Int. j. adv. multidisc. res. stud. 2023; 3(4):1090-1096

Received: 02-07-2023
Accepted: 12-08-2023

International Journal of Advanced Multidisciplinary Research and Studies

ISSN: 2583-049X

A New Method to Analyzing Speech to Detect Patients by Using Machine Learning Algorithms

Ali Najdet Nasret
Department of Electronics, Kirkuk Technical Institute, Northern Technical University Kirkuk, Iraq

Corresponding Author: **Ali Najdet Nasret**

Abstract
The progressive death of dopaminergic neurons in the substantia nigra causes motor system failure in the common neurodegenerative illness known as chronic degenerative disorder (CDD). Researchers have looked at a wide variety of signals, including electroencephalography (EEG), gait analysis, and speech analysis, in an effort to diagnose chronic degenerative disorder (CDD). For the vast majority (over 95%) of people with Chronic degenerative disorder (CDD), the study of speech is the primary technique utilized to improve speech-related issues. This research introduces the use of voice analysis as a fresh approach to the diagnosis of chronic degenerative disorders. In the first step, we use a Stochastic optimization (SO) to select the best features from among the collected data. Then, to separate healthy people from those with Chronic degenerative condition, a network based on support vector machines (SVMs) is employed. The dataset employed in this investigation is comprised of biological speech signals from 38 participants, including 32 with a chronic degenerative condition diagnosis and 9 healthy controls.
The subjects were asked to say the letter "A" out loud for a full four seconds. Extracted from the signals were a total of 29 features, both linear and non-linear properties. F0 (the fundamental frequency), jitter, and the noise-to-harmonics ratio were the focus of analysis for 15 of the aforementioned characteristics. These components have long been acknowledged for their crucial roles in shaping speech signals' defining features. Because of the obvious effect these qualities have on people with Chronic degenerative illness, a careful selection of the best possible qualities was made. The data was divided into groups based on how many ideal features they had. Using these 5 improved features, we were able to achieve a 95.53% accuracy rate in our classifications.

Keywords: Support Vector Machine, Chronic Degenerative Disorder, Speech Analysis, Stochastic Optimization

1. Introduction
The first documentation of Chronic degenerative disorder (CDD) was provided by James Parkinson in 1817, leading to the subsequent attribution of the illness's name to him. Chronic degenerative disorder (CDD) is a prevalent neurological ailment, ranking second in frequency after Alzheimer's disease. Current estimates indicate that the global population affected by CDD ranges from 4.5 to 7 million individuals. The majority of individuals afflicted with Chronic degenerative disorder (CDD) are typically aged 50 years or older; nevertheless, it is noteworthy that younger individuals might also experience the onset of this condition [1, 2]. Typically, the human brain contains neurons, referred to as brain cells, which are responsible for the production of dopamine. The neurons exhibit a notable level of localization inside the substantia nigra, a distinct part of the brain. Dopamine functions as a neurotransmitter, facilitating communication between the other regions and substantia nigra of the brain to regulate motor functions in the human body. Dopamine has a crucial role in facilitating the execution of coordinated muscular actions in humans. The onset of symptoms associated with Chronic degenerative disorder (CDD) normally occurs between the age range of 50 to 60 years.
These symptoms manifest gradually and are often overlooked by the affected individuals. The first manifestation that individuals with Chronic degenerative disorder (CDD) or their relatives often see is tremor. In the early stages, the tremor may present unilaterally, impacting either a single upper limb or lower limb, or only one lateral aspect of the body. Moreover, the tremor has the capacity to affect the muscles of the tongue, chin, and lips [3, 4, 5]. As the disease progresses, it is conceivable for the tremor to present bilaterally, impacting both hemispheres of the body. Other potential symptoms that may present themselves include feelings of depression and other emotional changes, with difficulties pertaining to eating, chewing, and speaking. Furthermore, individuals may have urinary difficulties or constipation, encounter skin issues, and face abnormalities in their sleep patterns. At now, Chronic degenerative disorder (CDD) lacks a definitive treatment; nevertheless,

pharmacological interventions known as dopaminergic agents have shown efficacy in mitigating muscular stiffness, enhancing motor function in terms of speed and coordination, and attenuating tremors. Several signals, such as electroencephalography (EEG), speech analysis, and gait analysis, have been used in the diagnosis of Chronic degenerative disorder (CDD). The recording of voice signals is considered to be the most ancient, straightforward, and least intrusive method for diagnosing Chronic degenerative disorder (CDD) [6, 7, 8].

Given that a significant proportion of individuals with Chronic degenerative disorder (CDD) have speech difficulties, it may be argued that speech analysis represents a logical and viable approach for CDD screening. The CDD dataset included in this paper has been examined by several experts in the field of speech analysis. The dataset has a total of 32 patients, with 24 individuals diagnosed with Chronic degenerative disorder and the other participants classified as healthy. In this article, M. Ene successfully derived a total of 29 linear and nonlinear features from the given dataset. The categorization approach included the use of three distinct kinds of probabilistic neural networks (PNN): incremental search (IS), Monte Carlo search (MCS), and hybrid search (HS). The concrete application has shown diagnostic accuracies ranging from 80% to 83%. An impressive 82.42% accuracy was achieved in classification utilizing the HS approach, showcasing its full potential. M. A. Little and coworkers used a strategy that comprised the extraction of characteristics that were similar to those previously used. Using the correlation equation to choose four ideal features, the Support Vector Machine (SVM) method achieved a classification accuracy of 92.6%. Four more optimal features similar to those employed in the prior research were selected by M. F. Caglar *et al*. Multi-Layer Perceptron (MLP), radial basis function (RBF), and Adaptive Neuro-Fuzzy Channel (ANFC) networks were used in the classification study, with the ANFC method used for feature selection. There was a 90.52% success rate in classification with the MLP, an 88.74% success rate with the RBF, and a 95.53% success rate with the ANFC. In this study, the authors, D. Gil and M. Johnson, conducted an investigation into the use of artificial neural networks (ANN) and support vector machine (SVM) networks for the purpose of diagnosing Chronic degenerative disorder (CDD). The authors' research used the same data sets. There was a 94% success rate in classifying data. This study investigates a strategy that uses a Stochastic optimization (SO) and a support vector machine (SVM) network as a classifier to pick out significant characteristics from a collection of extracted information. Several fields, including AI, image processing, and feature extraction, have found great success with the Stochastic optimization (SO) search paradigm. The Support Vector Machine (SVM) is a computer method for labeling things that employs a learning mechanism based on examples. Support Vector Machines (SVMs) have proven to be effective in a wide range of biological applications [9, 10]. Support vector machines (SVMs) are often used in the field of biomedicine for the purpose of automatically categorizing microarray gene expression patterns. The subsequent sections of the paper are structured in the following manner. Section 2 of the paper outlines the use of a Stochastic optimization approach to choose optimum features from the dataset. Additionally, the paper discusses the use of an SVM network for classification, as well as the process of data collecting and extraction of features from the dataset. Section 3 of the study delves into the examination of the efficacy of our approach while using different quantities of optimized characteristics. In order to assessment the effectiveness of the classifier, three statistical parameters will be used thereafter.

2. Substances and Techniques

General Outline of the Proposed Procedure

we provide a unique methodology for the detection and diagnosis of Chronic degenerative disorder (CDD) by using a hybrid technique that combines Stochastic optimization and support vector machine (SVM) network. The first segment of this study delineates our methodology for feature selection using a Stochastic optimization with the aim of attaining optimum outcomes. The subsequent portion of the study presents a comprehensive elucidation of the Support Vector Machine (SVM) network and the underlying justification for its use in the context of classification [11].

Evolutionary Algorithm

Based on evolutionary theory and natural selection, Stochastic optimization (SO) is an adaptable heuristic search technique. Data classification has been revolutionized by the approach being explored. It is well-known for its efficacy in selecting optimal characteristics. The phrase "solution" is more commonly referred to as a "chromosome" or "string" when discussing Stochastic optimizations. A population of chromosomes, or sequences that indicate a fusion of traits gleaned from the pool of viable solutions, is necessary for this strategy to work. A cost function, often known as a fitness function or assessment, is also crucial to have [12]. The above-mentioned procedure is responsible for determining whether or not each chromosome is healthy. The method operates on a finite set of chromosomes, known as the population, and draws inspiration from the principles of evolution. Crossover, inversion, and mutation are all chromosomal operations that occur naturally during reproduction and are passed on to the next generation. When two chromosomes exchange genetic information, it results in a new set of chromosomes that has a composite of characteristics from both parents. Chromosomal mutation results in the generation of a chromosome that has a striking resemblance to its parent chromosome, although with localized alterations occurring in some sections of the chromosome. The optimization procedure is executed in iterative phases referred to as generations. Different combinations of chromosomes are produced with the help of genetic operators like crossover, inversion, and mutation with each new generation [13].

In light of the population's stable size, only the most advantageous chromosomes are allowed to persist and advance to the following stage of reproduction. In order to facilitate an effective search, it is common for the crossover rate to be set at a very high number, often about 83%. Conversely, the mutation rate is frequently kept low, ranging from 1% to 14%. The iterative process continues until the population reaches a state of convergence, when all answers exhibit a reasonable degree of similarity and further investigation seems to provide diminishing returns. Alternatively, the process may terminate when an answer of satisfactory quality is obtained [14, 15].

Methodology for Choosing the Best Characteristics

The next section provides an explanation of the procedure for executing this algorithm to identify the optimal feature (pattern).

1. The entropy of each pattern may be determined by using Equation (1), whereas the entropy of the output (target) vector can be calculated using Equation (2).

$$H(X) = -\sum_{i=1}^{n} p(x_i) \log p(x_i) \quad (1)$$

$$H(Y) = -\sum_{i=1}^{n} p(y_i) \log p(y_i) \quad (2)$$

The feature vector is denoted by the variable x, whereas the target vector is denoted by y. p(x) and p(y) represent the attribute and goal probability density functions, respectively. The common information between all output and each pattern variables is calculated using equation (3).

$$I(X;Y) = H(X) - H(X|Y) = H(Y - H(Y|X))a \quad (3)$$

Equation (3) is used to compute the entropy of the patterns (H(X)), the entropy of the target vector (H(Y)), and the joint entropy of the patterns and target vector (H (X, Y)). This calculation is performed by using Equation (4).

$$H(X,Y) = \sum_{i=1}^{N}\sum_{k=1}^{N} -\log\left(p(x_i, y_k)\right) p(x_i, y_k) \quad (4)$$

And

$$H(Y|X) = H(X,Y) - H(X) \quad (5)$$

The next step is to use Equation (6) to get H(Y|X).

$$H(Y|X) = \sum_{x \varepsilon X} p(x) H(Y|X = x)$$

$$= \sum_{x \varepsilon X} p(x) \sum_{y \varepsilon Y} p(y|x) \log\left(\frac{1}{p(y|x)}\right) \quad (6)$$

2. In the context of the Stochastic optimization, the variable "n" represents the quantity of traits that are to be chosen, while the initial population is generated randomly from a pool of 206×n chromosomes. Hence, it can be seen that every chromosome is composed of a set of n genes, whereby the arrangement of the feature numbers is determined randomly. Furthermore, it is also conceivable for a certain feature number to occur many times within a single chromosome, following a random distribution.

3. Using Equation (7), we can get an overall measure of how well each chromosome patterns and targets match up.

$$V = \frac{1}{n} \sum_{i=1}^{n} I(X_i; Y_i) \quad (7)$$

The amount of information shared between features and targets is denoted by the "I" variable. Equation (8) is used to quantify the level of redundancy present in patterns and targets throughout each chromosome.

$$P = \frac{1}{n^2} \sum_{i=1}^{n} \sum_{j=1}^{n} I(X_i, Y_j) \quad (8)$$

4. Using Equation (9), we can calculate how healthy each chromosome is.

$$\phi = V - P \quad (9)$$

The primary aim of the evolutionary algorithm being suggested is to maximize the fitness function, which is mathematically given by Equation (9).

5. The rearrangement of chromosomes should be conducted in line with the fitness function that has been supplied.

6. Choose chromosomes with superior traits as parental units.

7. The process of using crossover and mutation is used to generate a novel population.

The chromosomes that exhibit the highest fitness function will be retained, while the other chromosomes will be eliminated. Subsequently, Steps 1-5 will be iteratively performed, and this process will persist until either the changes in the fitness of the chromosomes are below 0.03 or the algorithm achieves the set number of iterations. Ultimately, the chromosome exhibiting the highest level of fitness is picked, and the quantity of characteristics present inside such chromosome is regarded as the chosen features.

Vector Machine for Support Vectors

In the realm of localized neural networks, the Support Vector Machine (SVM) with a Gaussian kernel is rather common. This network has a single neuron serving as the output and a hidden layer made up of radial units. Our strategy for building this network and learning its parameters is based on using solely kernel functions, rather than directly processing signals from the hidden units. Despite the linear nature of the standard SVM, non-linear data may be utilized with this method by first applying a kernel function to indirectly translate the data into a linear feature space. Nevertheless, the creation of multiclass classifiers may be achieved by making slight modifications to the fundamental Support Vector Machine (SVM) algorithm, which is originally designed as a two-class classifier. In order to determine the maximum margin classifier, we analyze the function $f(x) = sgn(w \cdot x + b)$, where b and w represent the parameters that optimize the margin for the two classes. This analysis is conducted on a set of L linearly separable data points and their corresponding classes, denoted as $\{(x_1, y_1), (x_2, y_2), \ldots, (x_1, y_1)\}$. Here, $x_i \epsilon R^d$ belongs to the d-dimensional real space, while y_i takes values from the set {-1, 1}.

Here is a different representation of the classifier, written down with details on the input and output vectors:

$$f(x) = \text{sgn}\left(\sum_{i=1}^{L} \alpha_i y_i (x_i \cdot x) + b\right) \quad (10)$$

In order to get the biggest margin classifier, it is necessary to find the parameter α for each input vector. The bulk of α

values in this context exhibit a value of zero. However, inputs that possess non-zero α values are often denoted as support vectors because to their notable impact on the decision function. If the data set does not demonstrate linearity, the decision function used is:

$$f(x) = \operatorname{sgn}\left(\sum_{i=1}^{L} \alpha_i y_i K(x_i \cdot x) + b\right) \tag{11}$$

The process of transforming a non-linear input space into a linear one makes use of a kernel K. The largest margin classifier is often thought to exist in the linear space. A wide variety of kernels are available for selection. There are many different types of kernels used in machine learning techniques, however they may be broken down into four main groups: linear, polynomial, radial basis function, and hyperbolic tangent. Knowledge of the data and the features of different kernels may help mitigate the impact of the decision area on performance. If you're working with data that requires closed decision regions, for instance, an RBF kernel will serve you better than a linear or low-order polynomial one. As a result, the RBF kernel has been selected as the optimal option for this problem.

$$k(x_i, x) = \exp\left(-\frac{\|x_i - x\|}{2\sigma^2}\right) \tag{12}$$

In order to provide a more concise formulation of the RBF kernel, it is necessary to provide a parameter.

$$\lambda = -\frac{1}{2\sigma^2} \tag{13}$$

It is commonly accepted that the squared Euclidean distance between the two feature vectors is the formula $\|x_i - x\|$. The value of the free parameter ʎ is normally determined using empirical means.

The training of a Support Vector Machine (SVM) involves the resolution of a convex quadratic programming (QP) problem. This matter encompasses both equality and inequality restrictions, which are derived from the objective of increasing the margin. The solution approach computes the values of the nonzero parameters α that are introduced in the formulation and determines the support vectors that correspond to these values. In the context of data that is entirely separable, the values of α are restricted by the condition of being positive. On the other hand, when dealing with non-linearly separable data, the values of α are subject to the constraint of being within the range of 0 and C. The penalty parameter, represented as C, is an essential parameter that has to be established prior to the training of the Support Vector Machine (SVM). Further factors to be taken into account in the training of Support Vector Machines (SVMs) include the determination of an ideal training model by means of selecting a suitable kernel function and fine-tuning hyperparameters. In the context of multiclass support vector machines (SVM), a common approach involves training several two-class SVMs. During the classification phase, a voting method is used to determine the appropriate class assignment. Support Vector Machines (SVM) are deemed more suitable in this context because to their ability to explicitly quantify the degree to which individuals with Chronic degenerative disorder may be distinguished from healthy individuals based on dysphonia metrics. This approach addresses the challenge of accurately categorizing participants as either healthy or having Chronic degenerative disorder. By using this particular classification strategy, it is feasible to integrate many metrics in order to enhance discriminatory capabilities in practical applications.

3. Dataset

The research presented in the publication focused on the techniques used for extracting features in the context of voice problems that are often seen in the general population. The dataset included 197 instances of prolonged vowel phonations, with a total of 32 participants who were both male and female. Among these participants, 32 individuals were diagnosed with Chronic degenerative disorder (CDD). The duration since the diagnosis varied from 0 to 29 years, while the ages of the participants ranged from 47 to 86 years, with a mean of 66.3 years and a standard deviation of 10.2 years. Each subject's phonations were recorded, with an average of six measurements taken. The length of the measurements varied between 2 and 37 seconds. The phonations were recorded inside an IAC sound-treated booth using a head-mounted microphone (AKG C420) positioned at a distance of 9 cm from the lips. The speech signals were promptly captured and stored in a computer system using the CSL 4300B hardware, which is a product made by Kay Elemetrics. The sampling rate was set at 45.2 kHz, and the resolution was 17 bits. While the calibration of the samples is indeed influenced by amplitude normalization, the primary emphasis of this work lies in examining metrics that are not affected by variations in the absolute voice pressure level. To improve the robustness of the algorithms, it was imperative to conduct digital normalization of the amplitude for all samples prior to computing the measurements. Figure 1 illustrates the speech signals of a person without any health conditions and a patient who has been diagnosed with Chronic degenerative disorder (CDD), respectively.

Inferring Characteristics

A dataset was used to extract a total of 24 features, both linear and non-linear in nature. Table 1 provides a complete overview of the many traits, accompanied by succinct explanations.

The speech signal is characterized by 15 elements that may be attributed to four primary components: The ratio of noise to harmonics and jitter. F0 (fundamental frequency or pitch); and tremolo. These factors are considered to be of utmost significance in analyzing the voice signal.

According to the results, those with Chronic degenerative disorder and healthy controls vary significantly in the degree to which these parameters change. Consequently, certain characteristics that have been optimized are chosen from among these factors. The next section provides a description of each individual feature.

Flo (HZ): Minimum vocal fundamental frequency.

Fo (Hz): Average vocal fundamental frequency.

Fhi (Hz): Maximum vocal fundamental frequency.

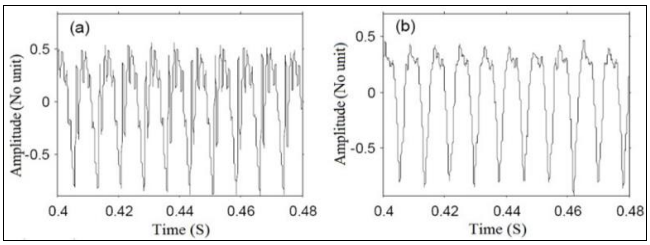

Fig. 1: (a) a person who is physically and mentally well; (b) a person who has been diagnosed with Chronic degenerative disorder

Table 1: This document presents a comprehensive compilation of extracted characteristics together with their corresponding descriptions

Features	Description
spread 1 spread 2 PPE	The fundamental frequency may be quantified in three nonlinear ways
DFA	The exponent of scaling for fractal signals
RCDDE D 2	Two Quantitative Metrics of Dynamical Complexity
NHR HNR	Two indicators of the amount of background noise relative to vocal tones
Jitter (%) Jitter (Abs) MDVP: RAP MDVP: PPQ Jitter: DDP	Several measures of variation in fundamental frequency

The jitter value is the mean absolute variation between consecutive fundamental frequency intervals divided by the mean period, expressed as a percentage.

$$Jitter(\%) = \frac{\frac{1}{N}\sum_{i=1}^{N-1}|T_i - T_{i-1}|}{\frac{1}{N}\sum_{i=1}^{N}T_i} \quad (14)$$

Within the given context, the symbol T_i is used to indicate the duration of the primary frequencies that are linked to the specific window labeled as "*i*." On the other hand, the symbol *N* is employed to designate the total count of windows present.

Jitter absolute refers to the fluctuation of the fundamental frequency from one cycle to the next, specifically denoting the mean absolute discrepancy between successive periods. This discrepancy is quantified as:

$$Jitter(ABS) = \frac{1}{N-1}\sum_{i=1}^{N-1}|T_i - T_{i-1}| \quad (15)$$

The number of fundamental frequency (F0) periods retrieved is denoted by *N*, and their respective durations are represented by the variable T_i.

Jitter, also known as Relative Average Perturbation (RAP), is a metric that quantifies the average absolute difference between a given period and the average of that period plus its two neighboring periods. The aforementioned number is then divided by the average duration in order to get a standardized metric for jitter.

$$Shimmer = \frac{\frac{1}{N-1}\sum_{i=1}^{N-1}|A_i - A_{i-1}|}{\frac{1}{N}\sum_{i=1}^{N}A_i} \quad (16)$$

The calculation of this metric involves measuring the average absolute difference between the amplitude of a certain period and the average amplitude of that period, as well as the average amplitudes of its four closest adjacent periods. The aforementioned number is thereafter divided by the mean amplitude of the specified time period.

The Harmonics-to-Noise Ratio (HNR) is a metric used to quantify the balance between harmonics and noise in a signal.

4. The Findings of the Study are as Follows

Before the commencement of the classification procedure aimed at differentiating individuals without Chronic degenerative disorder from those afflicted with the ailment, a Stochastic optimization was used to ascertain a collection of optimal features. The implementation of the SO and SVM classification methods was facilitated by the use of MATLAB software. In the classification process, after the use of a Stochastic optimization to identify influential characteristics, the subsequent steps include the application of training and testing processes employing these features. The dataset consists of many columns, each containing 197 distinct attributes. These properties are further separated into three segments, with 76% allocated for training purposes and 27% reserved for testing. The network was used in 100 instances for categorization, with varying quantities of features. The analysis of the data shown in Table 2 reveals that the use of certain attributes, namely Fhi (Hz), Fho (Hz), and jitter (RAP). resulted in the maximum degree of classification accuracy, which reached 95%. Furthermore, the study presents findings that indicate a classification accuracy of 94% for several auditory features, such as fundamental frequency low (Flo) in hertz, fundamental frequency high (Fhi) in hertz, fundamental frequency difference (Fho) in hertz, relative average perturbation (RAP) of jitter, absolute jitter (Jitter ABS). Moreover, an accuracy rate of 93.76% is attained in the classification process by using supplementary attributes like Flo (Hz), Fhi (Hz), Fho (Hz), jitter (RAP), Jitter (ABS), Jitter (%), and HNR. Table 2 displays the classification accuracy achieved by using the Support Vector Machine (SVM) classifier across different amounts of optimized features.

In order to assess the effectiveness of the suggested methodology, statistical measures including specificity, sensitivity, and overall classification accuracy were computed for different numbers of characteristics.

$$\text{Sensitivity} = \frac{NCH}{NTH} \times 100 \quad (17)$$

$$\text{Specificity} = \frac{NCPD}{NTPD} \times 100 \quad (18)$$

$$\text{Total classification accuracy} = \frac{NCH}{NTH} \times 100 \quad (19)$$

You can write NCCDD for the number of people who were correctly identified as having Chronic degenerative disorder, NTCDD for the total number of people who had Chronic degenerative disorder, NCH for the number of people who were correctly classified as being healthy, NCCP for the number of people who were correctly classified in the aggregate, and NTP for the total number of people who were included in the study. Table 3 presents the statistical

parameters' values corresponding to different numbers of characteristics. Figure 2 displays the graphical representations of the pairings of the first four significant traits that were derived via the use of a Stochastic optimization.

5. Discussion

The primary aim of this research endeavor was to use speech analysis as a diagnostic tool for the identification of Chronic degenerative disorder. The present study used a dataset of 32 people, out of whom 24 were diagnosed with Chronic degenerative disorder (CDD), while the other participants were classified as being in a healthy condition. A variety of linear and non-linear properties were obtained from the dataset. In specifically, a total of 15 distinct characteristics were extracted, with special emphasis on four key elements of speech: fundamental frequency (also known as pitch), jitter, and the ratio of noise to harmonics. Chronic degenerative condition patients differ significantly from healthy controls in 15 different ways, according to recent studies. Therefore, work was done to isolate desirable characteristics from this population. Choosing robust features is the first and most important step in improving classification precision. The process creates new populations by the use of genetic operators like selection, crossover, and mutation. The concepts of biological evolution, such as natural selection and genetic recombination, are reflected in these operators. The goal of a SO is to iteratively improve the quality of solutions by favoring those that are more fit, based on a fitness function. This iterative process continues until a satisfactory solution is obtained.

Table 2: Accuracy of classifications as a function of the number of characteristics

Features	N = 5	N = 8	N= 10
Accuracy	95±3.45	92.97±3.56	94.14±3.52

Table 3: Accuracy of classifications as a function of the number of characteristics

Feature Number	N = 5	N = 8	N= 10
Sensitivity	87.64	79.55	79.87
Specificity	96.12	90.34	93.08
Total classification accuracy	95.95	94.02	94.21

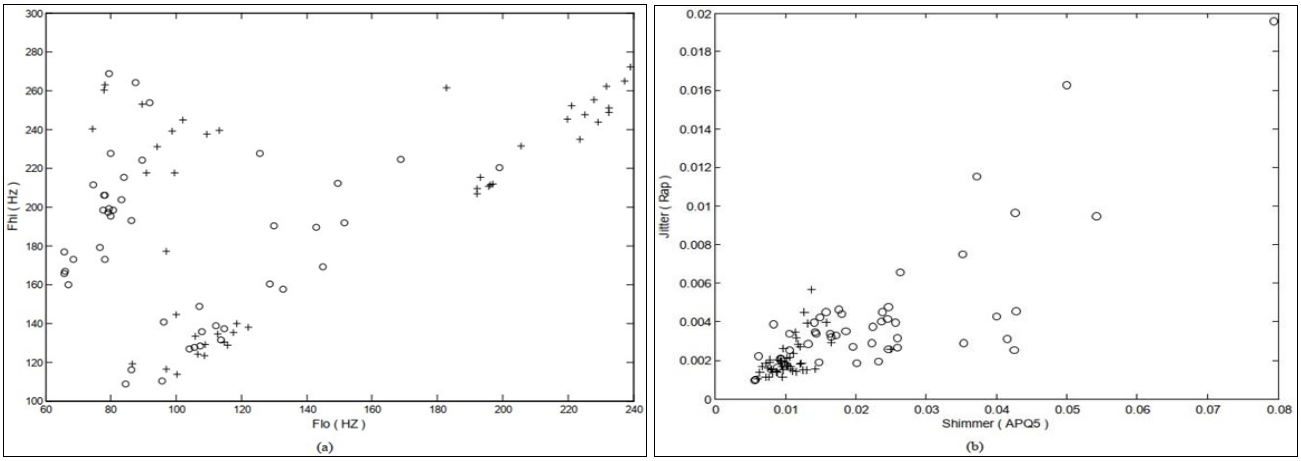

Fig 2: (a) Jitter (RAP) database (b) Fhi (Hz)-Flo (Hz) database are intended to be included in this investigation. In this context, "O" represents healthy individuals and "+" represents those with Chronic degenerative disorder

The data was acquired. Stochastic optimizations (SO) provide the ability to effectively handle expansive search spaces, resulting in a reduced likelihood of converging to local optimum solutions compared to other algorithms. The first step was using a Stochastic optimization to determine which characteristics are best at separating healthy individuals from those with Chronic degenerative disorder. Classifiers were then used to carry out the classification process, and a support vector machine (SVM) was ultimately chosen for this task. Support vector machines (SVMs) benefit from a kernel's increased flexibility in choosing a threshold that differentiates people with Chronic degenerative disorder from healthy persons. This threshold does not necessarily have to be linear and may vary in functional form throughout the dataset. The non-parametric and localized nature of the SVM allows for this flexibility. Moreover, a preliminary examination of the arrangement and grouping of pairs of measurements suggests that distinguishing individuals with Chronic degenerative disorder from healthy individuals using linear or hyperplane kernels may provide challenges. As a result, the kernel-SVM formulation with Gaussian radial basis kernel functions was chosen to be implemented. As previously stated, the determination of the parameter ʎ is reliant on experimental methods. Consequently, we conducted a systematic increment of the ʎ value within the range of 0 to 1. Notably, the most favorable classification accuracies were attained when the ʎ value was found to be 0.452.

After analyzing the classification process with various feature sets, it was discovered that the first four returned features Fho (Hz), Fhi (Hz), and jitter provided the greatest classification accuracy. However, results suggested that combining linear and non-linear data might improve classification accuracy. Our current focus is on creating a technique that uses linear and non-linear features in the classification process, with the end goal being the achievement of this aim. In addition, we will employ a fusion support vector machine (SVM) network to categorize people as healthy or afflicted with Chronic degenerative disorder (CDD).

6. Conclusion

In terms of prevalence among neurological disorders, chronic degenerative disease is second only to Alzheimer's. It affects every element of human functioning, although the most noticeable symptom is difficulty communicating

verbally. It has been suggested that speech analysis could be used as a diagnostic tool for chronic degenerative disorder (CDD), and several studies have been designed to explore this potential. This study looks into a novel approach to classifying individuals into two groups—those with and without a diagnosis of Chronic degenerative disorder—by combining Stochastic optimization with a support vector machine (SVM) network. In this research, we compare how well different classification methods perform when given different sets of features. three optimal features were used in this study: Fhi (Hz), Fho (Hz)a and jitter (RAP). This combination yielded the best extraction accuracy. Our method has been seen to be within a little margin of the accuracy of the gold standard.

7. References

1. Almeida JS, Rebouças Filho PP, Carneiro T, Wei W, Damaševičius R, Maskeliūnas R, *et al*. Detecting Parkinson's disease with sustained phonation and speech signals using machine learning techniques. Pattern Recognition Letters. 2019; 125:55-62.
2. Gozes O, Frid-Adar M, Greenspan H, Browning PD, Zhang H, Ji W, Siegel E. Rapid ai development cycle for the coronavirus (covid-19) pandemic: Initial results for automated detection & patient monitoring using deep learning ct image analysis. arXiv preprint arXiv:2003.05037, 2020.
3. Liu L, Zhao S, Chen H, Wang A. A new machine learning method for identifying Alzheimer's disease. Simulation Modelling Practice and Theory. 2020; 99:p102023.
4. Mathur R, Pathak V, Bandil D. Parkinson disease prediction using machine learning algorithm. In Emerging Trends in Expert Applications and Security: Proceedings of ICETEAS 2018. Springer Singapore, 2019, 357-363.
5. Liu X, Faes L, Kale AU, Wagner SK, Fu DJ, Bruynseels A, *et al*. A comparison of deep learning performance against health-care professionals in detecting diseases from medical imaging: A systematic review and meta-analysis. The lancet digital health. 2019; 1(6):e271-e297.
6. Hassan MD, Nasret AN, Baker MR, Mahmood ZS. Enhancement automatic speech recognition by deep neural networks. Periodicals of Engineering and Natural Sciences. 2021; 9(4):921-927.
7. Nasret AN, Noori AB, Mohammed AA, Mahmood ZS. Design of automatic speech recognition in noisy environments enhancement and modification. Periodicals of Engineering and Natural Sciences. 2021; 10(1):71-77.
8. Laylani LAASS, Coran ANN, Mahmood ZS. Foretelling Diabetic Disease Using a Machine Learning Algorithms. In 2022 International Conference for Advancement in Technology (ICONAT). IEEE, 2022, 1-5.
9. Kadhim IB, Nasret AN, Mahmood ZS. Enhancement and modification of automatic speaker verification by utilizing hidden Markov model. Indonesian Journal of Electrical Engineering and Computer Science. 2022; 27(3):1397-1403.
10. Lopez-de-Ipiña K, Alonso JB, Solé-Casals J, Barroso N, Henriquez P, Faundez-Zanuy M, *et al*. On automatic diagnosis of Alzheimer's disease based on spontaneous speech analysis and emotional temperature. Cognitive Computation. 2015; 7:44-55.
11. Suppa A, Asci F, Saggio G, Di Leo P, Zarezadeh Z, Ferrazzano G, *et al*. Voice analysis with machine learning: one step closer to an objective diagnosis of essential tremor. Movement Disorders. 2021; 36(6):1401-1410.
12. Aleem S, Huda NU, Amin R, Khalid S, Alshamrani SS, Alshehri A. Machine learning algorithms for depression: Diagnosis, insights, and research directions. Electronics. 2022; 11(7):p1111.
13. Kwekha-Rashid AS, Abduljabbar HN, Alhayani B. Coronavirus disease (COVID-19) cases analysis using machine-learning applications. Applied Nanoscience. 2023; 13(3):2013-2025.
14. Cihan P, Ozger ZB. A new approach for determining SARS-CoV-2 epitopes using machine learning-based in silico methods. Computational Biology and Chemistry. 2022; 98:p107688.
15. Charbuty B, Abdulazeez A. Classification based on decision tree algorithm for machine learning. Journal of Applied Science and Technology Trends. 2021; 2(1):20-28.