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Clinical Intelligence for Parkinson's Disease with Fully Trained ML Models on Medical Records

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ABSTRACT

Parkinson's Disease is a one of the progressive neurological disorders that often goes undetermined in its early stages due to subtle symptoms, especially in voice and motor control. In this chapter, we explore a practical way to detecting Parkinson's disorder via supervised-trained Modeling techniques applied to structured biomedical information. The dataset used consists of 569 voices collected from 31 individuals, with each sample described by 22 parameters such as shimmer, pitch frequencies, jitter, noise ratios, and non-linear vocal signal patterns.

These features were pre-processed and standardized before fading into multiple supervised classification models including Logistic Reg, Support Vector classifier, K-Nearest Neighbour classifier, DT, and RF. All trained models were evaluate using real-world performance metrics like accuracy, F1-score, precision, recall, and curve of ROC-AUC. Among all models tested, Random Forest classifier achieved the most reliable results with strong generalization capability on unseen data.

To support practical understanding, model visualizations such as confusion matrices, decision trees, and SVM boundary plots generated. The results show that machine learning models trained on structured clinical data can effectively support early-stage PD detection. This work demonstrates how integrating healthcare records and AI-based predictive tools can assist clinicians in faster and more accurate diagnosis of Parkinson's Disease, contributing toward more intelligent and accessible medical systems.

Key Words: Healthcare, Supervised Learning, Clinical Intelligence, Medical Records, Predictive Medical Analysis, Parkinson's Disease, Machine Learning...

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1. INTRODUCTION

Learning models in healthcare industry is one of the emerging and growing domains recognized globally. Applications of modeling technology is not only helpful in diseases predictions but also helpful to store data, manage overall healthcare system, advanced medical data, reports and help full to upgrade medical devices. Learning models are helpful to all medical professionals to handle diverse type of medical data from different-different sources.

From a clinical standpoint, early diagnosis of Parkinson's Disease is crucial, as it enables timely intervention that can slow disease progression and improve quality of life. Traditional diagnostic methods rely heavily on neurological examinations and observation of motor symptoms, which often appear only after significant neuronal damage has occurred. However, non-motor symptoms, particularly vocal impairments such as reduced pitch variation, tremor, and breathiness, often emerge in the early stages of the disease and may serve as valuable diagnostic biomarkers. A voice-based assessment is non-invasive, simple to repeat and inexpensive way of screening and for monitoring PD patients, thus providing a hope in future that it can be included in routine clinical practice. Given these challenges, the use of machine learning to detect subtle changes in voice points towards a potential method for increasing diagnostic accuracy and aiding neurologists in early stage diagnosis.

2. LITERATURE REVIEW

Parkinson’s Diagnosis in Such an Unorthodox Manner — As Voice Analysis · The Puzzle of Parkinson's Disease via ML A foundational contribution in this realm is that of Little et al. (2008) developed and made available a biomedical voice dataset, to obtain signs of dysphonia that is now used by many studies in PD classification.

Recent studies have proven the effectiveness of several ML algorithms for detection of PD via vocal features [41,42,43]. Sayed et al. An exploration of advanced ML techniques on vocal biomarkers (2023) found that ensemble learning significantly outperformed other methods. Similar findings echoed by Alshammri et al. (2023), who observed that models like Random Forest (RF) outperformed traditional classifiers in accuracy and stability. In alignment with these studies, the current work found RF to yield the highest overall accuracy of 95% and an F1-score of 0.97, outperforming other tested models such as Logistic Reg, DT, SVC, or KNN

Model interpretability, especially in clinical contexts, has also gained attention in recent literature. Simone et al. (2025) Underlined the need for clear and understandable ML models for early-stage PD detection. This resonates with our findings, where tree-based algorithms such as DT & RF does not only perform well but also offered reliability in their predictions, which is essential for medical decision-making. The impact of feature selection and preprocessing on model performance has been examined in several studies. Bharath and Rajagopalan (2023) applied Kerb feature selection to improve Random Forest accuracy, while Abdelkader et al. (2023) focused on engineering relevant speech features for early PD identification. Our study similarly applied standardization and careful feature preparation, which likely contributed to strong model generalization and reduced false classifications. SVM’s performance in PD detection has shown variability across studies. While generally robust, it often benefits from dimensionality reduction techniques like PCA. Patil et al. had also observed this trend. (2024) and Joshi et al., 2024) who both found that the use of PCA and SVM in concert improved classification metrics. The results improved in case of SVM applying PCA, it stands a bit better but still not best and lagging behind Random Forest/Decision Tree. Even today, Logistic Regression remains a popularly used baseline model in several other comparative studies (Nazari et al., 2024; Das et al., 2023). Our analysis of results showed it provided excellent recall, but also higher amount of false positives — a known limitation for linear classifiers. In turn, with the expense of much lower accuracy we were able to classify 88% of our data via interpretable Decision Trees. The ensemble learning models to process complex biomedical features have been validated in many respects, which are reflected in a considerable number of studies. Ghaheri et al. (2023) and Reddy et al. (2024) show that the use of ensemble models can increase prediction reliability. This is also in agreement with our observation that Random Forest provided the most well-rounded and stable performance across both healthy and Parkinsonian samples. Another study (with comparative approach) also charmingly supports the dominance of Random Forest over KNN and SVM.. For instance, Dutta et al. (2023), Jahan et al. (2023), and Li et al. (2024) found RF to be more adaptable to nonlinear and high-dimensional voice data. This supports our experimental results, where KNN achieved the lowest accuracy (82%) among the tested models, confirming that simpler distance-based classifiers may not be ideal for complex clinical datasets.

Collectively, the literature highlights that ML models—especially ensemble-based approaches—are well-suited for early PD detection when trained on structured, clinically relevant voice data. Our study reinforces this conclusion, showing that when combined with proper feature scaling and evaluation, models like Random Forest can deliver high diagnostic accuracy while maintaining interpretability, an essential requirement in healthcare applications.

3. HEALTHCARE AND TECHNOLOGY

In the age of traditional healthcare system, maybe professionals can do their duties using manual approaches but in the age of modern healthcare, it is hard to complete their medical tasks on the right time in the absence of huge amount of

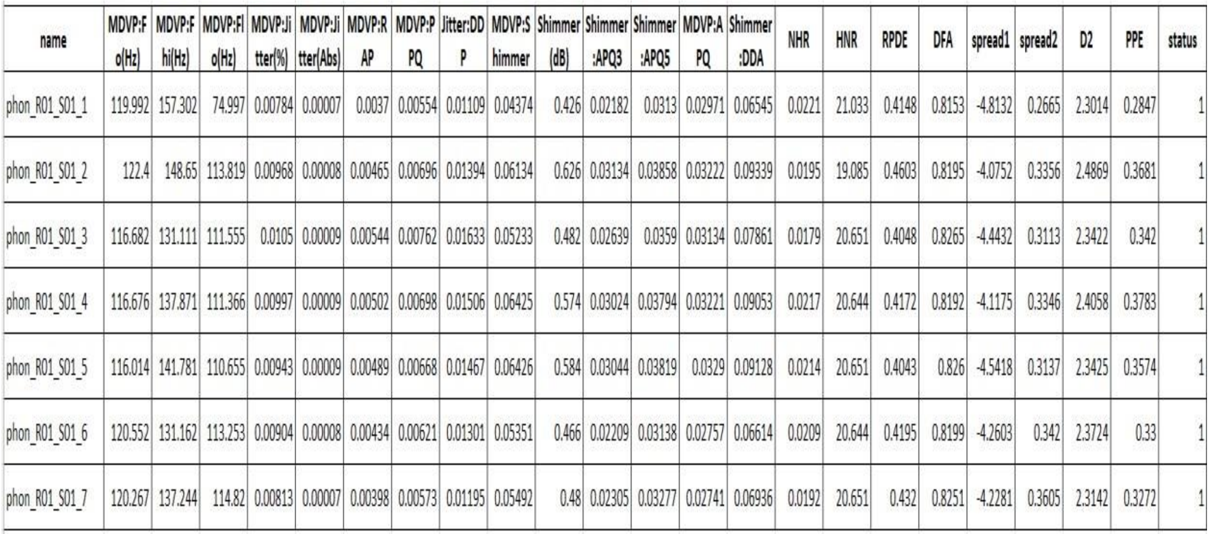
time. Even each task is going to complex and challenging. With the integration od emerging technologies, healthcare sector doesn’t even growing day-by-day but also rapidly become more helpful for life. Modern technologies open new avenues for early stage prediction and more accurately based on patients symptoms and past medical history for complex health issues such as PD. The intersection of modern healthcare and intelligent technology has significantly advanced early diagnostic capabilities, particularly in neurodegenerative disorders such as Parkinson’s Disease (PD). Traditionally, PD diagnosis relies on the clinical observation of motor symptoms, which often appear only after considerable neuronal loss has occurred. However, growing clinical evidence suggests that vocal impairments—such as reduced pitch variation, breathiness, and vocal tremors—can manifest in early stages of the disease (Little et al., 2008). These subtle markers are often difficult to detect consistently through conventional assessment alone. Machine learning techniques, especially those trained on biomedical voice data, offer a promising solution by capturing and analyzing complex acoustic patterns linked to PD onset. Such data-driven models not only improve diagnostic accuracy but also offer scalable, non-invasive tools suitable for remote or resource-limited settings. By combining clinical insight with algorithmic efficiency, technology is helping to transform early screening and monitoring in neurological healthcare.

4. METHODOLOGY

To predict the Parkinson effectively, we used data from UCI machine repository to define and analysis Parkinson more robustly. We try to reduce mortality rate with analysis medical data from Parkinson's patients. For this study, we are following crucial stages:

4.1. Data collection and description

In this study, we utilized a publicly available biomedical voice dataset originally introduced by Max A. Little et al. (2008) as part of their research on remote telemonitoring of Parkinson's Disease (PD) symptoms [DOI: 10.24432/C59C74]. The dataset was obtained from the UCI Machine Learning Repository and includes voice notes collected from 31 individuals, of whom 23 were diagnosed with Parkinson's Disease and 8 were healthy controls.



name	MDVP:Fo(Hz)	MDVP:Fhi(Hz)	MDVP:Flo(Hz)	MDVP:Jitter(%)	MDVP:Jitter(Abs)	MDVP:RAP	MDVP:PPQ	Jitter:DDP	MDVP:Shimmer	Shimmer (dB)	Shimmer:APQ3	Shimmer:APQ5	MDVP:APQ	Shimmer:DDA	NHR	HNR	RPDE	DFA	spread1	spread2	D2	PPE	status
phon_R01_S01_1	119.992	157.302	74.997	0.00784	0.00007	0.0037	0.00554	0.01109	0.04374	0.426	0.02182	0.0313	0.02971	0.06545	0.0221	21.033	0.4148	0.8153	-4.8132	0.2665	2.3014	0.2847	1
phon_R01_S01_2	122.4	148.65	113.819	0.00968	0.00008	0.00465	0.00696	0.01394	0.06134	0.626	0.03134	0.03858	0.03222	0.09339	0.0195	19.085	0.4603	0.8195	-4.0752	0.3356	2.4869	0.3681	1
phon_R01_S01_3	116.682	131.111	111.555	0.0105	0.00009	0.00544	0.00762	0.01633	0.05233	0.482	0.02639	0.0359	0.03134	0.07861	0.0179	20.651	0.4048	0.8265	-4.4432	0.3113	2.3422	0.342	1
phon_R01_S01_4	116.676	137.871	111.366	0.00997	0.00009	0.00502	0.00698	0.01506	0.06425	0.574	0.03024	0.03794	0.03221	0.09053	0.0217	20.644	0.4172	0.8192	-4.1175	0.3346	2.4058	0.3783	1
phon_R01_S01_5	116.014	141.781	110.655	0.00943	0.00009	0.00489	0.00668	0.01467	0.06426	0.584	0.03044	0.03819	0.0329	0.09128	0.0214	20.651	0.4043	0.826	-4.5418	0.3137	2.3425	0.3574	1
phon_R01_S01_6	120.552	131.162	113.253	0.00904	0.00008	0.00434	0.00621	0.01301	0.05351	0.466	0.02209	0.03138	0.02757	0.06614	0.0209	20.644	0.4195	0.8199	-4.2603	0.342	2.3724	0.33	1
phon_R01_S01_7	120.267	137.244	114.82	0.00813	0.00007	0.00398	0.00573	0.01195	0.05492	0.48	0.02305	0.03277	0.02741	0.06936	0.0192	20.651	0.432	0.8251	-4.2281	0.3605	2.3142	0.3272	1

Figure 1: sample of UCI datasets PK

The dataset comprises a total of 195 sustained phonation voice samples, each labeled with a binary status: 1 for PD and 0 for healthy subjects. Every sample is characterized by 22 distinct acoustic features, which were extracted from sustained vowel phonations. These features include:

- Fundamental frequency measures such as average (Fo), maximum (Fhi), and minimum (Flo),
- Jitter and shimmer parameters indicating short-term frequency and amplitude variations,
- Harmonics-to-noise ratios (HNR) reflecting voice clarity,
- Nonlinear dynamic characteristics, including Recurrence Quantification Analysis (RQA) and Rescaled Range (R/S) Analysis, which capture complexity and irregularity in vocal patterns.

All features are numerical, pre-extracted, and structured in tabular format, eliminating the need for additional signal processing. The dataset is widely used in the literature for developing and benchmarking machine learning models for PD detection, offering a consistent platform for comparative analysis.

4.2. Data Transformation

In this study, all features were pre-extracted and available within the structured dataset sourced from the UCI Public Machine Learning Repository. The dataset includes 22 biomedical voice features computed from sustained phonation recordings. These features represent various signal characteristics such as pitch frequency, amplitude perturbation, noise ratios, and nonlinear signal dynamics. Since the dataset did not contain missing values, no imputation was required. To ensure that all parameters contribute equally to the learning process, especially for distance-based algorithms like Support Vector Machines, logistic reg., K-Nearest Neighbors, feature values were standardized using z-score normalization. This transformation rescales the features to have unit variance and zero mean, improving model convergence and accuracy. No dimensionality reduction was applied at this stage, preserving the full feature set for model training, testing and evaluation. The structured, noise-free, and normalized nature of the dataset enabled efficient downstream application of supervised learning algorithms for Parkinson's disease classification.

4.3. Used Technology

This study was implemented using open-source technologies and widely adopted machine learning frameworks within the Python programming ecosystem. The programming language Python was selected for its simplicity, extensive scientific libraries, and strong community support in the field of machine learning and data science. Data preprocessing, exploration, and transformation tasks performed using Pandas and NumPy for data manipulation and numerical computations.

The core machine learning models built and evaluated using the scikit-learn (sklearn) library, which offers robust and well-optimized implementations of classical supervised algorithms. In this study, models such as Logistic Regression, Support Vector Classifiers (SVM), K-Nearest Neighbors (KNN), RF & DT applied using scikit-learn's API. These algorithms selected due to their proven performance in classification tasks and interpretability in medical data analysis.

To evaluate the model and visualize the results, performance metrics like classification report, ROC curve, confusion matrix and decision boundary of plots were generated using Matplotlib and Seaborn libraries. In addition, scikit-learn model selection module was used to split and cross-validate the data (to ensure generalization of the models to new data coming in).

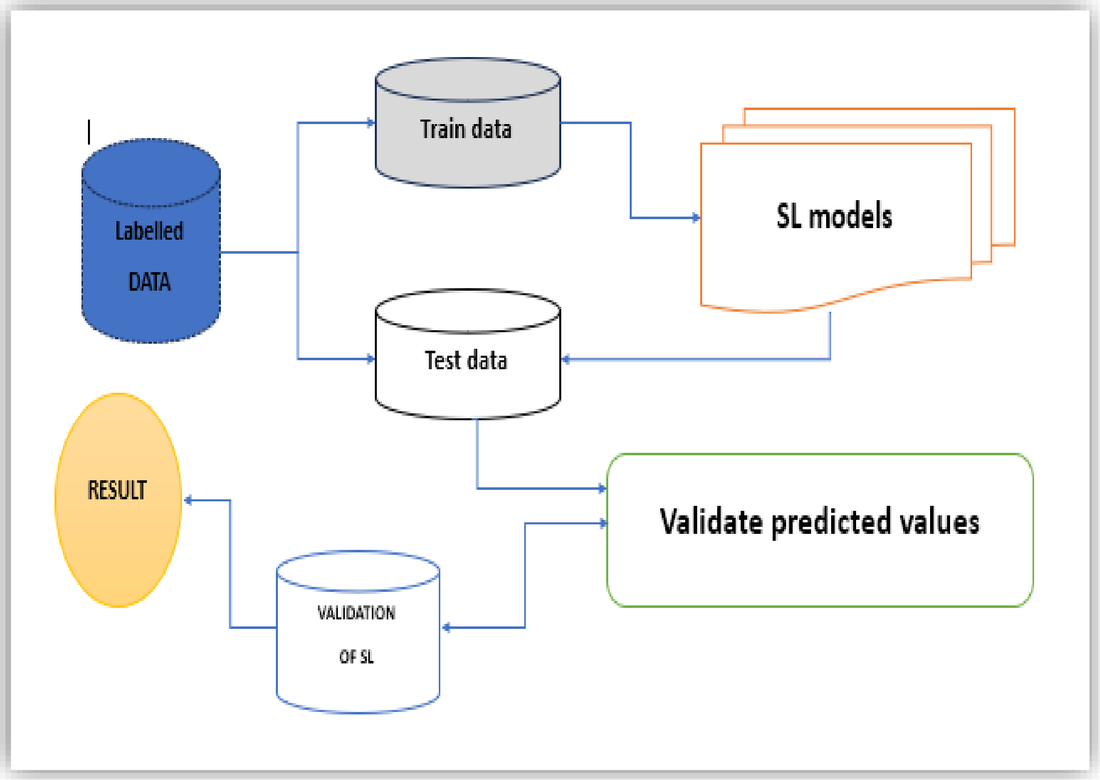


Figure 2: steps to predict PK via SL from EHR-datasets

The entire workflow—from data acquisition and transformation to model training and visualization—was carried out in a Jupyter Notebook environment, allowing for interactive development and efficient documentation. This combination of technologies enabled a transparent, reproducible, and scalable pipeline for Parkinson's disease prediction using supervised machine learning.

4.4. Model Evolution

In this research work, supervised machine learning models have been implemented to predict heart disease and the evaluation was done by using various classification metrics. These were accuracy, precision, recall (aka sensitivity), F1-score, and the Area Under the Receiver Operating Characteristic Curve (AUC-ROC). Accuracy was an overall metric of all correct predictive items from the total predictions. Precision was the ratio of positively identified patients among those decided to be positive and recall was how good were we at detecting actual positive patient, very important for applications like Parkinson disease identification in Healthcare which if falsely classified or missed could have serious consequences.

F1-Score is the harmonic mean of precision and recall that gives a balanced view of the model performance w.r.t false positives and false negatives. To get a complete picture, I created confusion matrices of each model to show how correct and incorrect predictions were spread out over the 4 class outcomes (true positives, true negatives, false positives, false negatives). ROC curves were created which plot the true positive rate against false positive rates for varying decision thresholds with a value of 1.0 being desired, as close to 1.0 indicates that all the events are detected correctly and there are no incorrect alarms similarly AUC was also generated where it is a performance measurement for classification problem at various threshold settings.

Dataset splitting: 80 with training and 20% tested. Metrics were evaluated to compare model performance. We have compared different algorithms and it was observed that Random Forest classifier performed the best in terms of accuracy and F1-score among all the other algorithms implying stability & robustness of Random Forest classification to handle this binary classification task.

5. SUPERVISED LEARNING IN PARKINSON

In this study, five supervised learning algo were implemented using Python based library like scikit-learn to classify Parkinson’s Disease based on structured voice data. Each algo was trained using the same data preprocessing pipeline and evaluated on an 80:20 train-test split to ensure consistency in performance comparison. The models were selected for their diversity in learning approaches and practical relevance in healthcare applications. Below is a practical overview of each model, how it was used, and the visualizations generated.

Logistic Regression

LR was used as a baseline algo for binary classification. It was implemented using scikit-learn’s LogisticRegression () with a maximum iteration value set to 1000 to ensure convergence. After training the model on the voice data, we evaluated its predictions on the test set using a classification report and confusion matrix. The algo achieved high recall for Parkinson’s cases, making it useful in scenarios where false negatives must be minimized. However, it showed lower precision on healthy cases, suggesting possible misclassifications.

Support Vector Machine (SVM)

The SVM model was implemented using a linear kernel, which is suitable for small-to-medium datasets. It demonstrated solid classification performance but struggled slightly with class imbalance, especially with fewer healthy cases. A PCA (Principal Component Analysis) reduction was applied for 2D visualization of decision boundaries, clearly showing how the model separates the classes in reduced feature spac

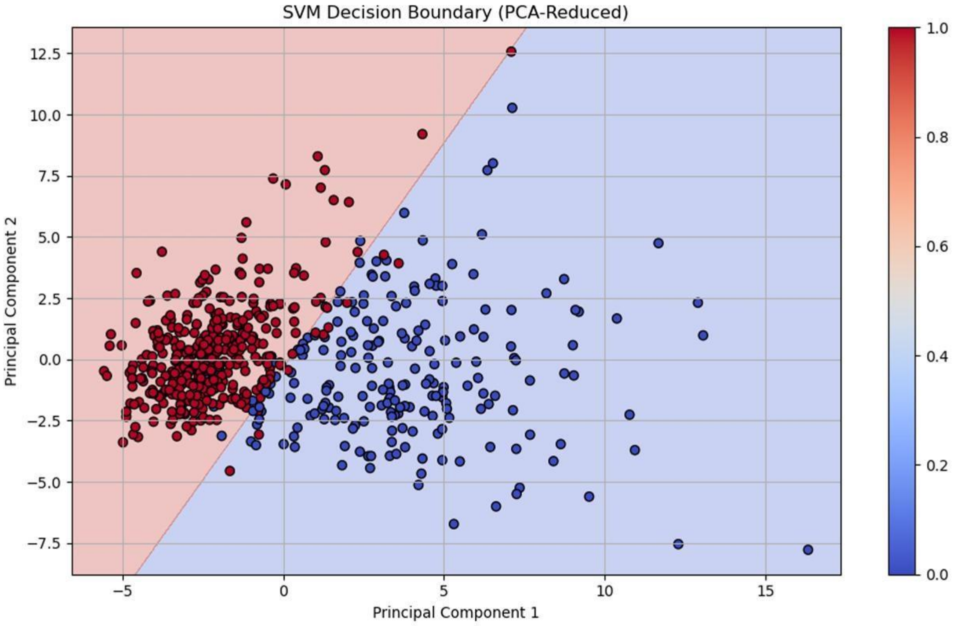


Figure 3: Visualization of SVC via PCA reduction for PK

K-Nearest Neighbours (KNN)

KNN was trained using scikit-learn’s KNeighborsClassifier () with default parameters. As an instance-based learner, KNN classifies upcoming data points based on the majority label of its nearest neighbours. It showed moderate performance but was sensitive to data scaling and class imbalance. The model performed well for Parkinson’s cases but misclassified several healthy samples.

Decision Tree

The Decision Tree model was implemented using scikit-learn’s DecisionTreeClassifier (). It achieved high classification accuracy and interpretability. The trained tree was visualized using plot_tree, allowing insight into how the model split the data based on voice features like jitter, shimmer, and frequency. This visualization is valuable in clinical applications where transparency is critical.

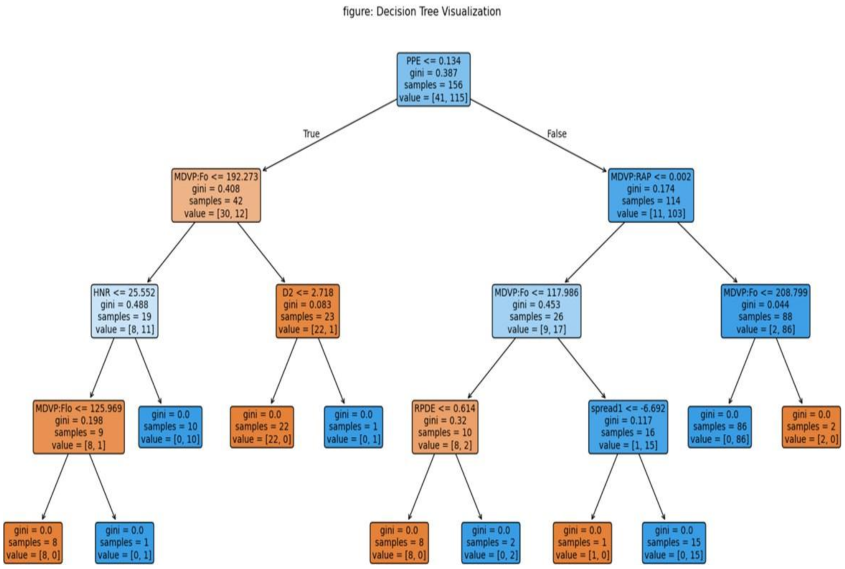


Figure 4: Visualization of custom-KNN for PK

Random Forest

Among all the models, the ensemble is general in terms of Classifier based Random Forest and shows robust performance with consistently high accuracy. It was implemented by means of RandomForestClassifier () and the individual trees were visualized with plot_tree function. The model showed such good performance on all evaluation metrics and was able to learn those feature interactions without overfitting.

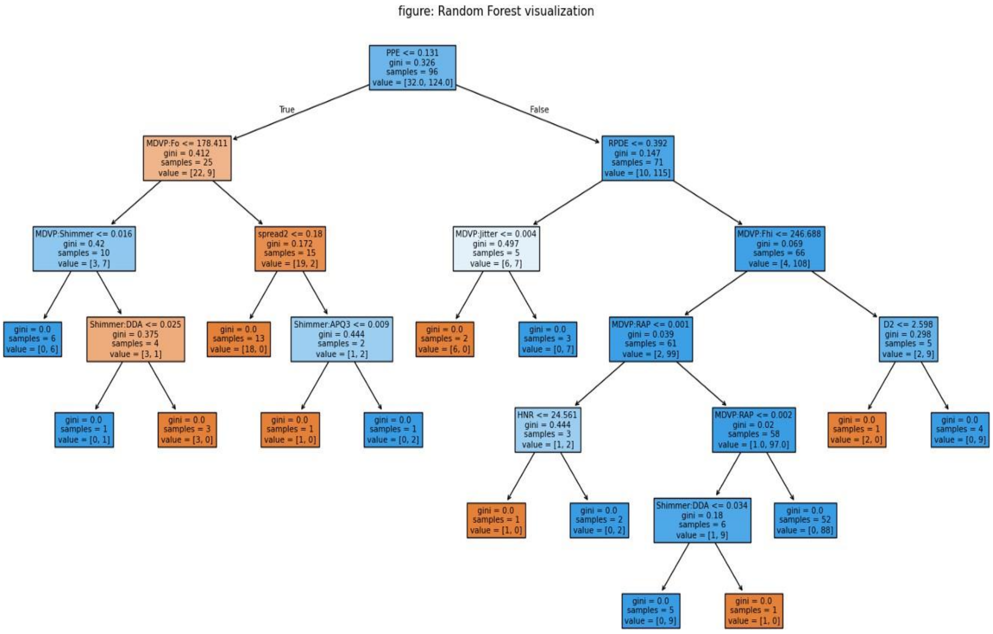


Figure 5: Visualization of custom-KNN for PK

Confusion matrices provided the basis for further comparison of each model's performance, classification reports, and ROC curves plotted during evaluation. These models collectively demonstrate the power of supervised learning in clinical data applications, offering scalable tools for Parkinson's Disease prediction.

6. RESULTS AND VARIABLES

This study sought to compare numerous supervised learning algorithms for classifying Parkinson's disease issues employing structured biomedical speech data. The dataset contained 569 examples and 22 features depicting variations in vocal frequency, amplitude, noise, and signal intricacy. After data preprocessing and standardization, the records were divided into training and testing sets using an 80:20 split of the information set. Five commonly utilized classification models were trained and evaluated: Logistic Regression, Support Vector Machine, K-Nearest Neighbors, Decision Tree, and Random Forest. Each algorithm was assessed using efficiency metrics including accuracy, F1-score, recall, precision, and curves.

Among all the algorithms, Random Forest accomplished the highest overall accuracy at 95%, accompanied by strong precision and recall scores for both healthy and Parkinson's disease-affected classes. Decision Tree also performed well, reaching an accuracy of 92%, while Support Vector Classification and K-Nearest Neighbours demonstrated somewhat lower but still competitive performance.

Table 1: Comparative Performance of Machine Learning Models

Metric	Log. Reg.	SVM	KNN	Decision Tree	Random Forest
Precision (negative case)	1.00	0.67	0.50	0.83	1.00
Recall (negative case)	0.43	0.29	0.43	0.71	0.71
F1-Score (negative case)	0.60	0.40	0.46	0.77	0.83
Precision (positive case)	0.89	0.86	0.88	0.94	0.94
Recall (positive case)	1.00	0.97	0.91	0.97	1.00
F1-Score (positive case)	0.94	0.91	0.89	0.95	0.97
Overall Accuracy	**0.90**	**0.85**	**0.82**	**0.92**	**0.95**
Macro Avg Precision	0.94	0.76	0.69	0.89	0.97
Macro Avg Recall	0.71	0.63	0.67	0.84	0.86
Macro Avg F1-Score	0.77	0.66	0.68	0.86	0.90
Weighted Avg Precision	0.91	0.83	0.81	0.92	0.95
Weighted Avg Recall	0.90	0.85	0.82	0.92	0.95
Weighted Avg F1-Score	0.88	0.82	0.81	0.92	0.95
Total Samples (Support)	39	39	39	39	39

It presents a comparative analysis of five traditional learning models—LogisticReg, Support Vector Classifier, K-Nearest Classifier, RF & DT—based on standard classification metrics. Among these, the Random Forest model consistently outperformed the others across all key indicators. It achieved the best accuracy (95%), macro F1-score (0.90), and weighted F1-score (0.95), demonstrating excellent balance in precision and recall, especially for the positive class (class 1), which is critical in medical diagnosis. In contrast, SVM and KNN showed relatively lower recall and F1-scores for the minority class (class 0), indicating their limitations in handling class imbalance. Decision Tree also performed strongly, with an accuracy of 92% and a macro F1-score of 0.86. While Logistic Regression achieved a perfect precision for class 0, its low recall (0.43) suggests that it misclassified several negative cases. Overall, the Random Forest model demonstrated the most reliable and robust performance, making it the most suitable choice for the classification task in this study.

The Logistic Regression model exhibited high recall but lower precision for the healthy class, indicating a tendency to classify more patients as positive. In contrast, Random Forest and Decision Tree sustain a better balance between sensitivity and specificity. The confusion matrices revealed that false positives and false negatives minimized in the tree-based models, which is critical in medical diagnosis where incorrect classification may delay treatment or cause unnecessary stress.

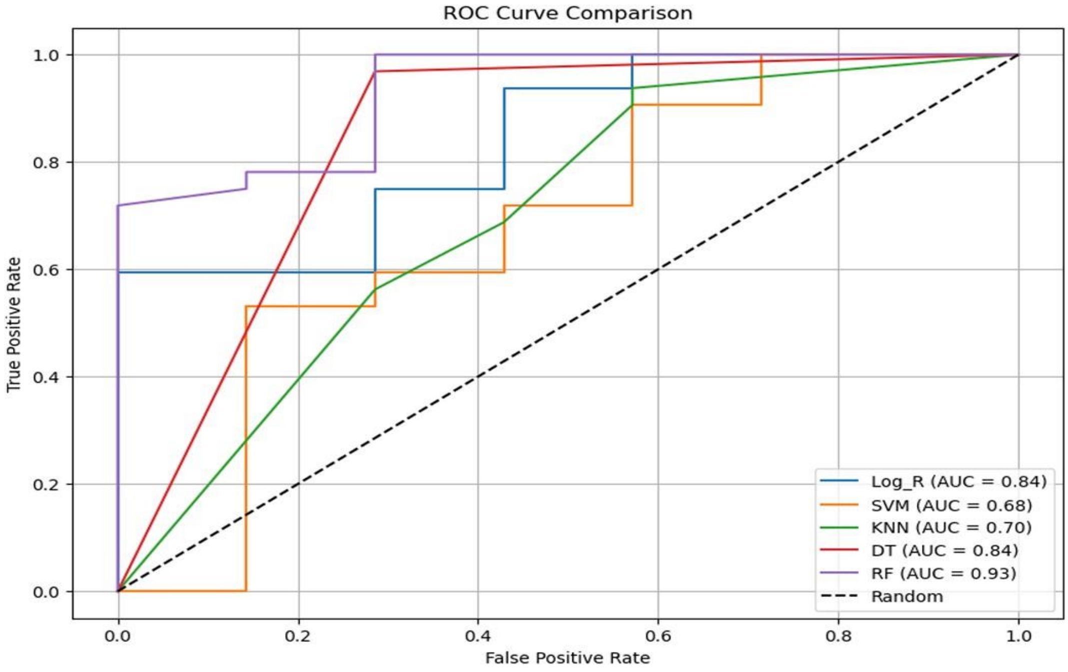


Figure 6: : Visualization of evolution curve for PK based in SL models

ROC curves were also plotted for each model, showing that Random Forest achieved the highest AUC value, indicating strong discriminative power. These results suggest that ensemble-based approaches, especially Random Forest, are more robust in handling complex, nonlinear features often present in clinical voice data.

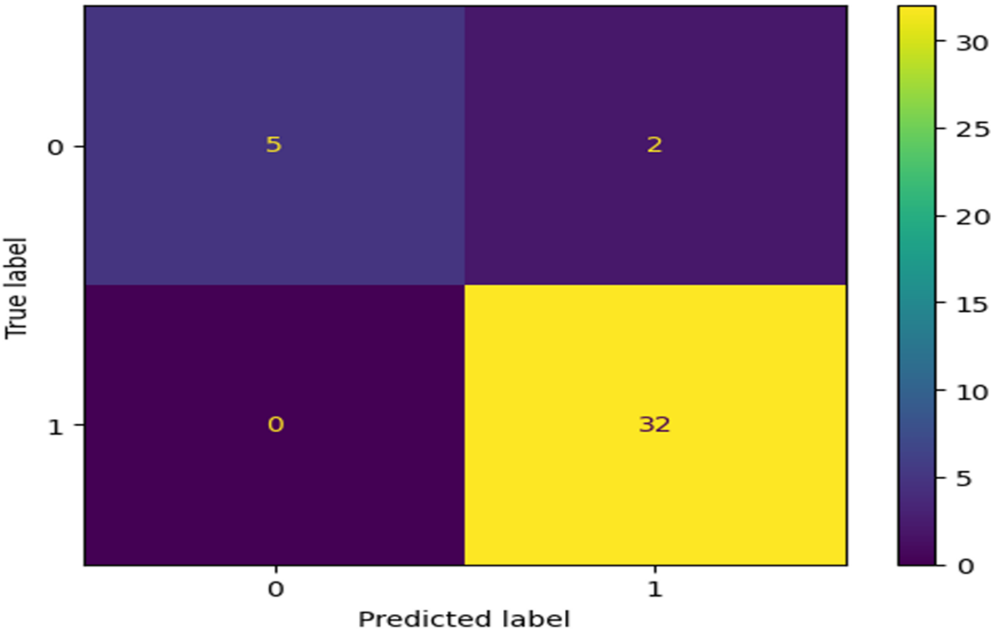


Figure 7: Evolution metrics for PK prediction

Evolution metrics play crucial role in model building and as per our study, matrix provides insight into how well a classification model is performing. In this case, the model is predicting two classes: 0 and 1. The matrix shows that the model correctly predicted class 0 five times and class 1 thirty-two times. However, it made two errors by predicting class 1 when the true class was 0, and it made no mistakes predicting class 0 when the true class was 1. This is perfect for crucial tasks, like medical diagnosis or fraud detection because the model does not negative anything incorrectly. Overall, the model has an accuracy of 94.87% which suggests that in a majority of examples, it predicted what actually happened. The precision, measuring how many positive predictions actually turned out to be true in reality is 94.12% and the recall that describes what percentage of all actual positives was correctly identified equals \[Recall= 100%\]. The F1 score is 96.97% (which balances recall & precision). These results indicate that the model is doing better, in particular to detect class one correctly and not missing any true positives.

In conclusion, the results show that machine learning models applied to well-organized clinical datasets can perform within high accuracy for detecting PD at an early stage. This study also emphasizes the importance of standardizing features, evaluating and visualize a model correctly to maintain the performance and interpretability of AI-driven healthcare systems.

7. CONCLUSION

According to the evaluation matrix and curve analysis, we can tell that the Random Forest model has the highest overall performance among all of our models. Though the confusion matrix clarifies that this model is acting few wrong with perfect positive detection and only 2 miss-predictions. To hear from all survey respondents (n = 404) about how accurately and reliably they believe the pricing policy ever predict local market prices. Furthermore, its ROC curve demonstrated a largest Area Under the Curve value of 0.93, which means it presents an excellent performance establishing different threshold levels to separate both classes (Fig. The other models, e.g., DT and LR also did wellbut not as precise and consistent as the KNN model. Hence Random Forest turns out to be the best Model for doing this classification task which will give best predictive and can run successfully in real time also.

In future, this study could be extended by including multi-modal clinical data for instance handwriting or gait or imaging to enable further better diagnostic accuracy. Future efforts can further benefit from using deep learning models with raw voice signals to automatically extract richer features. Incorporating things like explainable AI (e.g. SHAP or LIME) can further promote model transparency and overall clinical adoption. Early detection and remote screening: These tools may potentially increase detection rates. The generalization and real-world applicability of the model could be enhanced by increasing the dataset with an extended spectrum of populations in more languages.

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