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AN AUTOMATED PARKINSON'S DISEASE DIAGNOSIS: A FEATURE SELECTION APPROACH

Sibel ÇİMEN[1*], Bülent BOLAT[1]

[1] Yildiz Technical University, Faculty of Electrical and Electronics, Department of Electronics and Communication Engineering, Istanbul, Türkiye

Keywrods

Artificial Intelligence, Biomedical Computing, Biomedical Signal, Machine Learning, Supervised Learning.

Abstract

Parkinson's disease is one of the neurodegenerative disorders that significantly affect human health. Patients experience various negative effects such as tremors, walking disorders, and impaired speech. The disease also causes instability in walking, leading to tremors, and affects their writing skills. Studies on detection of disease generally focus on speech analysis. However, PD can be diagnosed by exploiting the loss of motor ability. In this work, a data set which was recorded at Cerrahpasa Faculty of Medicine, Istanbul University is considered. The data were collected from 15 healthy subjects and 57 with Parkinson's Disease.by a graphic tablet. Each subject asked to draw a spiral in two different conditions which are named as static spiral test (SST) and dynamic spiral test (DST) respectively, and the drawings transformed into X, Y and Z axis of movement, Grip Angle, and Pressure data. During the study, the effectiveness of SST and DST conditions are considered. Various machine learning algorithms have been tested to determine the best classifier. The effect of features was also considered by utilizing a feature elimination process. As a result, the best classification performance was obtained as 90,32% by using Kernel Naïve Bayes network with DST and SST + DST data, by omitting *Z* axis.

OTOMATİK PARKİNSON HASTALIĞI TEŞHİSİ: BİR ÖZELLİK SEÇİMİ YAKLAŞIMI

Anahtar Kelimeler

Yapay Zeka, Biyomedikal Hesaplama, Biyomedikal Sinyal, Makine Öğrenmesi, Eğiticili Öğrenme.

Öz

Parkinson hastalığı, insan sağlığını önemli ölçüde etkileyen nörodejeneratif bozukluklardan biridir. Hastalar, titreme, yürüme bozuklukları ve konuşma bozuklukları gibi çeşitli olumsuz etkiler yaşarlar. Hastalık ayrıca yürüme dengesizliğine, titremelere ve yazma becerilerini etkiler. Hastalığın tespiti üzerine yapılan çalışmalar genellikle konuşma analizine odaklanmaktadır. Ancak, Parkinson hastalığı motor yetenek kaybını kullanarak teşhis edilebilir. Bu çalışmada, İstanbul Üniversitesi Cerrahpaşa Tıp Fakültesi'nde kaydedilen bir veri seti incelenmektedir. Veriler, 15 sağlıklı denekten ve Parkinson hastalığı olan 57 denekten bir grafik tableti kullanılarak toplandı. Her denekten, sırasıyla statik spiral testi (SST) ve dinamik spiral testi (DST) olarak adlandırılan iki farklı koşul altında bir spiral çizmesi istenmiş ve çizimler X, Y ve Z eksenlerine hareket, Kavrama Açısı ve Basınç verilerine dönüştürülmüştür. Çalışma sırasında, SST ve DST koşullarının etkinliği dikkate alınmıştır. En iyi sınıflandırıcıyı belirlemek için çeşitli makine öğrenimi algoritmaları test edilmiştir. Özelliklerin etkisi, bir özellik elemesi süreci kullanılarak da dikkate alınmıştır. Sonuç olarak, Z eksenini ihmal ederek DST ve SST +DST verileri ile Kernel Naive Bayes ağı kullanılarak %90,32'lik en iyi sınıflandırma performansı elde edilmiştir.

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Yazar Kimliği / Author ID (ORCID Number)
Sibel Çimen, 0000-0003-3790-7362
Bülent Bolat, 0000-0002-2468-8618

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[*] Corresponding author: sblcmn@yildiz.edu.tr, +90212-383-59-16

AN AUTOMATED PARKINSON'S DISEASE DIAGNOSIS: A FEATURE SELECTION APPROACH

Sibel ÇİMEN[1†], Bülent BOLAT[1]
[1] Yildiz Technical University, Faculty of Electrical and Electronics, Department of Electronics and Communication Engineering, Istanbul, Türkiye

Highlights

- Parkinson's disease diagnosis was conducted using classical machine learning methods without heuristic approaches.
- Through feature selection, it was observed that data from the Z-axis had the least impact on Parkinson's disease diagnosis.
- It was observed that the diagnosis of Parkinson's disease using data from the Dynamic Spiral Test and Static Spiral + Dynamic Spiral Test was higher compared to data from the Static Spiral Test.

Purpose and Scope

This study focuses on the diagnosis of Parkinson's disease using machine learning methods that do not have a high computational load. Thus, it is aimed to develop an auxiliary tool that can work on simple personal devices and provide additional insight to physicians when necessary.

Design/methodology/approach

In this study, feature calculations were made on hand-drawn data and the obtained features were divided into test and training data sets. Feature selection was performed on data to determine the most effective features for diagnosis of Parkinson's disease. The data was applied to different classifiers to determine the best classifier for this problem.

Findings

As a result of the experiments, it was seen that the *Z* parameter was the least important feature. In most cases, removing the *Z* parameter increased the accuracy of the DST and SST + DST dataset. The best results were obtained by subtracting *Z* data for DST and merged data. Our results suggest that changes in the *Z* axis are less significant for the diagnosis of Parkinson's disease.

Originality

The originality of this study lies in demonstrating that the diagnosis of Parkinson's disease can be achieved by using simpler classifiers. Moreover, by applying a feature elimination method, it was shown that the Z axis information should be omitted. As a result, it was proven that Parkinson's data can be collected by using simpler hardware.

1. Introduction

Parkinson's disease is a neurodegenerative disease that generally affects 2-3% of the population aged 65 and over. Parkinson's disease occurs due to low dopamine release. Dopamine enables brain cells to communicate with each other, and disruption or loss of cells that produce dopamine causes low dopamine release (Chawla *et al.,* 2024, Kumar *et al.,* 2024). Thus, the person begins to develop Parkinson's disease. Clinical diagnosis can be made more easily in cases with advanced and fully developed classical motor features of Parkinson's disease. However, in the early phases of the disease, the error rate in clinical diagnosis can reach up to 24% (Poewe *et al*., 2017).

Various studies have been conducted on different data sets and detection methods for the diagnosis of Parkinson's disease (Alalayah *et al.,* 2023; Göker, 2023; Shafiq *et al.,* 2022; Soman *et al.,* 2023; Tsai *et al.,* 2023). These studies can assist doctors in diagnosing the disease. Along with physical effects, characteristic effects can also be observed in patients' speech (Alalayah *et al.,* 2023; Ali *et al.,* 2023; Guatelli *et al.,* 2023; Saleh *et al.,* 2024; Skodda, 2011; Uebelacker *et al.,* 2014; Zhao and Li, 2023; Yuan *et al., 2024*). Therefore, the detection of Parkinson's disease is also carried out using voice data, and various studies are being conducted on this subject. (Bolat and Bolat, 2010) can be given as an example of these studies. In this study, voice samples were taken from 31 people, 23 of whom had Parkinson's disease. The data obtained from these sound samples were used to classify. Four different classifiers were used for classification. These classifiers are probabilistic neural networks, generalized regression neural networks, support vector machine, and k-nearest Neighbors (k-NN) networks. Half of the data set consisting of sound samples was used

† Corresponding author: sblcmn@yildiz.edu.tr, +90212-383-59-16

as the training set and the other half was used as the test set.

In (Amato *et al.,* 2021), a multi-level analysis was conducted that progressively combined features extracted from the speech signal, the voiced segments, and the on-set/off-set regions. As a result, a total of 126 features emerged. Additionally, the performance of the feature fusion schemes was compared to identify the best model configuration, using 25 isolated words pronounced by each subject. The database consisting of 50 healthy controls and 50 PD patients, was used for validation and testing. An optimized k-NN model was implemented for the binary classification of PD patients versus healthy people, achieving a 94.3% accuracy in testing on the PC-GITA database.

Diagnosis of Parkinson's Disease using ANN (Çimen and Bolat, 2016) aims to investigate the effectiveness of artificial neural networks (ANNs) in diagnosing Parkinson's disease. The data used in this work include 150 participants' data, including 75 healthy individuals and 75 Parkinson's disease patients, and ANNs are utilized to classify the participants based on their clinical features. In this study, ANNs diagnosed Parkinson's disease with a high accuracy of up to 98%. Herewith, the study suggests that ANNs hold promise as a diagnostic tool for Parkinson's disease.

Parkinson's disease not only affects the patient's voice but also has a variety of physical complications such as slowing down in physical movements and reflexes, and altered writing abilities due to tremors in hand movements (Khatamino *et al.,* 2018; Kumar and Ghosh, 2023; Sankineni *et al.,* 2023), etc. Therefore, there are studies on this disease that use alternative methods rather than speech signals.

Mounika and her team worked on detecting Parkinson's disease by considering deep learning approaches and stated the success rate as 94.87% with RNN (Mounika and Rao, 2021). Tayal (Tayal, 2018), achieved a success rate of 91% by working with SVM. In his paper (Tiwari, 2016), Tiwari proposed a method using the random forest classifier and used this method on a data set with 20 features and used a feature selection algorithm in his study and the accuracy obtained was 90.3%.

Johri and Tripathi actualized the comparative analysis with various Machine Learning (ML) classifier algorithms like k-NN, XGBoost, SVM, and Random Forest and observed that Random Forest provides better performance with an accuracy of 90% (Johri and Tripathi, 2019).

Rabie Fadil et al (Fadil *et al.,* 2021) implied that the most suitable classifier was found by testing Random Forest, SVM, Decision Tree, Neural Network, kNN, and Gaussian Naive Bayes. The best classification performance was obtained using Random Forest with 80% accuracy.

In the study conducted in India (Sandhiya *et al.,* 2022), the spiral/wave drawing datasets taken from the machine learning repository at the University of California, Irvine was used and classification was performed with Random Forest Classifier and the accuracy was stated as 71.33%.

Elshewey et al compared 6 different ML methods and calculated performance metrics for all of the methods. During the test, hyperparameter tuning was performed. The test results also demonstrate that SVM outperformed the other methods with an accuracy of 92.3% (Elshewey *et al.,* 2023).

The organization of this paper is as follows. Section 2 describes the materials. Section 3 describes the methodology implemented to diagnose Parkinson's'. Section 4 presents our results of the methods applied in Section 3. Finally, Section 5 presents conclusions and discussion on the implications of the research.

2. Materials

In this study, a data set downloaded from the publicly available UCI Machine Learning Repository, which was initially provided by (Isenkul *et al.,* 2014) at the Department of Neurology Diagnostics within Istanbul University's Cerrahpasa Faculty of Medicine, is considered.

The Parkinson's disease handwriting data were collected by a graphic tablet at the Department of Neurology in Cerrahpaşa Faculty of Medicine, Istanbul University. The data set consists of 15 healthy individuals and 25 Parkinson's disease patients (Isenkul *et al.,* 2014) initially. Later, the Authors expanded the data set by adding new data taken from 32 Parkinson's disease patients.

During the data-collecting process, the Authors asked the subjects to perform two missions. In the first mission, three wound Archimedean spirals appeared on the graphic tablet and patients were asked to retrace the same spiral as much as possible using the digital pen. During the test, *X, Y,* and *Z coordinates, Pressure* and *Grip Angle* of the pen were taken on the graphic tablet and recorded as a time series. This mission is called Static Spiral Test (SST) (Isenkul *et al.,*

2014).

In the second mission, the patients were subjected to the Dynamic Spiral Test (DST). In DST, unlike SST, the Archimedean helix flashes at certain time intervals. These flashings force the patient to keep the pattern in mind and continue drawing. The purpose of this mission is to determine how the loss of information changes the patient's drawing performance. As a result of this test, it was observed that most of the patients continued to draw, but almost all of them lost the pattern (Isenkul *et al.,* 2014). Figure 1 shows examples of drawings made by healthy and Parkinson's subjects respectively.

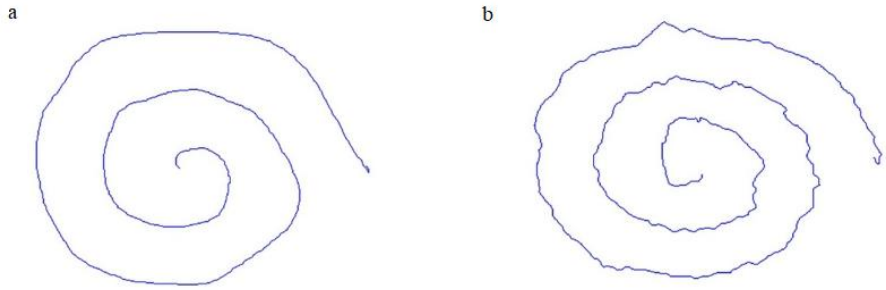

Figure 1. a) Healthy People Drawing, **b)** PD People Drawing (Isenkul *et al.*, 2014)

3. Method

As seen in Figure 1, there are distinct visual differences between healthy people and people with Parkinson's and it is possible to exploit these differences to develop an automatic diagnosis system. In this study, various ML methods were used to detect Parkinson's disease. First, the initial and additional data sets were merged, and a new data set consisting of 72 data was created. Then, during the first phase, SST and DST data were considered separately to determine whether one of these is distinctively better than the other. Finally, a new data set was created by combining these two and the learning process was repeated to see if any improvement could be acquired. In all trials, all features were used first, and then feature selection was performed to determine the most dominant features. During feature selection, features were removed from the data set one by one or in groups of two or three, and training and testing were performed. Since the number of features is small enough, a brute-force search was applied.

The proposed approach for Parkinson's disease diagnosis is described below (Figure 2). While training a model, first the standard deviations, averages, integrals, and standard deviations of the derivative of each feature were calculated. A feature elimination process was done on these features during preprocessing and a series of subsets were created. The generated data sets are divided into training and test data randomly. Non-heuristic classical ML networks were trained with the training sets and tested with the test data set.

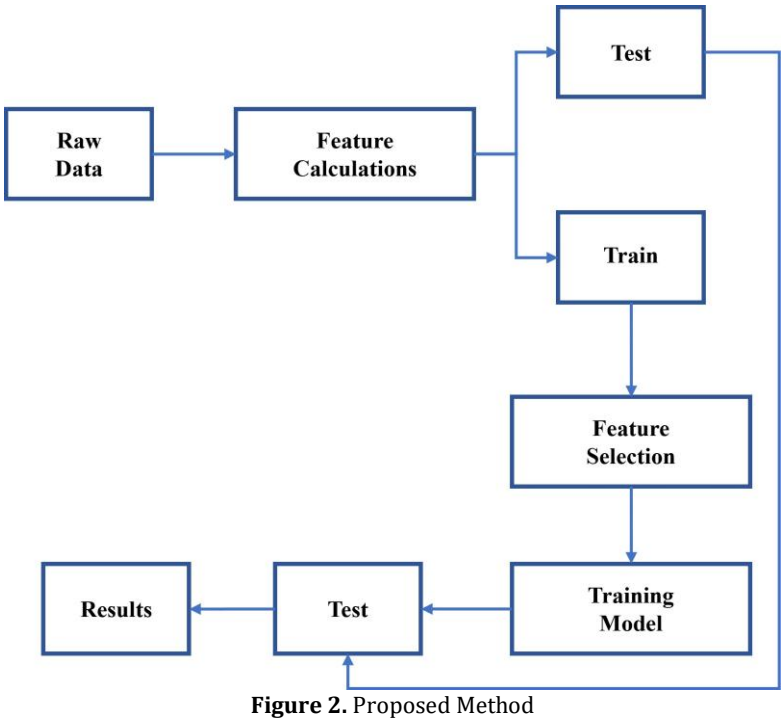

Figure 2. Proposed Method

In this study, 24 variations of 5 different supervised ML techniques (The MathWorks Inc., 2023) including Bayes, Discriminant & Regression, k-NN, Decision Tree, and SVM were fed by above mentioned data. The purpose was to identify the most effective classifier for Parkinson's patient classification by comparing it with other ML methods. To determine the most distinctive features, feature selection was applied to the data. The classifiers considered in this work are summarized below:

Bayes: A Bayesian network is a probabilistic graphical model used to describe random variables and their conditional relationships. In a Bayesian network, there are nodes and their parent nodes. Each parent node has a value and according to these values nodes have a probability distribution (Pearl, 1985). Probabilistic reasoning, decision-making, and prediction are among the applications for Bayesian networks. They are solution-oriented networks, especially for problems involving uncertainty such as medical diagnosis or financial forecasting.

The formula of the Bayes Theorem is as follows:

$$P(A|B) = P\frac{P(A|B)*P(A)}{P(B)} \quad (1)$$

where the probability P(A|B) is called the posterior probability, and the marginal probability of the event P(A) is called the prior probability.

SVM: Support-vector machine network is an ML algorithm used to solve classification problems with two groups. It works by mapping input vectors to a feature space with high dimensions and creating a linear decision surface in that space. The decision surface has unique properties that make the learning machine highly effective in generalizing (Cortes and Vapnik, 1995). The SVM aims to maximize the margin between two groups or classes.

New data point stated as x_{new} and the decision function can be explained according to the hyperplane by:

$$f(x_{new}) = \sum_{i=1}^{n} \alpha_i y_i K(x_i, x) + b \quad (2)$$

where the x is the new sample, α_i is the Lagrange multipliers, y_i is the labels of the training samples and b is bias term, and $f(x_{new})$ is the predicted class label and the $K(x_i, x)$ is the kernel function, which returns +1 and -1 (Di Caro, 2019). If the expression inside the function is positive, it returns +1 and if it is negative, it returns -1.

Discriminant & Regression: Discriminant network is a Bayesian network designed specifically for classification. It consists of a set of nodes representing input features and a single output node representing the class label. Each node has a conditional probability distribution (CPD) in the network. The distribution of the input nodes is estimated from the training data and the CPD of the output node is estimated using a discriminant function.

A regression network is a Bayesian network designed for regression tasks. It consists of nodes which represent the input features and a single output node representing the target variable. A regression network is used to calculate the expected value of the target variable, which is based on the values in the input variables.

Discriminant and regression networks can be trained using three different methods. These methods can be specified as maximum likelihood estimation, Bayesian parameter estimation, and gradient-based optimization. The choice of training method depends on the problem and data. Once the network is trained, it can be used to make predictions on new data by inferring the network using the observed values of the input variables.

k-NN: The k-NN is an algorithm that can be used in classification and regression, and this algorithm is non-parametric. It works by finding the k nearest neighbors to a new observation in the training set and using their values to make a prediction for the new observation. A k-NN model starts with a set of training data consisting of input-output pairs (X, Y). When a new input observation is received, the k closest training observations to that input based on some distance metric (such as Euclidean distance) are found. The output value for the new observation is then determined by taking the average (for regression) or majority vote (for classification) of the output values of its k nearest neighbors. The choice of k is an important hyperparameter that needs to be tuned for each problem. A smaller value of k leads to a more flexible model that can fit complex, nonlinear relationships in the data; but may also be more susceptible to noise and overfitting. A larger value of k leads to a smoother model that may also be less able to capture complex relationships in the data. Euclidian distance can be expressed with $\ell 2$-norm ($||\,.\,||_2$). The Euclidian distance is calculated between these two parameters and the k-NN is selected according to the smallest distance to the new data point. Implementation and interpretation of k-NN are easy and that is one of the advantages of the k-NN algorithm. K-NN does not require any assumptions about the underlying distribution of the data, making it easy to use in a wide range of applications. The biggest disadvantage of this network is seen in large data sets. It may not

perform well on large datasets and high-dimensional inputs if the training data is not representative of the base population.

Decision Tree: Decision tree is one of the predictive models for classification and regression. It divides the input space into smaller subsets based on the values of the input features and assigns a label or value to each leaf node of the tree. When making classification, decision trees assign a label to each leaf node based on the majority class of training examples reaching that node. For regression, it assigns a value to each leaf node based on the mean or median value of the training samples reaching the node.

Easy interpretation is one of the advantages of decision trees. Decision trees provide insight into important features and relationships in the data. However, they may be sensitive to small changes in the training data. If the decision tree is too deep or the stopping criteria are not set well, it may cause a tendency to over fit. To solve these problems, ensemble methods such as gradient boosting and random forests are often used to combine multiple decision trees into a more robust and accurate model.

4. Application and Results

In this work, detection of Parkinson's disease was carried out by using data obtained from SST and DST tests. First, two data sets were used separately to see if any of them were far better than others. Therefore, these data sets were merged into a single data set and the entire work was repeated to see if any improvement could be gained. The data set contains data from 15 healthy individuals and 57 PD patients. To perform a statistical confirmation test, the data was split into three parts equally, and a 3-fold cross-validation was applied.

While testing the performance of cross-validated data, feature elimination was conducted to observe the impact of specific features in Parkinson's disease diagnosis. Each feature was removed individually and in groups of two and three, and their success rates were evaluated by testing the 24 variations of the 5 supervised ML techniques. Due to the low number of features in the data set, heuristic methods were not required, and a brute-force feature elimination method was deemed adequate. The main reason for performing feature elimination is to eliminate noisy data if it exists. Features were obtained by calculating the standard deviation, mean, integral, and standard deviation of the derivative of each of the *X, Y, Z, Pressure,* and *Grip Angle* data.

Tables 1, 2, 3, and 4 show results obtained with SST data only. As seen in Table 1, Bagged Trees, one of the Decision Trees algorithms, achieved the best accuracy with 87.10% in almost every case. Table 2 clearly shows the effect of the Z parameter for the cases without *Z*, without Z and *Grip Angle*, and without *Z* and *Pressure*. As illustrated in Table 3, while not as effective as Decision Trees, SVM algorithms achieve an overall performance of 83.87%, ranking second. However, a review of the k-NN results presented in Table 4 indicates that this algorithm does not demonstrate a comparable level of performance.

Tablo 1. Decision Trees Accuracies for SST

	w/ all Features	w/o X	w/o Y	w/o Z	w/o Pressure	w/o Grip Angle	w/o Z-Grip	w/o Z-Pressure	w/o XYZ
Fine Tree	77,42%	80,65%	74,19%	77,42%	41,94%	77,42%	77,42%	41,93%	77,42%
Medium Tree	77,42%	80,65%	74,19%	77,42%	41,94%	77,42%	77,42%	41,93%	77,42%
Coarse Tree	77,42%	80,65%	74,19%	77,42%	41,94%	77,42%	77,42%	41,93%	77,42%
Boosted Trees	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%
Bagged Trees	87,10%	87,10%	87,10%	87,10%	87,10%	83,87%	87,10%	80,65%	87,10%
RUSBoosted Trees	74,19%	74,19%	54,83%	74,19%	38,71%	70,97%	61,29%	38,71%	67,74%

Table 2. Discriminant & Regression and Bayesian Accuracies for SST

	w/ all Features	w/o X	w/o Y	w/o Z	w/o Pressure	w/o Grip Angle	w/o Z-Grip	w/o Z-Pressure	w/o XYZ
Linear Discriminant	74,19%	74,19%	77,42%	64,51%	64,51%	80,65%	87,10%	45,16%	64,51%
Logistic Regression	51,62%	61,29%	67,74%	45,16%	35,48%	77,42%	67,74%	35,48%	77,42%
Gaussian Naive Bayes	67,74%	61,29%	77,42%	54,84%	74,20%	77,42%	48,39%	54,83%	35,48%
Kernel Naive Bayes	83,87%	80,65%	83,87%	83,87%	77,42%	83,87%	83,87%	77,41%	67,74%
Subspace Discriminant	80,65%	83,87%	80,65%	77,42%	67,74%	80,65%	80,65%	61,29%	80,65%

Table 3. SVM Accuracies for SST

	w/ all Features	w/o X	w/o Y	w/o Z	w/o Pressure	w/o Grip Angle	w/o Z-Grip	w/o Z-Pressure	w/o XYZ
Linear SVM	80,65%	80,65%	80,65%	77,42%	83,87%	80,65%	80,65%	58,06%	74,19%
Quadratic SVM	74,19%	74,19%	74,19%	70,94%	61,29%	80,65%	83,87%	35,48%	70,97%
Cubic SVM	74,19%	74,19%	83,87%	74,19%	54,83%	77,42%	80,65%	41,93%	80,65%
Fine Gaussian SVM	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%
Medium Gaussian SVM	83,87%	83,87%	83,87%	80,65%	83,87%	83,87%	83,87%	61,29%	83,87%
Coarse Gaussian SVM	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%

Table 4. k-NN Accuracies for SST

	w/ all Features	w/o X	w/o Y	w/o Z	w/o Pressure	w/o Grip Angle	w/o Z-Grip	w/o Z-Pressure	w/o XYZ
Fine k-NN	80,65%	80,65%	80,65%	70,97%	80,65%	80,65%	77,42%	48,37%	74,19%
Medium k-NN	74,19%	74,19%	83,87%	70,97%	74,19%	83,87%	87,10%	41,94%	80,65%
Coarse k-NN	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%
Cosine k-NN	83,87%	83,87%	80,65%	77,42%	74,19%	80,65%	87,10%	48,39%	80,65%
Cubic k-NN	80,65%	80,65%	83,87%	70,97%	64,51%	83,87%	83,87%	51,62%	77,42%
Weighted k-NN	83,87%	83,87%	83,87%	77,42%	77,42%	87,10%	83,87%	51,62%	80,65%
Subspace k-NN	77,20%	77,42%	77,42%	74,19%	70,97%	80,65%	80,65%	70,97%	77,42%

Tables 5, 6, 7, and 8 show the results of DST trials. Regarding to tables, the best solution is 90.32% with Kernel Naïve Bayes. In this case, the best solution was obtained two times; first by removing the *Z* parameter as in the previous, and by removing the *Z-Grip Angle*. The results indicate that the *Pressure* feature plays a significant role in the detection of PD. When the *Pressure* feature is excluded, a notable decline in detection accuracy is observed.

Table 5. Decision Trees Accuracies for DST

	w/ all Features	w/o X	w/o Y	w/o Z	w/o Pressure	w/o Grip Angle	w/o Z-Grip	w/o Z-Pressure	w/o XYZ
Fine Tree	87,10%	83,87%	87,10%	87,10%	87,10%	87,10%	87,10%	87,10%	35,49%
Medium Tree	87,10%	83,87%	87,10%	87,10%	87,10%	87,10%	87,10%	87,10%	35,49%
Coarse Tree	87,10%	83,87%	87,10%	87,10%	87,10%	87,10%	87,10%	87,10%	35,49%
Boosted Trees	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%
Bagged Trees	80,65%	77,42%	77,42%	83,87%	83,87%	83,87%	83,87%	87,10%	83,87%
RUSBoosted Trees	64,52%	67,74%	67,74%	64,52%	77,42%	64,52%	80,65%	64,52%	61,29%

Table 6. Discriminant & Regression and Bayesian Accuracies for DST

	w/ all Features	w/o X	w/o Y	w/o Z	w/o Pressure	w/o Grip Angle	w/o Z-Grip	w/o Z-Pressure	w/o XYZ
Linear Discriminant	54,84%	61,29%	64,52%	54,84%	58,06%	77,42%	80,65%	45,39%	48,39%
Logistic Regression	61,29%	67,74%	77,42%	58,06%	58,06%	74,19%	83,87%	45,39%	70,97%
Gaussian Naive Bayes	83,87%	74,20%	77,42%	74,19%	83,87%	87,10%	80,65%	77,42%	54,84%
Kernel Naive Bayes	87,10%	77,42%	87,10%	90,32%	83,87%	87,10%	90,32%	87,10%	80,65%
Subspace Discriminant	64,52%	64,52%	70,97%	67,74%	58,06%	83,87%	80,65%	58,06%	70,97%

Table 7. SVM Accuracies for DST

	w/ all Features	w/o X	w/o Y	w/o Z	w/o Pressure	w/o Grip Angle	w/o Z-Grip	w/o Z-Pressure	w/o XYZ
Linear SVM	64,52%	70,97%	70,97%	70,97%	54,84%	80,65%	83,87%	58,06%	58,06%
Quadratic SVM	70,97%	70,97%	67,74%	74,19%	51,61%	83,87%	83,87%	61,29%	61,29%
Cubic SVM	70,97%	74,19%	74,19%	70,97%	51,61%	87,10%	83,87%	51,61%	67,74%
Fine Gaussian SVM	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%
Medium Gaussian SVM	80,65%	80,65%	83,87%	83,87%	77,42%	83,87%	87,10%	67,74%	83,87%
Coarse Gaussian SVM	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%

Table 8. k-NN Accuracies for DST

	w/ all Features	w/o X	w/o Y	w/o Z	w/o Pressure	w/o Grip Angle	w/o Z-Grip	w/o Z-Pressure	w/o XYZ
Fine k-NN	83,87%	80,65%	80,65%	74,19%	70,975	80,65%	80,65%	67,74%	74,19%
Medium k-NN	61,29%	74,19%	67,74%	67,74%	58,06%	80,65%	77,42%	48,39%	67,74%
Coarse k-NN	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%
Cosine k-NN	70,97%	80,65%	74,19%	67,74%	64,52%	83,87%	83,87%	51,61%	67,74%
Cubic k-NN	70,97%	74,19%	64,52%	64,52%	61,29%	74,19%	77,42%	41,94%	64,52%
Weighted k-NN	74,19%	80,65%	80,65%	70,97%	64,52%	77,42%	80,65%	48,39%	70,97%
Subspace k-NN	80,65%	74,19%	77,42%	80,65%	77,42%	80,65%	80,65%	77,42%	77,42%

In the last experiments, SST and DST data were combined and the same training regime was applied to the classifiers. Tables 9, 10, 11, and 12 summarize the results of the last experiments. Once more, the best result was obtained by Kernel Naïve Bayes. The best accuracy, 90,32%, was the same as the DST trials. In this experiment, the redundant feature was the *Z* parameter again. These tables further illustrate the substantial importance of the *Pressure* feature in PD detection. Without the inclusion of *Pressure*, the performance drops to as low as 50%.

Table 9. Decision Trees Accuracies for SST + DST

	w/ all Features	w/o X	w/o Y	w/o Z	w/o Pressure	w/o Grip Angle	w/o Z-Grip	w/o Z-Pressure	w/o XYZ
Fine Tree	88,71%	80,65%	88,71%	88,71%	50,00%	87,10%	87,10%	50,00%	79,03%
Medium Tree	88,71%	80,65%	88,71%	88,71%	50,00%	87,10%	87,10%	50,00%	79,03%
Coarse Tree	88,71%	80,65%	88,71%	88,71%	51,61%	87,10%	87,10%	51,61%	80,64%
Boosted Trees	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%
Bagged Trees	87,10%	87,10%	82,25%	87,10%	88,71%	83,87%	83,87%	85,48%	83,87%
RUSBoosted Trees	82,26%	74,19%	70,97%	82,26%	75,81%	83,87%	83,87%	69,35%	72,58%

Table 10. Discriminant & Regression and Bayesian Accuracies for SST + DST

	w/ all Features	w/o X	w/o Y	w/o Z	w/o Pressure	w/o Grip Angle	w/o Z-Grip	w/o Z-Pressure	w/o XYZ
Linear Discriminant	67,74%	72,58%	66,13%	59,67%	59,67%	82,26%	79,03%	59,67%	56,45%
Logistic Regression	54,84%	67,74%	64,52%	61,29%	48,39%	72,58%	70,97%	90,32%	56,45%
Gaussian Naive Bayes	72,58%	70,97%	82,26%	66,13%	79,03%	80,65%	62,90%	67,74%	37,09%
Kernel Naive Bayes	85,48%	80,65%	80,65%	90,32%	83,87%	87,10%	88,71%	83,87%	67,74%
Subspace Discriminant	75,81%	77,42%	75,81%	75,80%	67,74%	83,87%	83,87%	61,29%	75,81%

Table 11. SVM Accuracies for SST + DST

	w/ all Features	w/o X	w/o Y	w/o Z	w/o Pressure	w/o Grip Angle	w/o Z-Grip	w/o Z-Pressure	w/o XYZ
Linear SVM	75,81%	75,81%	74,19%	74,19%	56,45%	85,48%	83,87%	51,61%	70,97%
Quadratic SVM	77,42%	75,81%	74,19%	74,19%	69,35%	85,48%	82,26%	46,77%	75,81%
Cubic SVM	77,42%	75,81%	75,81%	72,58%	61,29%	83,87%	82,26%	56,45%	79,03%
Fine Gaussian SVM	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%
Medium Gaussian SVM	83,87%	83,87%	83,87%	82,26%	83,87%	85,48%	82,26%	64,51%	82,26%
Coarse Gaussian SVM	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%

Table 12. K-NN Accuracies for SST + DST

	w/ all Features	w/o X	w/o Y	w/o Z	w/o Pressure	w/o Grip Angle	w/o Z-Grip	w/o Z-Pressure	w/o XYZ
Fine k-NN	82,26%	80,65%	83,87%	74,19%	75,81%	80,65%	80,65%	59,67%	72,58%
Medium k-NN	80,65%	82,26%	80,65%	74,19%	62,90%	79,03%	82,26%	51,62%	72,58%
Coarse k-NN	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%	83,87%
Cosine k-NN	83,87%	83,87%	82,26%	79,03%	72,58%	82,26%	85,48%	58,06%	77,42%
Cubic k-NN	79,03%	83,87%	77,42%	69,35%	54,84%	82,26%	82,26%	48,39%	70,97%
Weighted k-NN	83,87%	83,87%	79,03%	74,19%	75,81%	80,65%	85,48%	58,06%	77,42%
Subspace k-NN	80,65%	77,42%	79,03%	74,19%	77,42%	82,26%	83,87%	75,01%	79,03%

To provide a comparison to future works on this subject, different performance metrics were calculated for the best results for each classifier (*see* Table 13). The metrics evaluated in this work are as follows.

$$Accuracy = \frac{TP+TN}{TP+TN+FP+FN} x100 \quad (3)$$

$$Recall = \frac{TP}{TP+FN} x100 \quad (4)$$

$$Precision = \frac{TP}{TP+FP} x100 \quad (5)$$

$$F - Score = 2x\left(\frac{PrecisionxRecall}{Precision+Recall}\right) \quad (6)$$

where, TP, TN, FP, FN correspond to the True Positive, True Negative, False Positive and False Negative respectively.

Table 13. Performance Metrics for Static Spiral Test and Dynamic Spiral Test without *Z*

	Performance Metrics for Dynamic Spiral Test				Performance Metrics for Static and Dynamic Spiral Test			
	Fine Tree	Medium Tree	Coarse Tree	Kernel Naïve Bayes	Fine Tree	Medium Tree	Coarse Tree	Kernel Naïve Bayes
Accuracy	87,10%	87,10%	87,10%	90,32%	88,71%	88,71%	88,71%	90,32%
Recall	92,31%	92,31%	92,31%	100,00%	98,08%	98,08%	98,08%	96,15%
Precision	92,31%	92,31%	92,31%	89,66	89,47%	89,47%	89,47%	92,59%
F1-Score	92,31%	92,31%	92,31%	94,55%	93,58%	93,58%	93,58%	94,34%

Figure 3 summarizes the comparison of relevant studies and the proposed method for PD diagnosis, which is the Kernel Naïve Bayes algorithm that yields the highest results.

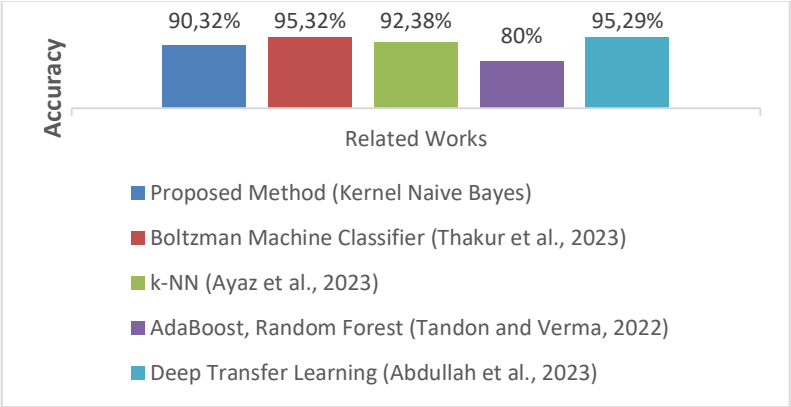

Figure 3. Performance Comparison of the Proposed Method with Related Works

Table 14. Hyperparameter of the Algorithms

Method	Max # of splits	Split Criterion	Ensemble Method	Learner Type	# of learners	Learning Rate	Subspace Dimension	Covariance Structure
Fine Tree	100	Gini's diversity index	-	-	-	-	-	-
Medium Tree	20	Gini's diversity index	-	-	-	-	-	-
Coarse Tree	4	Gini's diversity index	-	-	-	-	-	-
Boosted Trees	20	-	AdaBoost	-	30	0,1	-	-
Bagged Trees	40	-	Bag	-	30	0,1	-	-
RUSBoosted Trees	20	-	RusBoost	-	30	0,1	-	-
Linear Discriminant	-	-	-	-	-	-	-	Full
Logistic Regression	-	-	-	-	-	-	-	-
Gaussian Naive Bayes	-	-	-	-	-	-	-	-
Subspace Discriminant	20		Subspace	Discriminant	30	0,1	10	-
Subspace k-NN	20		Subspace	Nearest Neighbors	30	0,1	10	-

For all experiments, hyperparameters of the algorithms were presented in Tables 14 and 15. The Box Constraint Level parameter is crucial for SVM algorithms, and its variation can significantly impact performance. Therefore, in the context of this one-class classification problem, experiments were repeated using the SVM algorithm under conditions DST and SST + DST, specifically excluding the Z feature. It was observed that changes in this parameter did not have a positive effect on performance, as presented in Tables 16 and 17.

While examining the results, one can claim that SVM and k-NN algorithms gave lower results for SST and DST regardless of the kernel used. The proposed method, Kernel Naïve Bayes, showed the highest results for both DST and combined data. Therefore, one can conclude that a DST and a merged version of the tests were better for detecting Parkinson's rather than a SST.

When the features are considered, it is clearly seen that the *Z* and *Z-Grip Angle* parameters are the least important features. In most cases removing the *Z* parameter increased the accuracy of the SST data set. In some cases, removing the *Z-Grip Angle* gave a better result than removing the *Z*, but in general, removing the Z was better. For the DST data, it is seen that *Z-Grip Angle* is the most redundant feature. However, the same results were achieved by removing Z data for DST and combined data also. Therefore, these results concluded that the variations on z-axis are less significant for the diagnosis of Parkinson's. Unlike the Z parameter, performance was negatively affected when Pressure was not used, which emphasizes the importance of the Pressure parameter in the diagnosis of Parkinson's disease.

Table 15. Hyperparameter of the Algorithms

Method	Kernel Type	Box Constraint Level	Manual Kernel Scale	Num of neighbors	Distance Metric	Distance Weight
Kernel Naive Bayes	Gaussian					
Linear SVM	Linear	1				
Quadratic SVM	Quadratic	1				
Cubic SVM	Cubic	1				
Fine Gaussian SVM	Gaussian	1	1,1			
Medium Gaussian SVM	Gaussian	1	4,5			
Coarse Gaussian SVM	Gaussian	1	18			
Fine k-NN				1	Euclidian	Equal
Medium k-NN				10	Euclidian	Equal
Coarse k-NN				100	Euclidian	Equal
Cosine k-NN				10	Cosine	Equal
Cubic k-NN				10	Minkowski	Equal
Weighted k-NN				10	Euclidian	Squared Inverse

Table 16. SVM Hyperparameters Comparison for DST Trials

	Box Constraint Level=1	Box Constraint Level=2	Box Constraint Level=5	Box Constraint Level=10
Linear SVM	70,97%	70,97%	70,97%	64,52%
Quadratic SVM	74,19%	67,74%	70,97%	70,97%
Cubic SVM	70,97%	70,97%	70,97%	70,97%
Fine Gaussian SVM	83,87%	83,87%	83,87%	83,87%
Medium Gaussian SVM	83,87%	83,87%	80,65%	80,65%
Coarse Gaussian SVM	83,87%	83,87%	77,42%	67,74%

Table 17. SVM Hyperparameters Comparison for SST + DST Trials

	Box Constraint Level=1	Box Constraint Level=2	Box Constraint Level=5	Box Constraint Level=10
Linear SVM	74,19%	74,19%	75,81%	75,81%
Quadratic SVM	74,19%	70,97%	67,74%	67,74%
Cubic SVM	72,58%	70,97%	66,13%	64,52%
Fine Gaussian SVM	83,87%	83,87%	83,87%	83,87%
Medium Gaussian SVM	82,26%	82,26%	80,65%	79,03%
Coarse Gaussian SVM	83,87%	80,65%	75,81%	75,81%

5. Conclusions and Discussions

Parkinson's disease is one of the neurodegenerative diseases which affects people's quality of life negatively. Early detection of PD affects positively patients' quality of life. In this work, a PD diagnosis method based on motor abilities was presented. The data was obtained from a digital graphic tablet. Each patient performed two drawing tasks which are named as static spiral test and the dynamic spiral test. The drawings were recorded as *X, Y and Z* components of pen movement, *Grip Angle*, and *Pressure*. The PD patients' tremors can be seen on the shapes by eye on the drawings. Since the differences in the drawings will also be reflected in the data obtained from the tablet, the classification of this data may be a guiding factor in detecting PD.

The aim of this study is to detect PD in a very simple way without the need for heuristic approaches and by using simple ML algorithms. In recent years, deep learning algorithms-based approaches to PD diagnosis have gained popularity. To our knowledge, deep networks usually produce better results than traditional ML methods. However, deep learning algorithms require a mass amount of data, greater processing power, and computation time, hence consuming more energy. Therefore, to be more energy-efficient, if possible, traditional methods should be preferred.

In this work, PD diagnosis was made by using SST and DST data covering a total of 15 healthy and 57 people with PD. Regarding the results, the Kernel Naïve Bayes network outperformed other methods, with a performance of 90,32% with DST and merged data. The results can compete with the state of the art.

By analyzing the results deeper, one can claim that the *Z* parameter is the least important feature. In most cases, removing the *Z* parameter increased the accuracy of the SST data set. The best results were obtained by removing *Z* data for DST and merging data. These results led us to conclude that variations in the z-axis are less significant for the diagnosis of Parkinson's. As a result, it is thought that it may be more appropriate to increase DST-like tests in the diagnosis of Parkinson's disease and to use these tests as an auxiliary tool in the diagnosis of the disease. While performing these tests, simpler hardware that does not measure the *Z* axis, such as a mobile phone or a personal

tablet, may be preferred for the diagnosis of PD.

Conflict of Interest

No conflict of interest was declared by the authors.

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