JTH: Journal of Technology and Health *ISSN 3025-1168*
Vol. 4, No. 1, 2026, pp. 379 ~ 392
Open Acces: *https://doi.org/10.61677/jth.v4i1.838*

OPTIMIZATION AND EVALUATION OF SUPPORT VECTOR MACHINE PERFORMANCE FOR PARKINSON'S DISEASE CLASSIFICATION USING BIOMEDICAL DATA

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Received May 12, 2026; Revised May 28, 2026; Accepted June 2, 2026; Published June 4, 2026

ABSTRACT

Dysphonia, hypophonia, and decreased pitch variation are common vocal deficits linked to Parkinson's disease, a progressive neurological illness. These anomalies can be used as non-invasive biomarkers to identify diseases early. Using biomedical speech data, this work attempts to optimize and assess the Support Vector Machine (SVM) algorithm's performance for Parkinson's disease categorization. The UCI Machine Learning Repository provided the dataset, which included 195 observations with 23 biological voice variables, such as jitter, shimmer, and characteristics related to frequency. Cleaning, standardization, and dividing the dataset into 80% training and 20% testing sets were all part of the data preprocessing procedure. To find the best SVM configuration, Grid Search and k-fold cross-validation were used for hyperparameter tuning. The findings of the experiment demonstrated that the Radial Basis Function (RBF) kernel.

Keywords: *Parkinson's disease. Support vector machine, Biomedical voice data, Machine learning, Hyperparameter optimization*

INTRODUCTION

Parkinson's disease is the second most prevalent neurological condition in the world and a significant global health concern. Parkinson's disease has significantly increased in prevalence over the past few decades, according to the most recent global epidemiological statistics. In 2021, the sickness affected about 11.77 million people worldwide, a more than 270% rise from 1990. Due to aging populations and longer life expectancies, Parkinson's disease is one of the neurological disorders that is spreading the fastest in the world (Li et al., 2025). Motor symptoms such as bradykinesia, stiffness, resting tremors, and postural instability are caused by the death of dopaminergic neurons in the substantia nigra (Postuma et al., 2015). Parkinson's disease affects non-motor functions, such as speech and voice production difficulties, in addition to motor symptoms. Dysphonia, or changes in vocal qualities, affects about 90% of Parkinson's patients as the disease progresses. These voice abnormalities often appear in the early stages and may not be recognized directly by patients. Biomedical voice signals, such as jitter and shimmer, contain important acoustic information that can be utilized as non-invasive biomarkers for Parkinson's disease detection and diagnosis (Fernández-García et al., 2021; Majda-Zdancewicz et al., 2024).

Because medical treatment is typically more effective when given in the early stages of the disease, early detection of Parkinson's disease is critical to improve patient quality of life (Tysnes & Storstein, 2017). A delayed diagnosis could accelerate the illness's

progression and reduce the effectiveness of treatment. The creation of clinical decision support systems based on machine learning is becoming more crucial to help doctors identify Parkinson's disease early. Because Parkinson's disease frequently results in subtle vocal abnormalities, such as jitter, shimmer, reduced pitch variation, and speech instability, which may be difficult to identify through traditional clinical observation alone, this approach is especially pertinent for biological voice data. High-dimensional and complex voice features can be analyzed by machine learning algorithms, which can also find hidden patterns and provide highly accurate predictive models. For early Parkinson's disease screening and diagnosis, voice-based machine learning techniques provide a useful, non-invasive, and affordable option. Biological data and a number of machine learning classification techniques, such as Random Forest and Naive Bayes, have been used to identify Parkinson's disease (Orozco-Arroyave et al., 2016). Support Vector Machine (SVM) has continuously shown better performance, especially for high-dimensional medical datasets with small sample sizes. SVM is a great fit for challenging biomedical classification tasks since it can create ideal hyperplanes using kernel functions (Rahman et al., 2023).

Even if SVM performs well, choosing the right hyperparameters is crucial to its efficacy. Overfitting and poor classification accuracy, which often falls between 0.80 and 0.90 in many Parkinson's disease investigations, might result from improper parameter selections (Ahammad et al., 2024). In this work, biological speech data is used to optimize and assess SVM performance for Parkinson's disease classification. Support Vector Machine (SVM) has been shown in earlier research to be capable of detecting Parkinson's disease from biological voice data. Many still use traditional SVM configurations, don't adjust the hyperparameters, or put classification accuracy ahead of careful model interpretation. The suggested approach uses Grid Search and k-fold cross-validation for systematic hyperparameter tuning to increase classification accuracy and lower the risk of overfitting in SVM-based Parkinson's disease diagnosis. In contrast to earlier studies, this study provides both strong prediction accuracy and clinically interpretable insights into significant biological speech aspects by combining improved SVM modeling with Explainable Artificial Intelligence (XAI) approaches including Permutation Importance and SHAP analysis.

Parkinson's disease is a degenerative neurological condition that mostly affects motor function, but it can also cause significant non-motor symptoms including dysphonia or trouble speaking. Parkinson's patients with dysphonia experience symptoms like hypophonia, hoarseness, irregular speech rate, monotone pitch, and decreased vocal quality. These symptoms are linked to abnormalities in laryngeal muscle control, cognitive decline, and emotional disturbances (Liu et al., 2025; Stemple et al., 2020). Due to their frequent occurrence in the early stages of the disease and their role as early diagnostic indications, these voice-related anomalies have garnered a lot of attention. The correct diagnosis and management of Parkinson's disease depend on an understanding of the pathological and clinical features of dysphonia.

Parkinson's disease is better understood and diagnosed thanks in large part to biomedical data. To detect abnormalities related to disease, a variety of biomedical data have been used, such as structural and functional Magnetic Resonance Imaging (MRI/fMRI), Positron Emission Tomography (PET), electroencephalography (EEG), gait analysis, and voice signal analysis (Chang et al., 2023; Schröter et al., 2025). Because minor irregularities in speech prosody and articulation may manifest before to the onset of severe motor symptoms, voice signal analysis in particular has shown great promise

(Kent & Vorperian, 2018). While Electronic Health Records (EHRs) offer longitudinal clinical data that supports disease monitoring and therapy evaluation, biological biomarkers and genetic information also aid in understanding the molecular underpinnings of Parkinson's disease (Bloem et al., 2021). Combining various scientific data sources provides a more thorough and impartial method for identifying diseases and making treatment decisions.

Research on disease classification has been greatly impacted by the quick growth of artificial intelligence, especially machine learning. Computer systems can learn patterns from data and create prediction models without explicit programming thanks to machine learning (ML) (Mitchell, 1997). ML algorithms can handle high-dimensional biomedical information in medical applications and find intricate patterns that are challenging to find with traditional analytical techniques (LeCun et al., 2015). Many machine learning algorithms, such as Random Forest, Naive Bayes, and SVM, have been used to classify Parkinson's disease. SVM is one of these methods that has garnered a lot of interest because to its remarkable capacity for generalization and its effectiveness while managing datasets with large feature dimensions and small sample sizes.

Finding the best hyperplane to split classes with the largest margin is the aim of the supervised learning method Support Vector Machine (SVM) (Purba et al., 2025). SVM uses kernel functions like Polynomial and Radial Basis Functions (RBF) to transform non-linear datasets into higher-dimensional feature spaces where linear separation is possible (Wildah et al., 2020). To differentiate between healthy people and Parkinson's patients, biological speech characteristics including jitter, shimmer, and entropy are mapped into multidimensional feature spaces. It has been demonstrated that applying kernel-based transformation enhances classification performance, especially when utilizing the RBF kernel because of its adaptability in representing intricate decision boundaries (Mohammad Annan Makruf Mustofa et al., 2025).

Even while SVM shows promise, the model's efficacy is mostly contingent on choosing the right hyperparameters, particularly the regularization parameter C and the kernel value gamma (γ). These parameters influence the balance between maximizing classification accuracy and minimizing overfitting. Hyperparameter optimization techniques like Grid Search are commonly used to identify the ideal parameter combinations that improve classification performance, particularly Area Under the Curve (AUC), sensitivity, and specificity (Putra & Pramartha, 2025). The potential of SVM for Parkinson's disease classification has been shown in earlier research, but many of these studies still have issues with poor parameter tuning and inadequate integration of biological characteristics with thorough model validation. Further research focused on systematic SVM improvement and performance evaluation is still needed to improve the reliability and accuracy of Parkinson's disease diagnosis systems.

This study's goal is to assess and improve the SVM approach for classifying Parkinson's disease utilizing biomedical speech data. This study also compares the optimized SVM model with other classification methods to assess how well it distinguishes Parkinson's patients from healthy individuals.

RESEARCH METHODS

In order to assess and improve the performance of the Support Vector Machine (SVM) algorithm for Parkinson's disease classification utilizing biomedical voice data, this work combines an experimental research technique with a quantitative approach. Data preparation, model training, hyperparameter tuning, testing, and validation were all

part of the experimental process. An 80:20 ratio was used to split the dataset into training and testing sets. The classification model was developed using the training data, and the expected performance was assessed using the testing data. Grid Search and k-fold cross-validation were used for hyperparameter optimization to find the best SVM configuration and lessen the risk of overfitting. Using a variety of evaluation measures, the performance of the improved SVM model was contrasted with that of other classification techniques, especially Random Forest and Naive Bayes.Since the study concentrated on objective assessment and statistical evaluation of model performance using classification metrics including accuracy, precision, recall, F1-score, and Area Under the Curve (AUC), the quantitative approach was chosen (Asri Mulyani et al., 2025; Danis Rifa Nurqotimah et al., 2024). The experimental design enabled systematic comparison between different SVM hyperparameter configurations and optimization strategies, allowing the results to be scientifically validated and generalized.

Data gathering, preprocessing, model construction, hyperparameter optimization, and performance evaluation were the steps in the research process. The Parkinson's Disease dataset, which was created from biomedical voice recordings, was the biomedical dataset utilized in this investigation. The UCI Machine Learning Repository is where it was obtained. The collection contained 195 voice recordings from 31 participants, including those with a diagnosis of Parkinson's disease and healthy control persons. The dataset contained twenty-three biological voice features that are associated with vocal characteristics, including jitter, shimmer, and frequency-related measurements. These characteristics are often used to identify speech impairments linked to Parkinson's disease. The chosen dataset included biological voice characteristics linked to the categorization of Parkinson's illness. The biomedical voice data were obtained from sustained phonation recordings, particularly the sustained vowel /a/, collected from study participants and provided through the UCI Machine Learning Repository. Voice recordings were processed to extract 23 acoustic features representing vocal characteristics associated with Parkinson’s disease. These features included frequency-based features like fundamental frequency (MDVP:Fo), non-linear voice metrics like noise-to-harmonic ratio (NHR), recurrence period density entropy (RPDE), and pitch period entropy (PPE), as well as vocal instability metrics like jitter and shimmer. The voice acquisition and feature extraction procedures, which followed the standardized method used in the initial dataset development, enabled reliable biomedical speech analysis for Parkinson's disease detection. By addressing missing values, eliminating duplicates, identifying outliers, and using normalization or feature scaling techniques as needed, data pretreatment was carried out to enhance data quality. To enable accurate model evaluation, the dataset was then split into training and testing sets using standard data partitioning ratios.

Due to its exceptional ability to handle high-dimensional and non-linear biological datasets with small sample sizes, SVM was the primary classification method employed in this work (Junus et al., 2023). The model included a number of independent variables, such as SVM kernel types, regularization parameter C, gamma (γ) parameter, biological characteristics collected from voice signals, and feature selection techniques. Parkinson's disease categorization outcomes and model performance indicators made up the dependent variables. A number of kernel functions, including Linear, Polynomial, and Radial Basis Function (RBF), were evaluated in order to identify the optimal classification model. The optimal set of parameters that will enhance classification

performance was found using Grid Search techniques for hyperparameter optimization. The SVM classification model can be expressed mathematically as

$$f(x)_{= \omega^T \emptyset(x)+b}$$

Where f(x) represents the prediction function, www denotes the weight vector, $\omega^T \emptyset(x) + b$ is the mapping function that transforms input data into a higher-dimensional feature space, and bbb represents the bias term [23]. To achieve optimal classification, SVM attempts to maximize the separating margin while minimizing classification errors. For non-linear classification, kernel functions were applied using the kernel trick approach, expressed as:

$$K(x_i, x_j) = \emptyset(x_i)^T \emptyset(x_j)$$

In this study, the Radial Basis Function (RBF) kernel was primarily utilized because of its flexibility in handling complex biomedical patterns. The RBF kernel function is defined as:

$$K(x_i, x_j) = \exp\left(-\gamma \|x_i - x_j\|^2\right)$$

Where γ is the kernel parameter that regulates each training sample's effect range. Data analysis was conducted through several systematic stages, including preprocessing, data partitioning, model optimization, validation, and performance evaluation. During preprocessing, the dataset underwent cleaning procedures, including checking for missing values, removing duplicate records, and applying feature normalization to ensure comparable scales among biomedical voice variables. After processing, the dataset was split into training and testing sets in an 80:20 ratio. The training set was used to create the classification model, and the testing set was used to assess the expected performance. Grid Search was used for hyperparameter optimization to determine the ideal set of SVM parameters, such as kernel type, regularization parameter (C), and gamma (γ). During the optimization phase, K-fold cross-validation was used to decrease overfitting and increase model reliability. Lastly, the model's performance was compared with Random Forest and Naive Bayes classifiers using confusion matrix analysis and classification measures like accuracy, precision, recall, F1-score, sensitivity, specificity, and AUC.
Contains the types of research methods and research approaches carried out along with the steps in detail. The author must explain what is done at each stage. It is not recommended to only explain in theory without explaining the actions taken by the researcher.

RESULTS AND DISCUSSION

Dataset Description and Preprocessing

The UCI Machine Learning Repository provided the dataset for this work, which included 195 observations with 23 biological voice characteristics associated with Parkinson's disease. The dataset included 48 healthy control samples and 147 Parkinson's disease samples, as shown in Table 1, demonstrating an uneven class distribution. The dataset was split into 80% training data and 20% testing data in order to construct and assess the model. Table 1. The dataset summary provides an overview of the aspects of the dataset, including the data source, number of observations, feature dimensions, and class distribution. The greater percentage of Parkinson's cases in comparison to healthy

samples raises the possibility of a class imbalance problem that could affect classification performance and necessitates careful consideration when evaluating the model.

Descriptive statistical analysis was conducted to examine the distribution of biomedical voice features. As shown in Table 2, several vocal biomarkers exhibited considerable variability across observations. Features related to voice perturbation, such as MDVP (%), Jitter, MDVP, MDVP (dB), Shimmer:APQ3, Shimmer:APQ5, and Shimmer:DDA, demonstrated different mean values and standard deviations, reflecting variations in vocal characteristics commonly associated with Parkinson's disease. For example, the feature MDVP (dB) showed a relatively large standard deviation (0.1949), indicating substantial variability among subjects.

Furthermore, the overall distribution of the biomedical voice features is illustrated in Figure 1. The figure highlights the heterogeneity of the dataset and shows that several attributes possess different value ranges and distribution patterns. Such variability may affect the learning process of machine learning algorithms, particularly distance-based classifiers such as Support Vector Machines (SVM).

During the preprocessing phase, feature normalization was used to convert all variables into a similar scale because several features showed large numerical ranges and comparatively significant standard deviations. This step was required to enhance the stability and prediction performance of the SVM model and to stop features with higher numerical values from affecting the classification process. The normalized dataset was then used to train and evaluate the classification models.

Table 1 Dataset Summary

Description	Value
Data Source	UCI Machine Learning Repository
Total Data	195
Training Data	80%
Testing Data	20%
Number of Features	23
Parkinson's Class	147
Healthy Class	48

Table 2 Descriptive Statistics of Biomedical Features

Feature	Count	Mean	Std	Min	Max
MDVP:Jitter (%)	195.0	0.0062	0.0048	0.00168	0.03316
Jitter:DDP	195.0	0.0099	0.0089	0.00204	0.06433
MDVP:Shimmer	195.0	0.0297	0.0189	0.00954	0.11908
MDVP:Shimmer (dB)	195.0	0.2823	0.1949	0.085	1.302
Shimmer:APQ3	195.0	0.0157	0.0102	0.00455	0.05647
Shimmer:APQ5	195.0	0.0179	0.0120	0.0057	0.0794
Shimmer:DDA	195.0	0.0470	0.0305	0.01364	0.16942

	name	MDVP:Fo(Hz)	MDVP:Fhi(Hz)	MDVP:Flo(Hz)	MDVP:Jitter(%)	\
0	phon_R01_S01_1	119.992	157.302	74.997	0.00784	
1	phon_R01_S01_2	122.400	148.650	113.819	0.00968	
2	phon_R01_S01_3	116.682	131.111	111.555	0.01050	
3	phon_R01_S01_4	116.676	137.871	111.366	0.00997	
4	phon_R01_S01_5	116.014	141.781	110.655	0.01284	

	MDVP:Jitter(Abs)	MDVP:RAP	MDVP:PPQ	Jitter:DDP	MDVP:Shimmer	...	\
0	0.00007	0.00370	0.00554	0.01109	0.04374	...	
1	0.00008	0.00465	0.00696	0.01394	0.06134	...	
2	0.00009	0.00544	0.00781	0.01633	0.05233	...	
3	0.00009	0.00502	0.00698	0.01505	0.05492	...	
4	0.00011	0.00655	0.00908	0.01966	0.06425	...	

	Shimmer:DDA	NHR	HNR	status	RPDE	DFA	spread1	\
0	0.06545	0.02211	21.033	1	0.414783	0.815285	-4.813031	
1	0.09403	0.01929	19.085	1	0.458359	0.819521	-4.075192	
2	0.08270	0.01309	20.651	1	0.429895	0.825288	-4.443179	
3	0.08771	0.01353	20.644	1	0.434969	0.819235	-4.117501	
4	0.10470	0.01767	19.649	1	0.417356	0.823484	-3.747787	

	spread2	D2	PPE
0	0.266482	2.301442	0.284654
1	0.335590	2.486855	0.368674
2	0.311173	2.342259	0.332634
3	0.334147	2.405554	0.368975
4	0.234513	2.332180	0.410335

Figure 1 Distribution of Biomedical Voice Features in the Parkinson

SVM Hyperparameter Optimization

To enhance the SVM model's classification performance, hyperparameter adjustment was carried out. In this work, the optimal parameter configuration was found using Grid Search and k-fold cross-validation. Among the parameters analyzed were the regularization parameter (C), kernel type, and gamma (γ). These variables significantly affect the decision boundary, model complexity, and generalization ability of the classifier.

Table 3 shows that the Radial Basis Function (RBF) kernel with regularization values of C = 10 and γ = 0.1 created the ideal hyperparameter configuration. The ability of the RBF kernel to capture non-linear correlations in biomedical speech data which are commonly observed in tasks involving the classification of Parkinson's disease led to its selection. While γ = 0.1 allowed the model to efficiently capture local data patterns without significantly overfitting, the selected value of C = 10 offered a suitable balance between maximizing the decision margin and minimizing classification mistakes.

The ideal parameter values found using the Grid Search process are compiled in Table 3. For biomedical speech characteristics linked to Parkinson's illness, the experimental findings showed that this configuration produced the greatest classification performance among the assessed parameter combinations, offering an efficient trade-off between predictive accuracy and model generalization.

The enhanced hyperparameters were used to train the final SVM model, and accuracy, precision, recall, F1-score, specificity, AUC-ROC, and confusion matrix analysis were used to evaluate the model's performance.

Table 3 Best Hyperparameter Configuration

Parameter	Best Value
C	10
Gamma	0.1
Kernel	RBF

Model Performance Evaluation

Several classification metrics, including accuracy, precision, recall, F1-score, specificity, and AUC-ROC, were used to compare SVM's performance against Random Forest and Naive Bayes. With an AUC-ROC value of 0.99, the optimized SVM model demonstrated the best discriminative performance among the assessed classifiers, as shown in Figure 2, demonstrating an exceptional capacity to differentiate Parkinson's patients from healthy people. The results demonstrated that the optimized SVM model performed the best overall, with an accuracy of 94.87%, recall of 96.55%, precision of 96.55%, F1-score of 96.55%, specificity of 90.00%, and an AUC-ROC value of 0.99. Figure 3, which compares the confusion matrices of SVM, Random Forest, and Naive Bayes, provides more proof of the model's efficacy. Twenty-eight true positive (TP), nine true negative (TN), one false positive (FP), and just one false negative (FN) case were found by the SVM confusion matrix analysis. These findings show that SVM was quite successful in differentiating Parkinson's patients from healthy people while preserving balanced sensitivity and specificity, which are crucial for medical diagnosis.

The model rarely failed to detect Parkinson's patients, as evidenced by the low frequency of false negatives, which lowers the possibility of missed diagnoses. Although one false positive case was observed, the model maintained strong diagnostic reliability, supported by its high recall (96.55%) and AUC (0.99), as shown in Figure 2, demonstrating excellent discriminative capability for Parkinson's disease classification.

In comparison, Random Forest also produced competitive results, achieving an AUC-ROC value of 0.97 and a confusion matrix consisting of 28 TP, 8 TN, 2 FP, and 1 FN, as illustrated in Figures 2 and 3. However, its overall performance remained slightly lower than that of SVM. Meanwhile, Naive Bayes achieved the lowest classification performance, with an AUC-ROC value of 0.87 and a confusion matrix consisting of 16 TP, 10 TN, 0 FP, and 13 FN. Naive Bayes's assumption of feature independence may have contributed to its frequent failure to detect Parkinson's cases, as evidenced by the comparatively high number of false negatives. As a result, it is less appropriate for coupled biological speech data. Overall, compared to Random Forest and Naive Bayes, the improved SVM model consistently demonstrated greater classification performance and better handling of non-linear biological patterns, as shown by the ROC curve comparison in Figure 2 and the confusion matrix comparison in Figure 3.

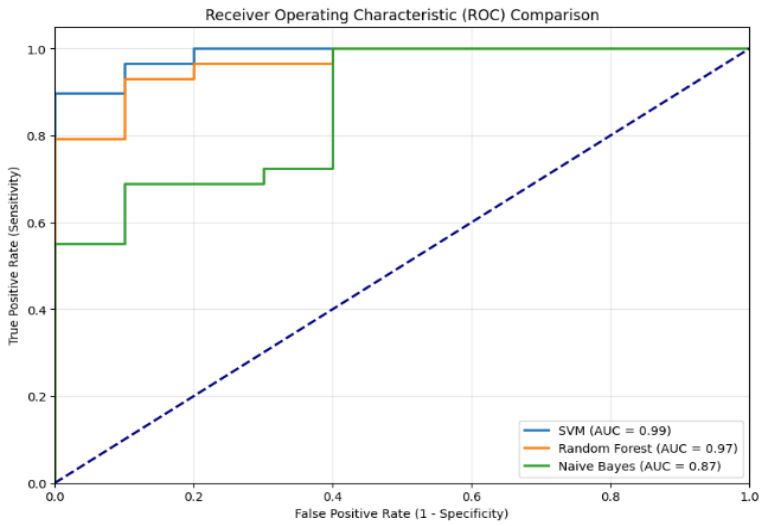

Figure 2. ROC Curve Comparison

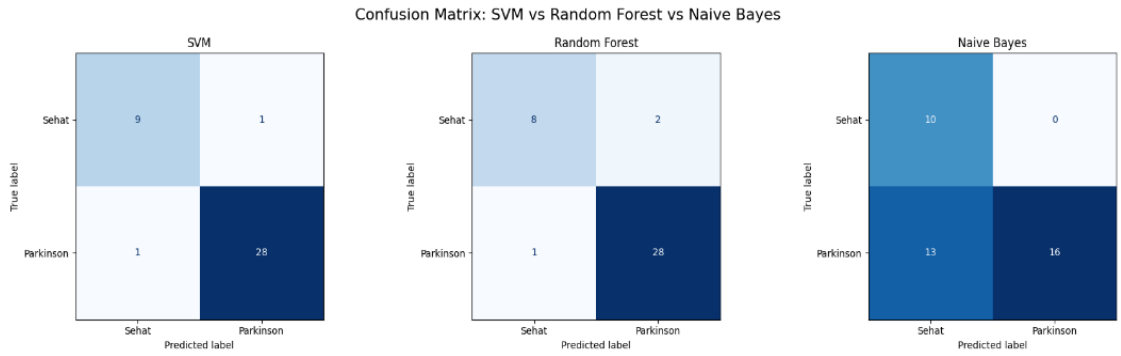

Figure 3. Confusion Matrix Comparison

Feature Importance Analysis

Permutation Importance and SHAP were used in feature importance analysis to determine the most significant biomedical voice characteristics in the classification of Parkinson's illness. The results revealed that features such as MDVP:Fo(Hz), spread1, spread2, and PPE were the most significant contributors to model predictions. These features are strongly associated with vocal instability, pitch variation, and dysphonia characteristics commonly observed in Parkinson's patients. SHAP analysis further demonstrated that higher values of spread1, spread2, and PPE increased the probability of Parkinson's classification, while lower fundamental frequency values contributed positively to Parkinson's predictions. These findings are clinically consistent with symptoms such as hypokinetic dysarthria, vocal tremor, and reduced pitch variation in Parkinson's disease. The consistency between technical results and clinical interpretation indicates that voice-based biomedical analysis has strong potential as a non-invasive early detection method for Parkinson's disease.

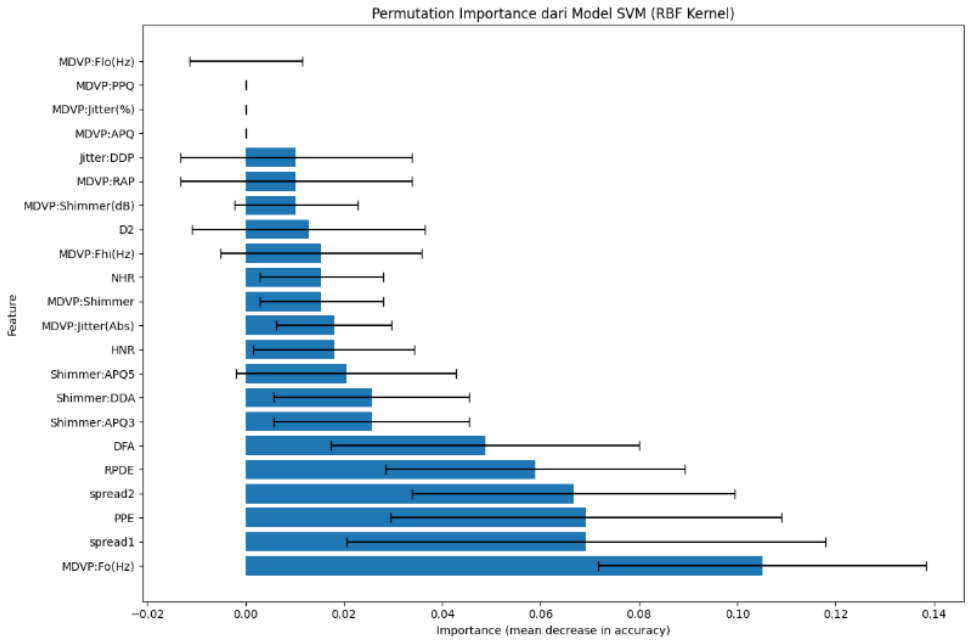

Figure 4. Permutation Importance Visualization

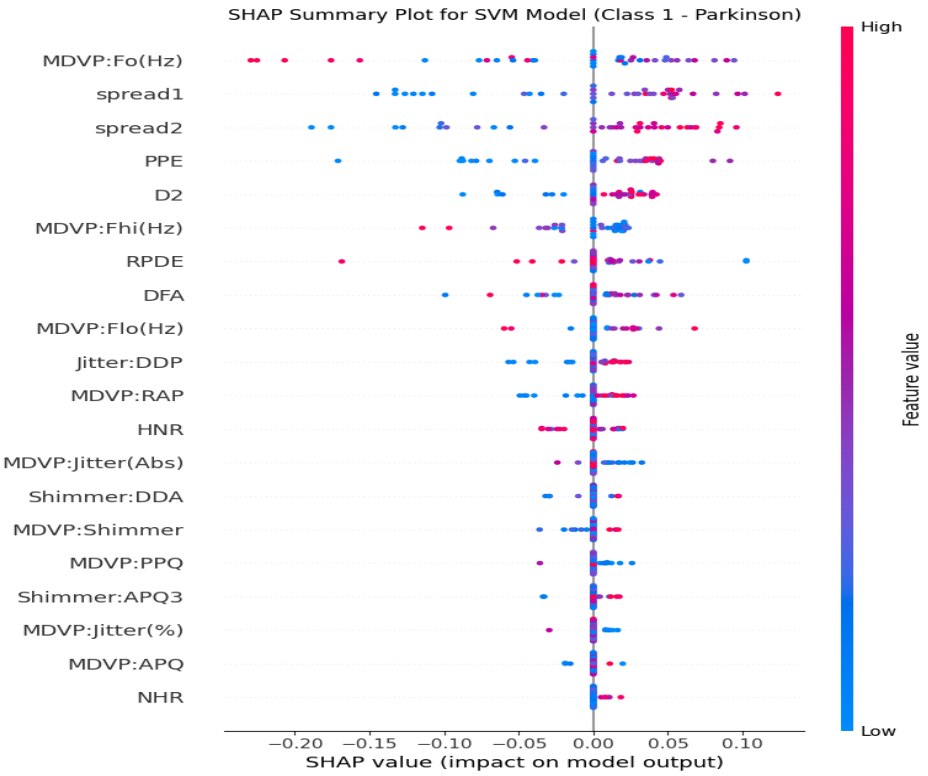

Figure 5. SHAP Summary Plot

The study's findings show that, while classifying Parkinson's illness using biomedical speech data, the SVM model with the RBF kernel outperformed Random Forest and Naive Bayes. SVM consistently outperformed the other models on several evaluation metrics, such as accuracy, recall, and AUC, demonstrating a strong ability to distinguish Parkinson's sufferers from healthy individuals. With an accuracy of 94.87%, recall of 96.5%, and AUC of 0.99, the optimized SVM model demonstrated its efficacy in biological classification tasks. These findings are consistent with recent studies demonstrating that SVM is among the best algorithms for voice-based Parkinson's disease detection. Several recent research have demonstrated that SVM provides good classification performance for biological voice data because it can handle high-dimensional and non-linear patterns. Ali et al. (2024) showed that SVM optimization combined with feature refinement significantly improved Parkinson's disease detection accuracy. Similarly, Neto (2024) reported that SVM remained highly competitive compared with ensemble and neural network approaches across multiple Parkinson's datasets. Ahammad et al. (2024) also demonstrated that SVM achieved reliable performance in speech-based Parkinson's classification, particularly when appropriate feature extraction and parameter optimization techniques were applied.

Furthermore, recent studies by Purba et al. (2025) and Putra and Pramartha (2025) highlighted that hyperparameter tuning plays a critical role in improving SVM generalization and classification performance in medical datasets. These findings corroborate the current work by indicating that optimized SVM models are still very relevant and effective for detecting Parkinson's disease utilizing biomedical speech data. The significance of parameter tuning and feature selection in biomedical classification was highlighted by research by Ali et al. (2024), which showed that SVM optimization combined with feature refinement considerably increased classification accuracy in

Parkinson's speech samples. Neto (2024) further reported that SVM remained highly competitive with ensemble and neural network models across multiple Parkinson's datasets, indicating its continued relevance despite rapid developments in deep learning approaches. Ahammad et al. (2024) revealed similar results, showing that SVM achieved consistent and reliable performance in speech-signal-based Parkinson's disease identification when supported by effective feature extraction and optimization techniques. Additionally, according to studies by Fernández-García et al. (2021) and Majda-Zdancewicz et al. (2024), biomedical voice features like jitter, shimmer, phonation stability, and prosodic characteristics are clinically relevant indicators of Parkinson's disease because they reflect vocal impairments like dysphonia and hypokinetic dysarthria. These findings support the present study, where features related to vocal instability and pitch variation played a significant role in classification performance.

Feature importance analysis revealed that MDVP:Fo(Hz), PPE, spread1, and spread2 were the most influential features in Parkinson's classification. These traits are clinically associated with vocal abnormalities that are common indicators of Parkinson's disease, such as dysarthria, hypophonia, and monopitch. The agreement between machine learning outcomes and clinical features indicates that voice-based biomedical analysis has significant promise as a non-invasive early detection method for Parkinson's disease.

The integration of explainable artificial intelligence (XAI), thorough performance evaluation, and systematic SVM hyperparameter optimization into a single framework for Parkinson's disease classification utilizing biological voice data is what makes this work novel. Unlike many previous studies that primarily concentrated on improving classification accuracy or comparing machine learning algorithms, this study uses Grid Search-based hyperparameter tuning with k-fold cross-validation to achieve optimal model generalization while concurrently applying Permutation Importance and SHAP analysis to improve interpretability.

Additionally, this work evaluates predictive performance using a range of measures, including accuracy, precision, recall, F1-score, specificity, and AUC, and demonstrates congruence between machine learning outputs and clinically significant speech abnormalities associated with Parkinson's disease. The proposed approach provides a more comprehensive and clinically interpretable framework for non-invasive Parkinson's disease identification when compared to earlier SVM-based studies. These techniques improved the model's interpretability and performance. The comparatively limited dataset size, the lack of testing in real-world noisy environments, and the lack of comparison with deep learning techniques like CNN and LSTM models are some of the study's other shortcomings. This work demonstrates that biomedical speech feature-based optimized SVM models offer a dependable and successful method for classifying Parkinson's illness. The suggested approach has a great chance of being used in early Parkinson's disease diagnostic decision support systems due to its excellent classification performance and clinically interpretable outcomes.

CONCLUSION

The results of the study demonstrate how well the enhanced Support Vector Machine (SVM) model classifies Parkinson's disease using biomedical voice data. Grid Search hyperparameter adjustment significantly improved model performance, while the RBF kernel provided the best configuration for handling non-linear data patterns. The SVM model demonstrated exceptional classification and generalization capabilities, outperforming Random Forest and Naive Bayes with an accuracy of 94.87%, recall of

96.55%, and AUC of 0.99. Confusion matrix and ROC curve analyses confirmed that SVM produced very low classification errors, particularly false negatives, which are critical in medical diagnosis. Feature importance analysis also revealed that voice-related features such as MDVP:Fo(Hz), PPE, spread1, and spread2 were the most influential indicators in detecting Parkinson's disease, and these findings were clinically consistent with vocal symptoms such as monopitch, dysarthria, and vocal tremor.

Despite the encouraging outcomes, this study still has a number of drawbacks, such as the short dataset size and the lack of testing in noisy real-world settings. It is advised that future studies make use of larger and more varied datasets, investigate deep learning techniques like CNN and LSTM for temporal voice pattern capture, and incorporate multimodal biological data like motion sensors and medical records. The practical use of early Parkinson's disease detection may be improved by the creation of telemedicine or mobile-based solutions. It is also advised to further enhance model interpretability using Explainable AI approaches, such as SHAP and LIME, to boost reliability and transparency in clinical applications.

ACKNOWLEDGMENT

The study paper's acknowledgments, which are included at the conclusion, should at the very least list the funding sources that made the work possible. Although there may be other recognizable contributors to the paper or the data it contains, their caliber of work may not warrant their inclusion as authors. If there is a research grant contract number, you may also include it.

REFERENCES

Ahammad, S. A., Sankaran, A., & Kumar, L. S. (2024). Detection of Parkinson's Disease using Machine Learning Algorithms from Speech Signals. *2024 International Conference on Signal Processing, Computation, Electronics, Power and Telecommunication (IConSCEPT)*, 1–6. https://doi.org/10.1109/IConSCEPT61884.2024.10627874

Asri Mulyani, Sarah Khoerunisa, & Dede Kurniadi. (2025). Perbandingan Kinerja Algoritma KNN dan SVM Menggunakan SMOTE untuk Klasifikasi Penyakit Diabetes. *Jurnal Nasional Teknik Elektro Dan Teknologi Informasi*, *14*(1), 25–34. https://doi.org/10.22146/jnteti.v14i1.15198

Bloem, B. R., Okun, M. S., & Klein, C. (2021). Parkinson's disease. *The Lancet*, *397*(10291), 2284–2303. https://doi.org/10.1016/S0140-6736(21)00218-X

Chang, H., Liu, B., Zong, Y., Lu, C., & Wang, X. (2023). EEG-Based Parkinson's Disease Recognition via Attention-Based Sparse Graph Convolutional Neural Network. *IEEE Journal of Biomedical and Health Informatics*, *27*(11), 5216–5224. https://doi.org/10.1109/JBHI.2023.3292452

Danis Rifa Nurqotimah, Naseh Khudori, A., & Siwi Pradini, R. (2024). Implementasi Algoritma Support Vector Machine (SVM) Untuk Klasifikasi Penyakit Stroke. *Journal of Applied Computer Science and Technology*, *5*(2), 179–185. https://doi.org/10.52158/jacost.v5i2.817

Fernández-García, S., Dumitrache, C. G., & González-López, J. A. (2021). Acoustic analysis of the voice in patients with Parkinson's disease and hypokinetic dysarthria. *Revista de Logopedia, Foniatría y Audiología*, *41*(3), 142–150.

https://doi.org/10.1016/j.rlfa.2020.04.002

Junus, C. Z. V., Tarno, T., & Kartikasari, P. (2023). Klasifikasi Menggunakan Metode Support Vector Machine dan Random Forest untuk Deteksi Awal Risiko Diabetes Melitus. *Jurnal Gaussian*, *11*(3), 386–396. https://doi.org/10.14710/j.gauss.11.3.386-396

Kent, R. D., & Vorperian, H. K. (2018). Static measurements of vowel formant frequencies and bandwidths: A review. *Journal of Communication Disorders*, *74*, 74–97. https://doi.org/10.1016/j.jcomdis.2018.05.004

LeCun, Y., Bengio, Y., & Hinton, G. (2015). Deep learning. *Nature*, *521*, 436–444. https://doi.org/10.1038/nature14539

Li, M., Ye, X., Huang, Z., Ye, L., & Chen, C. (2025). Global burden of Parkinson's disease from 1990 to 2021: a population-based study. *BMJ Open*, *15*(4), 1–10. https://doi.org/10.1136/bmjopen-2024-095610

Liu, V., Smith, D., & Yip, H. (2025). Prevalence and Treatment of Dysphonia in Parkinson's Disease: A Cross-Sectional National Database Study. *Laryngoscope Investigative Otolaryngology*, *10*(3), 1–8. https://doi.org/10.1002/lio2.70149

Majda-Zdancewicz, E., Potulska-Chromik, A., Nojszewska, M., & Kostera-Pruszczyk, A. (2024). Speech Signal Analysis in Patients with Parkinson's Disease, Taking into Account Phonation, Articulation, and Prosody of Speech. *Applied Sciences*, *14*(23), 1–30. https://doi.org/10.3390/app142311085

Mitchell, T. M. . (1997). *Machine Learning*. McGraw-Hill.

Mohammad Annan Makruf Mustofa, Sucipto, & Arie Nugroho. (2025). Penerapan Random Forest Untuk Deteksi Dini Penyakit Parkinson's Dengan Data Frekuensi Suara. *Jurnal Qua Teknika*, *15*(02), 25–37. https://doi.org/10.35457/quateknika.v15i02.4563

Orozco-Arroyave, J. R., Hönig, F., Arias-Londoño, J. D., Vargas-Bonilla, J. F., Daqrouq, K., Skodda, S., Rusz, J., & Nöth, E. (2016). Automatic detection of Parkinson's disease in running speech spoken in three different languages. *The Journal of the Acoustical Society of America*, *139*(1), 481–500. https://doi.org/10.1121/1.4939739

Postuma, R. B., Berg, D., Stern, M., Poewe, W., Olanow, C. W., Oertel, W., Obeso, J., Marek, K., Litvan, I., Lang, A. E., Halliday, G., Goetz, C. G., Gasser, T., Dubois, B., Chan, P., Bloem, B. R., Adler, C. H., & Deuschl, G. (2015). MDS clinical diagnostic criteria for Parkinson's disease. *Movement Disorders*, *30*(12), 1591–1601. https://doi.org/10.1002/mds.26424

Purba, M. E., Situmorang, A. Z., & Lubis, M. W. P. (2025). Perbandingan Pengklasifikasian Penyakit Parkinson Menggunakan Algoritma Naive Bayes, Random Forest, dan Regresi Logistik. *Jurnal Sifo Mikroskil*, *26*(1), 21–36. https://doi.org/10.55601/jsm.v26i1.1466

Putra, I. N. A. M., & Pramartha, C. (2025). Optimasi Hyperparameter Algoritma Support Vector Machine dalam Klasifikasi Penyakit β-Thalassemia. *Jurnal Nasional Teknologi Informasi Dan Aplikasinya*, *3(2)*, 283–293. https://ejournal2.unud.ac.id/index.php/jnatia/article/view/1460

Rahman, S., Hasan, M., Sarkar, A. K., & Khan, F. (2023). Classification of Parkinson's Disease using Speech Signal with Machine Learning and Deep Learning Approaches. *European Journal of Electrical Engineering and Computer Science*, *7*(2), 20–27. https://doi.org/10.24018/ejece.2023.7.2.488

Schröter, N., Groppa, S., Rijntjes, M., Gonzalez-Escamilla, G., Urbach, H., Jost, W. H., & Rau, A. (2025). Neuroimaging in advanced Parkinson's disease: insights into pathophysiology, biomarkers, and personalized therapies. *Journal of Neural Transmission*, *132*(11), 1655–1664. https://doi.org/10.1007/s00702-025-02942-y

Stemple, J. C. ., Roy, N., & Klaben, B. (2020). *Clinical voice pathology : theory and management*. Plural Publishing Inc.

Tysnes, O.-B., & Storstein, A. (2017). Epidemiology of Parkinson's disease. *Journal of Neural Transmission*, *124*(8), 901–905. https://doi.org/10.1007/s00702-017-1686-y

Wildah, S. K., Agustiani, S., S, M. R. R., Gata, W., & Nawawi, H. M. (2020). Deteksi Penyakit Alzheimer Menggunakan Algoritma Naïve Bayes Dan Correlation Based Feature Selection. *Jurnal Informatika*, *7*(2), 166–173. https://doi.org/10.31294/ji.v7i2.8226