting the disease as there isn't one specific test that can guarantee the existence of the disease. There have been previous approaches that used deep learning models to do this. The deep learning models being "black-box" models give accurate results while not giving any reasoning for the prediction. To make more interpretable and explainable models we have chosen a few machine learning algorithms that are known to do as such and have achieved accuracies that are on par with the previous approaches of deep learning while using these models. In the future we wish to identify the features that are responsible for classification by their future importance and rank them to see which features are having a greater impact on the classification.

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