

APPLICATION OF MACHINE LEARNING FOR THE PREDICTION OF THE PARKINSON'S DISEASE

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ABSTRACT

Parkinson's disease (PD) is a dopamine receptor neurological disorder. Parkinson's disease primarily contributes to movement issues. It can slowly trigger a person to shift. A progressive neurological disorder characterised by both motor (movement) and non-motor symptoms is Parkinson's. Every person will experience and display an individual presentation of the condition apart from several common symptoms. Parkinson's disease is a progressive neurodegenerative disease caused by the death of substantive nigra cell dopamine. There is no accurate test that differentiates Parkinson's disease from other disorders with similar clinical presentations. The diagnosis is mostly a historical and clinical diagnosis in this research paper, Feature Selection with Machine Learning Classifier based approach is proposed to enhance the classification accuracy, Precision, True Positive Rate and reduces the error rates like False Positive Rate, and Miss Rate. For the proposed approach, different feature selection techniques like Information Gain, Gain Ratio, Chi-Square, Correlation-based, and Fisher Exact test are analyzed with six Machine Learning classifiers like Artificial Neural Network, Support Vector Machine, Gradient Boosting Tree, Bagging, Random Forest, and Decision Tree. In this research work, Chi-Square feature selection with Gradient Boosting Tree classifier will enhance the classification accuracy of Parkinson's disease and also it reduces the error rates.

Key words: Machine Learning, Parkinson's disease, prediction, classification, feature selection, Random Forest, Decision Tree, Boosting, Bagging, Gradient Boosting Tree.

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1. INTRODUCTION

One of the biggest public health challenges in the world is Parkinson's disease (PD). About a million people have Parkinson's in the US, although the amount of Parkinson's in the world is

about five million. It is well-known. So, Parkinson's disease needs to be predicted in early stages, so that the appropriate care can be scheduled early. The motor symptoms are commonly recognised to people with Parkinson's disease but there is growing research on the prediction with non-motor symptoms of Parkinson's disease before engine disease. If it is possible to predict early and accurately, a patient may obtain the necessary care. Rapid Eye Movement (REM) Sleep Behaviour Disorder (SBD) and olfactory loss are considered non-motor symptoms. In early prediction, the development of machine learning models that can help to predict the disease can play an important role.

The chronic, degenerative neurological disorder is Parkinson's disease (PD). In fact, it is unclear the principal cause of Parkinson's disease. However, the combination of environmental and genetic factors has been investigated to play an important part in PD [1]. In order to explain Parkinson's disease in general, it is treated as a central nervous system condition arising from cell loss from different areas of the brain. Substantia nigra cells that make dopamine also contain these cells. Dopamine plays an important role in movement synchronization. It functions for the transport of signals inside the brain as a chemical transmitter. Patients suffer from motion disorder because of the loss of these cells. The PD symptoms can be divided into two groups, i.e. non-engine and motor symptoms. Many people are conscious of the motor symptoms, which human beings can experience visually. Those signs include resting tremor, movement slowness (bradykinesia), postural instability (equilibrium problems) and rigidity [2][3] as well as a cardinal symptom. The timeframes for observation of non-motor symptoms are now known. These symptoms are called symptoms that do not respond to dopamine. These signs include cognitive dysfunction, sleep issues, smell loss, constipation, speech or swallowing, unexplained pain, drooling, constipation and low blood pressure. However, when used together with other biomarkers of cerebrospinal fluid measurement (CSF) and dopamine transporter imaging, these characteristics will enable us to predict PD.

2. RELATED WORKS

Huang, Guan-Hua, et al [4] The aim of this paper was to predict phases of PD patients through their functional brain pictures. The authors used multivariate statistical methods (linear discriminatory analysis, vector support, decision tree and multi-layered perceptrons [MLP]), group learn models (random forest [RF] and adaptive boosting), and deep convolutional neural network (CNN).

El Maachi, Imanne, Guillaume-Alexandre Bilodeau, and Wassim Bouachir [5] proposed a new Parkinson smart method of detecting gait knowledge based on deep learning techniques. The authors have been developing a deep neural network (DNN) classification by using a 1D convolutionary (1D-Convnet) neural network. The proposed model processes 18 1D-signals from vertical soil reaction force (VGRF) sensors. The first component of the network is composed of 18 parallel 1D-Convnet inputs. The second component is a completely linked network linking the 1D Convnets' concatenated outputs for a final ranking.

Salmanpour, Mohammad R., et al [6] In view of increasing awareness of non-motor symptoms in Parkinson's disease, the authors review the optimum use of MCA (Montréal Cognitive Assessment (MoCA) prediction methods in year 4 from longitudinal data obtainable in years 0 and 1. In the Parkinson's Progression Marker Initiative (PPMI) database, the authors selected n=184 PD subjects (93 features). Selected were a number of robust forecast algorithms and sub-set feature selector algorithms (FSSAs). followed by the automatic hyperparameter set-up. In each of the trainings, training confirmation and final tests (10 random arrangements) the authors used 65%, 5% and 30% of the patientes, respectively. The prediction of cognitive outcome can be enhanced by the use of appropriate optimization methods (including automatic hyperparameter tuning).

Su, Chang, Jie Tong, and Fei Wang [7] This research reviews the literature concerned with the use of machine learning models in genetic and transcriptomic data analysis in PD and recognises remaining problems and accordingly indicates potential orientations. The use of machine learning certainly improves genetic PD and transcriptomic efficiency to accelerate PD research. Existing studies have shown the great potential for machine learning to detect hidden patterns within genetic or transcriptomic data and thus to discover clues that underlie pathology and pathogenesis. Progress will help us to reliably identify, pronounce and manage PD by tackling the remaining challenges.

Mostafa, Salama A., et al [8] This paper aims to enhance Parkinson's disease diagnosis by evaluating various methods of assessment of features and of classification based on the study of speech disorders. This paper is designed to find an optimal solution to the problem I by proposing a new Multi-Feature Evaluation Method (MFEA) with the implementation of a multi-agent system (ii) with 5 separate classification schemes: Decision Tree, Naive Bayes, Neural network, Random Forests, and Support for Parkinson Vector Machines, and (iii) testing the MFEA.

3. PROPOSED FRAMEWORK FOR PARKINSON'S DISEASE PREDICTION WITH MACHINE LEARNING APPROACH

3.1. Artificial Neural Network Classifier

Neural Network [9] [21][22] was based on the organic neuron used for prediction. Neural Network Let's get the single neuron to learn. A single neuron with a single input is shown in figure 1. The provided equation describes the single input neuron where O is the output, σ is the sigmoid function, ξ is the neuron's input and ω is the weight which connects the input to the neuron.

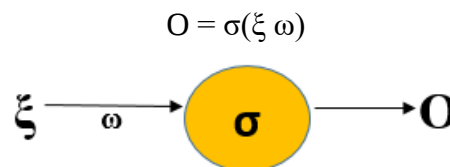


Figure 1 Single input neuron

So, when a neuron has multiple inputs as shown in Figure 2, it is the MLP which consists of inputs connected to the layer by weight. The neuron then takes several inputs and produces a result called a multilayer perceptron. A multi-layer experience is seen in the diagram.

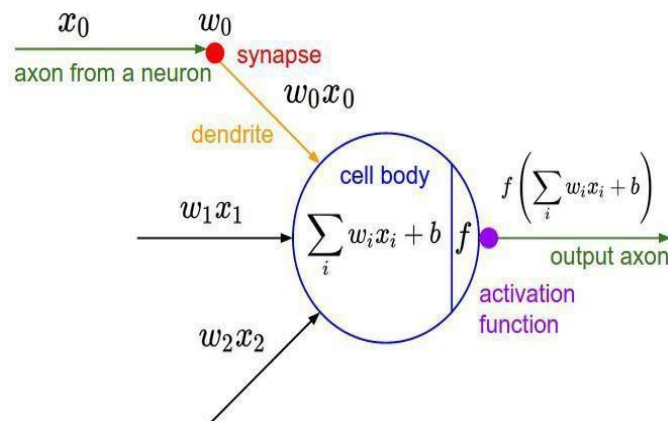


Figure 2 Multilayer perceptron

$$O = \sigma(\xi_1 \omega_1 + \xi_2 \omega_2 + \dots + \xi_k \omega_k) + \Theta$$

where O is the output.

σ is the sigmoid function or transformed function.

ξ is the input to the neuron.

ω is the weight of input (1 to k).

Θ is the bias.

3.2. Support Vector Machine Classifier

A hyperplane separating support vector machine is described. The approach performance is an ideal hyperplane that categorises new instances. This modern hyper plane in a two-dimensional space divides a plane into two sections where each class lies on one side. It results better for complex problems with classification. Every data element is marked with a value for each function that represents the coordination of the plane as a point in n-dimension. The SVM [10] [23] is categorised very efficiently that distinguishes both groups.

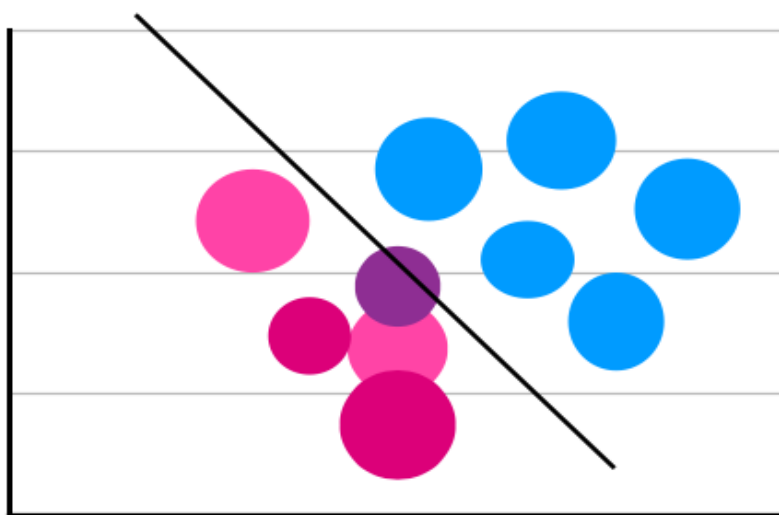


Figure 3 Support Vector Machine Hyper plane classifying two classes

3.3. Gradient Boosting Classifier

Sequentially, gradient boosting (GB) generates new models from an array of weak models that can minimise loss functions for each new model. The function of loss is determined by the descent of gradients. Using the loss function, every new model matches the observations more accurately and improves overall accuracy. Boosting, however, must finally be stopped; the model appears to overfit otherwise. The stop criterion may be an accuracy level or a maximum number of models.

GBDT [11] [24] is a community model of sequence-trained decision-making trees. GBDT learns the decision trees in any iteration by adapting negative gradients (also called residual failures). The key expense in GBDT is to learn decision bodies and finding the best split points is the most time-consuming aspect to learn a decision tree. One of the most common dividing dots is the pre-sort algorithm, listed with pre-sorting function values all possible dividing points. This algorithm is straightforward and can find the optimum splits, but both training speeds and memory use are ineffective.

3.4. Bagging Classifier

Bagging is an ensemble algorithm [12] [25] [26]; bagging methods form a powerful group of algorithms, which combine multiple cases of black box estimators in random sub-sets of the original data set, and then aggregate their predictions effectively to work out and formulate the final prediction. In order to minimise variances between the basic estimators, the storage methods make an enormous effort by efficiently incorporating randomization in its construction. Take a scenario in which, for scenario The Decision Tree, you have a learner. Often, with Bootstrap technology, you have sought to boost its accuracy and variance.

- You eventually generate several samples of your data set categorised as a training set using a next scheme approach: you can randomly imagine every variable in your training set and then pull it back. This results in a situation in which some of the training elements in the new sample are present several times and some unintentionally are missing. The samples must be the same size as the train package.
- On each produced sample you can train your student to achieve efficient results and refine the model.
- You use the algorithm to estimate the average number of students if they regress, or to vote if they are graded.

3.5. Random Forest Classifier

Random Forest is one of the techniques of master learning used for grading and regression. It's a sort of ensemble approach that transforms a group of weak models into a powerful model when combined. Several tresses are generated in the random forest. Each tree should be categorised by voting for that class. A classification. The forest prefers the highest vote classification. Figure 4 shows the method of selection by random forest [13] [21] [26]. Take the test to assess the features and decide trees in order to forecast the results and to store the results.

- For each expected result, determine the votes.
- Consider the heavily voted forecast result as the final forecast.

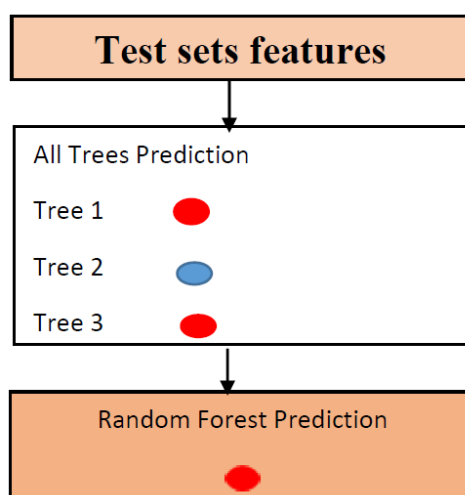


Figure 4 Prediction process taken by random forest

3.6. Decision Tree Classifier

Decision tree algorithm [14] is a supervised research algorithm used for the problems of classification and regression. Its main goal is to build a training model that can be used to predict

Parkinson 's decisions by training data sets. It tries to solve the problem by node or node hierarchy. There are three nodes:

- Root
- Internal Nodes
- Leaf Nodes

Root node is the entire sample that is subsequently divided into nodes known as leaf nodes which display the attribute divided into leaf nodes representing the class Labels.

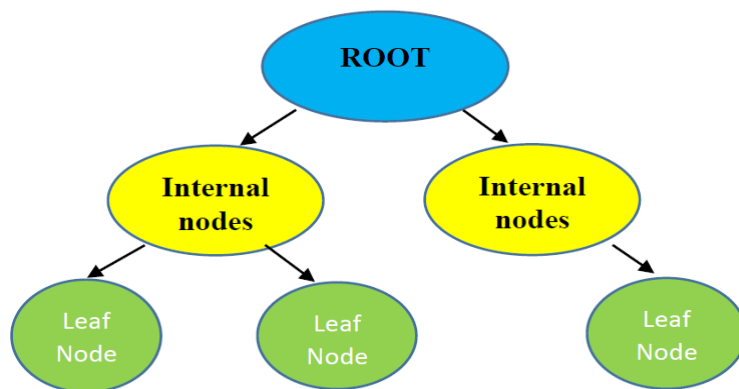


Figure 5 Representation of the Decision Tree

3.7. Proposed Research Methodology with Feature Selection Technique

A feature selection algorithm is given in this research paper based on Chi-Square in order to predict Parkinson disease using algorithms for machine learning. The comparison of other functional approaches for the classification of Parkinson's disease is often compared with the Chi-Square. The methods for selecting features such as correlation-based role selection, the gain ratio, chi-square-based feature selection, the Fishers Exact Test are used to predict Parkinson's disease.

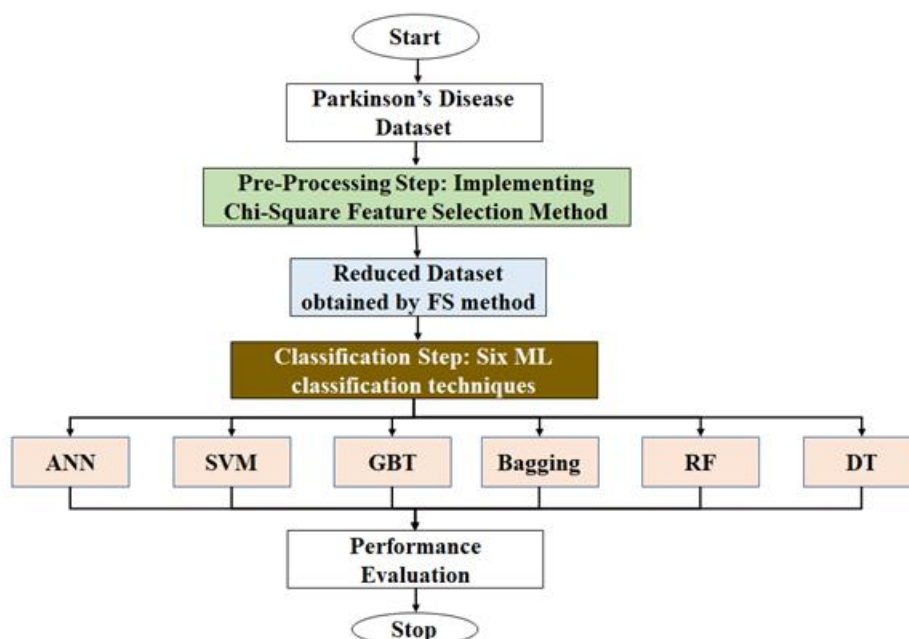


Figure 6 Proposed Framework for Predicting Parkinson's Disease

3.7.1. Correlation based Feature Selection

In this algorithm, the relation between all features and the output class is determined and the heuristic correlation assessment function is used to select the appropriate feature subset [15]. It tests the relation between nominal and categorical features such that discrete values are used for numerical features. The correlation function shall be selected by the equation given.

$$r_{zc} = \frac{K\bar{r}_{zi}}{\sqrt{K + K(K-1)\bar{r}_{ii}}}$$

Where r_{zc} denotes the relationship between features and class variable, K represents the number of features, $\bar{r}_{zi}$ indicates the mean value of correlated feature-classes and $\bar{r}_{ii}$ represents the mean value of inter-correlated features.

3.7.2. Information gain Ratio Feature Selection

The amount of data obtained by the term in a text for class prediction is determined by knowledge. Knowledge gains It selects the appropriate information value in relation to the generation of a subgroup on the class attribute. In order to evaluate characteristics, data conjecture indexes are often needed. The ultimate aim of this work is to provide an unwanted range of data gain or the entropy value for whole data is also calculated [16]. It is a selection algorithm for supervised, univariate, simple, solid, symmetrical and entropy-based features. The following information is given for the function X and class Y :

$$\text{Informationgain}(X,Y) = H(X) - H(X|Y)$$

Where $H(X)$, $H(X|Y)$ is calculated on X and Y for entropy values. X entropy can be computed as

$$H(X) = -\sum_i P(x_i) \log_2(P(x_i))$$

$X|Y$ entropy calculation is shown below:

$$H(X|Y) = -\sum_j P(y_j) \sum_i P(x_i | y_j) \log_2(P(x_i | y_j))$$

In the same way, this approach calculates the ratio on behalf of every attribute separately and selects 'm' as its most appropriate function, i.e. it regards the most significant function F with a high information gain. The main downside of this algorithm is that it chooses an attribute with high data gains that can or may not be more insightful. The knowledge gain cannot manage redundant characteristics because the characteristics are chosen universally.

3.7.3. Gain Ratio Feature Selection

The Gain Ratio is the updated information gain version. It considers daughter nodes in which an attribute divides the class data. This restricts the love that the knowledge gaining process has four attributes and enormous potential values [17]. Equation offers a ratio of benefit.

$$\text{GainRatio} = \frac{\text{InformationGain}}{H(X)}$$

When we forecast variable Y, we normalise information gain by breaking it into X entropy and vice versa. As a consequence of this normalisation the value of the gain ratio is between 0 and 1. Gain ratio = 1 means that X information totally predicts Y and no relation between Y and X is = 0. = 0. In comparison to information gain, it favours variables with less value.

3.7.4. Chi-Square Feature Selection Method

Chi-Square feature selections have two parameters viz., observed and expected frequency. It is calculated by MapReduce techniques [18]. The weights of the attributes can also be discovered. The corresponding attributes are the highest weight attributes. This method analyzes the class label. This is used for selecting the variable of the predictor. This attribute value with 'r' and 'c' class number is defined as

$$x^2 = \sum_{i=1}^r \sum_{j=1}^c \frac{(O_{ij} - E_{ij})^2}{E_{ij}}$$

Where O_{ij} is the number of 'i' value occurrences in class 'j'. E_{ij} is the number of events predictable with the value 'i' and the class 'j'.

3.7.5. Fisher's Exact Test

The Fisher score can be used to select the appropriate characteristics using a well-known fishermen ratio definition and a heuristic policy to create a value for characteristics [19]. The profit is:

- Define the features applicable to any particular issue.
- Reduces issue size and storage in your machine.
- Minimize calculation time to increase prediction accuracy as well.
- Strengthen the classification by eliminating irrelevant characteristics and noise.

4. RESULT AND DISCUSSION

4.1. Description of the dataset

Parkinson's disease dataset is considered from the Kaggle repository [20]. Table 1 depicts the features and its description of the dataset.

Table 1 Description of the Dataset

Feature number	Feature Name
1	Name (ASCII subject name and recording number)
2	MDVP:Fo(Hz) - Average vocal fundamental frequency
3	MDVP:Fhi(Hz) - Maximum vocal fundamental frequency
4	MDVP:Flo(Hz) - Minimum vocal fundamental frequency
5	MDVP:Jitter(%)
6	MDVP:Jitter(Abs)
7	MDVP:RAP
8	MDVP:PPQ
9	Jitter:DDP
10	MDVP:Shimmer
11	MDVP:Shimmer(dB)
12	Shimmer:APQ3
13	Shimmer:APQ5

14	MDVP:APQ
15	Shimmer:DDA
16	NHR – Measures of Ratio of noise to Tonal components in the voice
17	HNR – another Measures of Ratio of noise to Tonal components in the voice
18	RPDE – Nonlinear Dynamical Complexity Measure
19	D2 – Another Nonlinear Dynamical Complexity Measure
20	DFA Signal fractal scaling exponent
21	spread1 - nonlinear measures of fundamental frequency variation
22	spread2- nonlinear measures of fundamental frequency variation
23	PPE - nonlinear measures of fundamental frequency variation
24	Status - Healthy status of the subject 1 – Parkinson’s disease 0 - Healthy

4.2. Number of Features obtained by Feature Selection Techniques

Table 2 gives the number of features obtained by implementing the feature selection techniques like Correlation based Feature Selection (CFS), Information Gain (IG), Gain Ratio (GR), Chi-Square, and Fisher Exact Test. From the table 2, it is clear that the Chi-Square Feature Selection method gives a smaller number of features when comparing with other feature selection methods.

Table 2 Number of Features obtained by Feature Selection Methods

Feature Selection Method	Number of Features obtained
Original Dataset	24
Correlation based Feature Selection Method	18
Information Gain	19
Gain Ratio	16
Chi-Square	14
Fisher Exact Test	20

4.3. Performance Analysis of the Feature Selection Methods

The performance metrics like Classification Accuracy, True Positive Rate (TPR), Precision, False Positive, and Miss Rate are considered in this paper to evaluate the performance of the feature selection methods in the prediction of Parkinson’s disease using different Machine Learning classifiers.

Table 3 gives the classification accuracy obtained by the feature selection methods using various classifiers. Table 4 depicts the True Positive Rate (in %) obtained by Feature Selection Methods using different classifiers. Table 5 presents the precision (in %) obtained by the feature selection methods using various classifiers. Table 6 depicts the False Positive Rate (in %) obtained by the feature selection methods using various classifiers. Table 7 gives the miss rate (in %) obtained by the feature selection methods using various classifiers.

Table 3 Classification accuracy (in %) obtained by Feature Selection Methods using different classifiers

Feature Selection Methods	Classification Accuracy (in %) by Classification Techniques					
	ANN	SVM	GBT	Bagging	RF	DT
Original Dataset	44.27	45.31	49.21	43.98	41.65	42.86
Correlation based FS	68.51	68.76	69.73	67.31	66.82	65.41
Information Gain	64.33	65.74	69.81	62.23	63.71	65.43
Gain Ratio	64.43	64.74	66.64	64.34	61.82	62.77
Chi-Square	89.44	85.75	89.15	79.81	80.53	81.22
Fisher’s Exact	72.65	73.21	73.76	68.92	69.16	70.88

Table 4 True Positive Rate (in %) obtained by Feature Selection Methods using different classifiers

Feature Selection Methods	True Positive Rate (in %) by Classification Techniques					
	ANN	SVM	GBT	Bagging	RF	DT
Original Dataset	51.42	51.73	49.62	49.89	49.34	48.88
Correlation based FS	72.16	71.78	72.57	71.72	70.62	69.96
Information Gain	70.53	70.43	70.95	68.73	67.46	69.57
Gain Ratio	65.46	65.66	67.37	63.42	61.78	62.87
Chi-Square	88.54	87.72	89.22	86.34	85.62	81.11
Fisher's Exact	68.26	66.54	64.57	66.91	65.17	67.49

Table 5 Precision (in %) obtained by Feature Selection Methods using different classifiers

Feature Selection Methods	Precision (in %) by Classification Techniques					
	ANN	SVM	GBT	Bagging	RF	DT
Original Dataset	44.72	48.16	50.61	43.43	44.31	45.76
Correlation based FS	67.67	67.52	72.51	66.97	65.43	66.81
Information Gain	58.39	57.61	60.43	55.64	54.32	59.45
Gain Ratio	57.68	57.52	59.52	54.43	52.16	58.65
Chi-Square	83.18	85.24	85.42	81.53	79.72	78.18
Fisher's Exact	55.85	56.21	61.28	65.89	64.25	55.32

Table 6 False Positive Rate (in %) obtained by Feature Selection Methods using different classifiers

Feature Selection Methods	False Positive Rate (in %) by Classification Techniques					
	ANN	SVM	GBT	Bagging	RF	DT
Original Dataset	66.25	59.17	55.61	66.54	67.26	56.36
Correlation based FS	34.31	32.54	26.51	35.36	35.34	33.54
Information Gain	33.53	34.51	25.42	32.53	35.34	34.25
Gain Ratio	35.61	34.63	27.43	33.31	34.34	35.48
Chi-Square	7.62	7.84	6.73	10.25	17.33	20.09
Fisher's Exact	31.97	31.77	23.14	31.56	33.13	32.88

Table 7 Miss Rate (in %) obtained by Feature Selection Methods using different classifiers

Feature Selection Methods	Miss Rate (in %) by Classification Techniques					
	ANN	SVM	GBT	Bagging	RF	DT
Original Dataset	48.58	48.27	50.38	50.11	50.66	51.12
Correlation based FS	27.84	28.22	27.43	28.28	29.38	30.04
Information Gain	29.47	29.57	29.05	31.27	32.54	30.43
Gain Ratio	34.54	34.34	32.63	36.58	38.22	37.13
Chi-Square	11.46	12.28	10.78	13.66	14.38	18.89
Fisher's Exact	31.74	33.46	35.43	33.09	34.83	32.51

From the table 3, table 4, table 5, table 6 and table 7, it is clear that the Chi-Square Feature Selection with Gradient Boosting Tree (GBT) classifiers increased the classification accuracy, TPR, Precision, and also it reduced the error rates like FPR and Miss Rate.

5. CONCLUSION

Parkinson's disease (PD) is a common neurodegenerative disease, which has attracted more and more attention. Many artificial intelligence methods have been used for the diagnosis of PD. Feature selection plays an essential role in data mining pre-processing step and also several data mining machine learning methods are finding difficult to handle large amounts of irrelevant features. Therefore, there is a demand for suitable feature selection approach. Recently, the diagnosis of neurodegenerative diseases based on the neuroimaging data has been extensively

studied. In this research work, the performance of the different six classifiers like ANN, SVM, GBT, Bagging, RF, and DT are evaluated with Feature Selection techniques like Information Gain, Gain Ratio, Chi-Square, Correlation based, Fisher's Exact are evaluated for the prediction of Parkinson's disease. From the result obtained, it is clear that the Chi-Square Feature Selection with Gradient Boosting Tree classifier performs better in the prediction of Parkinson's disease, than the other feature selection techniques with other classifiers.

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