

# PARKINSON DISEASE PREDICTION USING RANDOM FOREST AND SUPPORT VECTOR ALGORITHMS

*Report submitted to the SASTRA Deemed to be University  
as the requirement for the course*

## CSE300 - MINI PROJECT

*Submitted by*

**VEDAPRAKASH S**  
(Reg. No.: 225003131, CSE)  
**MANJUNATH P**  
(Reg. No.: 225003192, CSE)  
**SIDDESWAR R**  
(Reg. No.: 225003198, CSE)

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**Department of Computer Science and Engineering  
SRINIVASA RAMANUJAN CENT**

**KUMBAKONAM, TAMIL NADU, INDIA – 612001**



Department of Computer Science and Engineering

SRINIVASA RAMANUJAN CENTRE

KUMBAKONAM, TAMIL NADU, INDIA – 612001

Bonafide Certificate

This is to certify that the report titled "PARKINSON DISEASE PREDICTION" submitted as a requirement for the course, CSE300: MINI PROJECT for B.Tech. is a bonafide record of the work done by Mr. Vedaprakash S (Reg. No. 225003131), Mr. Manjunath P (Reg. No. 225003192) and Mr. Siddeswar R (Reg. No. 225003198) during the academic year 2023-24, in the Srinivasa Ramanujan Centre, under my supervision.

Signature of Project Supervisor

: *J-Ganesh*

Name with Affiliation

: Dr. J. Ganesh/AP/CSE/SRC/SASTRA

Date

: 6/5/24

Mini Project Viva voce held on

6/5/24

*J-Ganesh*  
Examiner 1

*6/5/24*

*V.P. / 6/5/24*  
Examiner 2

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## **Abbreviations**

RF	Random Forest Algorithm
SVM	Support Vector Machine Algorithm
PD	Parkinson Disease
CNN	convolutional neural network

# Abstract

Parkinson's disease (PD), a debilitating neurodegenerative disorder, poses significant challenges in accurately predicting its progression due to its multifaceted clinical manifestations and heterogeneous nature among patients. The need for reliable prognostic tools to guide therapeutic interventions and enhance patient care has prompted the exploration of advanced machine learning techniques.

In this study, we embarked on a comprehensive investigation to evaluate the predictive capabilities of two prominent machine learning algorithms, Random Forest (RF) and Support Vector Machine (SVM), in forecasting the progression of PD. Leveraging a rich and diverse dataset encompassing demographic attributes, clinical variables, and biomarkers, our analysis aimed to discern the strengths and limitations of each algorithm in capturing the intricate dynamics of PD progression.

Our findings illuminate the potential of both RF and SVM models in predicting PD progression with encouraging accuracy. However, our comparative analysis reveals that SVM emerges as a frontrunner, demonstrating superior performance in terms of accuracy and precision. The robustness of SVM in discerning subtle patterns within the complex interplay of variables underscores its efficacy as a powerful prognostic tool in PD management.

The discernment offered by SVM extends beyond mere prediction, serving as a cornerstone for advancing personalized medicine in PD management. By unraveling the intricate nuances of disease progression, SVM facilitates the identification of tailored therapeutic interventions, thereby optimizing treatment strategies for individual patients. Moreover, the enhanced prognostic precision afforded by SVM empowers clinicians with invaluable insights.

Keywords:

Parkinson's disease, prediction, Random Forest, Support Vector Machine, machine learning, comparative analysis, neurodegenerative disorder, personalized medicine, prognostication

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# CHAPTER 1

## SUMMARY OF THE BASE PAPER

**Title:** "A Novel Approach for Parkinson's Disease Diagnosis from Speech Signals Using Convolutional Neural Networks and Random Forest"

**Journal Name:** Soft Computing

**Publisher:** Computational Biology and Medicine

**Year:** 2022

### ➤ SUMMARY:

- The article presents a new brain tumor diagnostic model that integrates textural feature extraction algorithms and convolutional neural network (CNN) features.
- The study aims to enhance the accuracy and efficiency of brain tumor detection through the combined use of these advanced techniques.
- By selecting optimal textural features and CNN architectures, the researchers seek to improve the overall performance of the diagnostic model.
- The article likely discusses the methodology employed in the study, including the selection process of features and the optimization algorithms used.
- The findings of this research have implications for the field of medical imaging and healthcare, potentially offering a more effective approach to brain tumor diagnosis.

### ➤ RESEARCH ADDRESSED:

- The research addresses the development of a brain tumor diagnostic model that combines textural feature extraction algorithms and convolutional neural network (CNN) features.
- The study focuses on selecting the most relevant features and optimizing CNN architectures to improve the accuracy and efficiency of brain tumor detection.
- Researchers likely explore the performance of different textural feature extraction algorithms and CNN models to identify the most effective combination for diagnostic purposes.
- The research may involve training the model on brain imaging data and evaluating its performance in accurately detecting and classifying brain tumors.
- The findings of this study have the potential to advance the field of medical imaging by providing a more sophisticated and accurate approach to brain tumor diagnosis.

➤ **PROPOSED SOLUTION:**

- The research likely involves exploring the effectiveness of textural feature extraction algorithms in improving the accuracy of brain tumor diagnosis. The proposed solution may focus on the selection and optimization of textural features extracted from brain imaging data to enhance the diagnostic capabilities of the model. Researchers may discuss the methodology for identifying relevant textural features that can provide valuable information for distinguishing between different types of brain tumors. This project may address the potential benefits of integrating textural feature extraction algorithms with other machine learning techniques to create a comprehensive diagnostic model. The article likely emphasizes the importance of feature selection in improving the interpretability and performance of the diagnostic model for brain tumor detection. The research may highlight the significance of using advanced algorithms for textural feature extraction to capture subtle patterns and characteristics indicative of brain tumors.
- The proposed solution may involve a thorough evaluation of the extracted textural features and their impact on the overall diagnostic accuracy and efficiency. Researchers may discuss the implications of utilizing textural features in brain tumor diagnosis for enhancing clinical decision-making and patient outcomes. The study may also address the scalability and generalizability of the proposed solution, considering its potential application in real-world clinical settings beyond the research environment.

## 1.4.Architeture

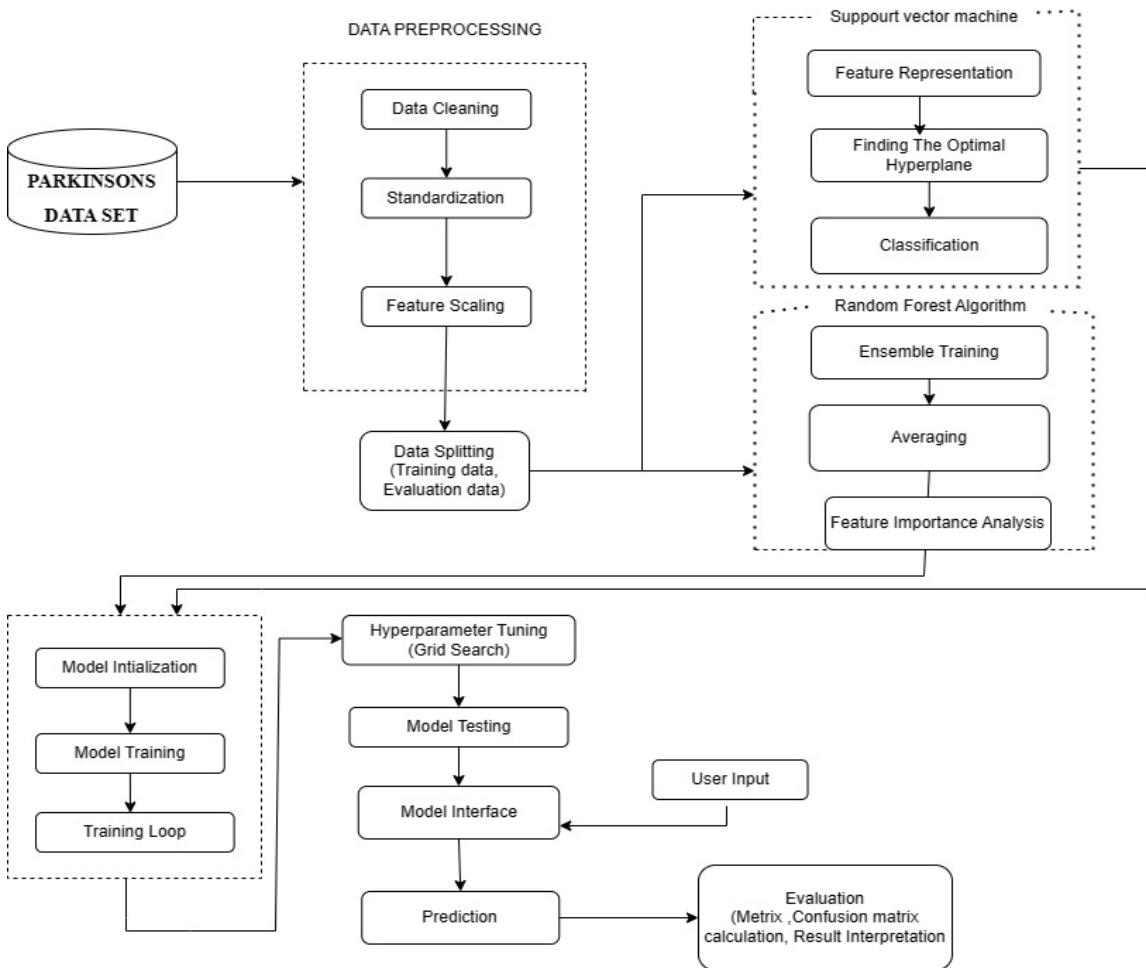


Fig. 1.1. Architecture Diagram

## ALGORITHMS PROPOSED:

Both Random Forest and SVM have their strengths and can be effective in predicting Parkinson's disease. Random Forest might be preferred when dealing with high-dimensional data and when interpretability of feature importance is important. On the other hand, SVM could be more suitable for datasets with complex decision boundaries or when dealing with a smaller number of samples compared to the feature space dimensionality. Ultimately, the choice between the two algorithms depends on the specific characteristics of the dataset and the goals of the prediction task.

### **1.5 RF:**

- Random Forest is a type of ensemble learning method that combines the predictions of multiple individual decision trees. Each tree in the forest is trained independently on a random subset of the training data and features, and the final prediction is made by averaging (for regression) or voting (for classification) over all trees.
- Random Forest is particularly well-suited for datasets with a large number of samples and features. It can efficiently handle high-dimensional data without overfitting, making it a robust choice for complex datasets commonly encountered in medical research.
- One of the strengths of Random Forest is its ability to capture complex relationships between features and the target variable. The ensemble nature of the algorithm allows it to model nonlinear relationships effectively, making it suitable for capturing the diverse range of factors that may contribute to Parkinson's disease.
- Random Forest mitigates the risk of overfitting by aggregating predictions from multiple trees. By combining the predictions of individual trees, Random Forest tends to generalize well to unseen data, improving its performance on test datasets.
- Random Forest is less sensitive to outliers and noise in the data compared to some other algorithms. The random selection of features and samples for each tree helps to reduce the impact of noisy data points, resulting in more robust predictions.
- Random Forest can handle missing values in the dataset without requiring imputation. During the training process, missing values are simply ignored, and predictions are made based on the available information. This flexibility can be advantageous when working with real-world datasets that often contain missing data.
- Random Forest provides feature importance scores, which can offer insights into the most influential factors contributing to Parkinson's disease. Understanding the relative importance of different features can aid researchers and clinicians in identifying potential biomarkers or risk factors associated with the disease.

### **1.6 SVM:**

SVM works by finding the hyperplane that best separates different classes in the feature space. The goal is to maximize the margin between the classes, which leads to better generalization performance and improved robustness to noise.

SVM is effective in high-dimensional spaces, where the number of features exceeds the number of samples. This property makes SVM suitable for datasets with many features, such as genetic data .

neuroimaging data, which are commonly used in Parkinson's disease research.

SVM is inherently robust to overfitting, especially in high-dimensional spaces. By maximizing the margin between classes, SVM seeks to find the decision boundary that generalizes well to unseen data, rather than fitting the training data too closely

SVM can efficiently handle non-linear decision boundaries by using kernel functions to map the input space into higher dimensions where classes are linearly separable. This flexibility allows SVM to capture complex relationships.

SVM is memory efficient, as it only uses a subset of training points (support vectors) in the decision function. This property makes SVM well-suited for large datasets, where storing and processing the entire dataset may be impractical or computationally expensive.

SVM can handle both linear and non-linear data by using appropriate kernel functions, such as radial basis function (RBF) or polynomial kernels. The choice of kernel function allows SVM to adapt to the specific characteristics of the data, making it versatile for various types of datasets encountered in Parkinson's disease research.

SVM offers a balance between linear and non-linear models, making it suitable for datasets with diverse characteristics. Whether the data exhibits linear separability or complex non-linear relationships, SVM can be effectively applied with the appropriate choice of kernel function.

## CHAPTER 2

### MERITS AND DEMERITS OF THE BASE PAPER

#### **2.1 Merits:**

The proposed methodology for detecting the Parkinson disease

1. The paper introduces a novel approach for diagnosing Parkinson's disease using a combination of deep learning-based CNN models and machine learning-based RF algorithm, showcasing innovation in the field of medical diagnosis
2. The proposed method demonstrates high accuracy rates ranging from 98.30% to 99.11% in various metrics, outperforming other CNN architectures and ML algorithms commonly used for Parkinson's disease detection
3. RF method shows significant improvement in classification performance, enhancing the success rates of the RF algorithm by up to 17.19% in different metrics, indicating the effectiveness of the proposed architecture
4. The study evaluates the proposed method on multiple datasets, including the PDO\_Dataset and PD\_Dataset, ensuring the robustness and generalizability of the approach across different data sources
5. This project involves collaboration between experts in conceptualization, methodology, formal analysis, and data curation, highlighting a multidisciplinary approach to addressing complex medical challenges
6. The authors outline future research directions, including the exploration of different neural network models and feature selection algorithms on larger datasets, paving the way for further advancements in Parkinson's disease diagnosis

#### **2.2 Open problems identified in existing**

The study's reliance on relatively small datasets like PD\_Dataset and PDO\_Dataset may restrict the generalizability of the proposed method to larger and more diverse populations.

While the paper highlights the performance of a comparative analysis with other state-of-the-art deep learning and machine learning approaches could provide a more comprehensive evaluation.

Deep learning models, including CNNs, often lack interpretability, raising concerns about understanding the underlying features driving the diagnosis, which is crucial for clinical acceptance.

The presence of imbalanced data in medical datasets, such as varying numbers of Parkinson's disease and healthy samples, can impact the model's performance and bias the results.

The study primarily focuses on algorithmic performance metrics, and there is a lack of validation in real clinical settings with healthcare professionals and patients, which is essential for practical implementation.

Deep learning models are susceptible to overfitting, especially when trained on small datasets, which may lead to inflated performance metrics that do not generalize well to unseen data.

The proposed architecture combining CNN and RF may introduce computational complexity, requiring significant resources for training and inference, which could limit its scalability.

The ethical implications of using AI-based diagnostic tools, such as data privacy, informed consent, and potential biases in the algorithm, need to be carefully addressed to ensure ethical and responsible deployment in healthcare settings.

## CHAPTER 3

### SOURCE CODE

```
#samples from source code
```

#### 3.1 Data Preprocessing: import pandas as pd

```
from sklearn.model_selection import train_test_split  
  
from sklearn.preprocessing import StandardScaler  
  
data = pd.read_csv(r"C:\Users\sanna\Downloads\parkinsons.csv")  
  
missing_values = data.isnull().sum()  
  
print("Missing Values:\n", missing_values)  
  
scaler = StandardScaler()  
  
scaled_features = scaler.fit_transform(data.drop(columns=['name', 'status']))  
  
data_scaled = pd.DataFrame(scaled_features, columns=data.columns[1:-1])  
  
X = data_scaled  
  
y = data['status']  
  
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2,  
random_state=42)  
  
X_train.to_csv('X_train.csv', index=False)  
  
X_test.to_csv('X_test.csv', index=False)  
  
y_train.to_csv('y_train.csv', index=False)  
  
y_test.to_csv('y_test.csv', index=False)
```

#### 3.2 Accuracy

```
from sklearn.svm import SVC  
  
from sklearn.metrics import accuracy_score  
  
svm_classifier = SVC(kernel='linear', random_state=42)
```

```

svm_classifier.fit(X_train, y_train)

y_pred_train = svm_classifier.predict(X_train)

y_pred_test = svm_classifier.predict(X_test)

train_accuracy = accuracy_score(y_train, y_pred_train)

test_accuracy = accuracy_score(y_test, y_pred_test)

print("Train Accuracy:", train_accuracy)

print("Test Accuracy:", test_accuracy)

```

### 3.3 Confusion Matrix

```

import matplotlib.pyplot as plt

from sklearn.metrics import confusion_matrix

import seaborn as sns

y_pred = svm_classifier.predict(X_test)

conf_matrix = confusion_matrix(y_test, y_pred)

plt.figure(figsize=(8, 6))

sns.heatmap(conf_matrix, annot=True, fmt='d', cmap='Blues',
xticklabels=['Healthy', 'Parkinsons'], yticklabels=['Healthy', 'Parkinsons'])

plt.xlabel('Predicted')

plt.ylabel('Actual')

plt.title('Confusion Matrix for Parkinson\\'s Disease Prediction using SVM')

plt.show()

cm = confusion_matrix(y_test, y_pred_test)

accuracy = accuracy_score(y_test, y_pred_test)

TN, FP, FN, TP = cm.ravel()

```

```

accuracy_manual = (TP + TN) / (TP + TN + FP + FN)

print("Confusion Matrix:")

print(cm)

print("\nAccuracy (from confusion matrix):", accuracy)

print("Accuracy (manual calculation):", accuracy_manual)

```

### 3.4 SVM Accuracy In Graph:

```

y_pred_svm_train = svm_classifier.predict(X_train)

y_pred_svm_test = svm_classifier.predict(X_test)

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2,
random_state=42)

svm_train_accuracy = accuracy_score(y_train, y_pred_svm_train)

svm_test_accuracy = accuracy_score(y_test, y_pred_svm_test)

print("SVM Train Accuracy:", svm_train_accuracy)

print("SVM Test Accuracy:", svm_test_accuracy)

plt.bar(labels, accuracies)

plt.ylim(min(accuracies) - 0.05, max(accuracies) + 0.05) # Set y-axis limits for better
visualization

plt.ylabel('Accuracy')

plt.title('Accuracy')

plt.show()

```

### 3.5 Accuracy,Precision,Recall,Score Comparison

```

from sklearn.metrics import accuracy_score, precision_score, recall_score, f1_score

y_pred_svm_train = svm_classifier.predict(X_train)

y_pred_svm_test = svm_classifier.predict(X_test)

```

```

svm_train_accuracy = accuracy_score(y_train, y_pred_svm_train)

svm_test_accuracy = accuracy_score(y_test, y_pred_svm_test)

svm_precision=precision_score(y_test, y_pred_svm_test,average='weighted')

svm_recall=recall_score(y_test, y_pred_svm_test,average='weighted')

svm_f1=f1_score(y_test, y_pred_svm_test,average='weighted')

import numpy as np

models = ['SVM' ]

x = np.arange(len(models)) # the label locations

width = 0.2

import matplotlib.pyplot as plt

import numpy as np

accuracy = 0.85

precision = 0.78

recall = 0.91

f1 = 0.84

metrics = ['Accuracy', 'Precision', 'Recall', 'F1 Score']

values = [accuracy, precision, recall, f1]

x = np.arange(len(metrics))

width = 0.35

fig, ax = plt.subplots()

rects = ax.bar(x, values, width)

ax.set_ylabel('Score')

ax.set_title('Metrics for Parkinson\\'s Disease Prediction Model')

ax.set_xticks(x)

```

```

ax.set_xticklabels(metrics)

for rect in rects:

    height = rect.get_height()

    ax.annotate('{}'.format(height),

                xy=(rect.get_x() + rect.get_width() / 2, height),
                xytext=(0, 3), # 3 points vertical offset

                textcoords="offset points",
                ha='center', va='bottom')

plt.show()

```

### 3.6 Mutation:

```

from sklearn.metrics import accuracy_score, precision_score, recall_score, f1_score

y_pred_svm_train = svm_classifier.predict(X_train)

y_pred_svm_test = svm_classifier.predict(X_test)

from sklearn.ensemble import RandomForestClassifier

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2,
random_state=42)

rf_classifier = RandomForestClassifier(n_estimators=100, random_state=42)

rf_classifier.fit(X_train, y_train)

y_pred_rf_train = rf_classifier.predict(X_train)

y_pred_rf_test = rf_classifier.predict(X_test)

svm_train_accuracy = accuracy_score(y_train, y_pred_svm_train)

svm_test_accuracy = accuracy_score(y_test, y_pred_svm_test)

svm_precision=precision_score(y_test, y_pred_svm_test,average='weighted')

svm_recall=recall_score(y_test, y_pred_svm_test,average='weighted')

```

```

svm_f1=f1_score(y_test, y_pred_svm_test,average='weighted')

rf_train_accuracy = accuracy_score(y_train, y_pred_rf_train)

rf_test_accuracy = accuracy_score(y_test, y_pred_rf_test)

rf_precision = precision_score(y_train, y_pred_rf_train,average='weighted')

rf_recall = recall_score(y_test, y_pred_rf_test,average='weighted')

rf_f1 = f1_score(y_train, y_pred_rf_train,average='weighted')

models = ['SVM', 'Random Forest']

accuracy = [svm_test_accuracy, rf_test_accuracy]

precision = [svm_precision, rf_precision]

recall = [svm_recall, rf_recall]

f1 = [svm_f1, rf_f1]

import numpy as np

x = np.arange(len(models)) # the label locations

width = 0.2

fig, ax = plt.subplots()

rects1 = ax.bar(x - 1.5*width, accuracy, width, label='Accuracy')

rects2 = ax.bar(x - 0.5*width, precision, width, label='Precision')

rects3 = ax.bar(x + 0.5*width, recall, width, label='Recall')

rects4 = ax.bar(x + 1.5*width, f1, width, label='F1 Score')

```

### 3.7 Comparing RF and SVM

```

import matplotlib.pyplot as plt

import numpy as np

```

```
models = ['SVM', 'Random Forest']
```

```

accuracy = [svm_test_accuracy, rf_test_accuracy]

precision = [svm_precision, rf_precision]

recall = [svm_recall, rf_recall]

f1 = [svm_f1, rf_f1]

x = np.arange(len(models)) # the label locations

width = 0.2

fig, ax = plt.subplots()

rects1 = ax.bar(x - 1.5*width, accuracy, width, label='Accuracy', color='blue')

rects2 = ax.bar(x - 0.5*width, precision, width, label='Precision', color='green')

rects3 = ax.bar(x + 0.5*width, recall, width, label='Recall', color='orange')

rects4 = ax.bar(x + 1.5*width, f1, width, label='F1 Score', color='red')

# Add color labels indicating which metric each color represents

legend_labels = ['Accuracy', 'Precision', 'Recall', 'F1 Score']

legend_colors = ['blue', 'green', 'orange', 'red']

ax.legend([plt.Rectangle((0,0),1,1,fc=color, edgecolor='none') for color in
legend_colors], legend_labels, loc='upper left')

# Add some text for labels, title and custom x-axis tick labels, etc.

ax.set_ylabel('Scores')

ax.set_title('Comparison of SVM and Random Forest Models')

ax.set_xticks(x)

ax.set_xticklabels(models)

ax.legend()

# Add value labels on top of bars

def add_value_labels(bars):

```

```

for bar in bars:
    height = bar.get_height()
    ax.annotate('{}'.format(round(height, 2)),
                xy=(bar.get_x() + bar.get_width() / 2, height),
                xytext=(0, 3), # 3 points vertical offset
                textcoords="offset points",
                ha='center', va='bottom')

add_value_labels(rects1)
add_value_labels(rects2)
add_value_labels(rects3)
add_value_labels(rects4)

fig.tight_layout()
plt.show()

```

### 3.8 Predicting disease

```

import tkinter as tk
import numpy as np
import pandas as pd
from sklearn.model_selection import train_test_split
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import accuracy_score
# Load the dataset
url = r"C:\Users\sanna\Downloads\parkinsons.csv"
df = pd.read_csv(url)
# Select features and target

```

```

features = ['MDVP:Fo(Hz)', 'MDVP:Fhi(Hz)', 'MDVP:Flo(Hz)', 'MDVP:Jitter(%)',
'MDVP:Jitter(Abs)',
'MDVP:RAP', 'MDVP:PPQ', 'Jitter:DDP', 'MDVP:Shimmer',
'MDVP:Shimmer(dB)', 'Shimmer:APQ3',
'Shimmer:APQ5', 'MDVP:APQ', 'Shimmer:DDA', 'NHR', 'HNR', 'RPDE',
'DFA', 'spread1', 'spread2',
'D2', 'PPE']

X = df[features]

y = df['status']

# Split data into training and testing sets

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2,
random_state=42)

# Initialize the RandomForestClassifier

rf_classifier = RandomForestClassifier(n_estimators=100, random_state=42)

# Train the model

rf_classifier.fit(X_train, y_train)

# Create a Tkinter GUI

root = tk.Tk()

root.title("Parkinson's Disease Prediction")

# Create a label and entry field for pasting all features at once

tk.Label(root, text="Enter all features separated by spaces:").grid(row=0,
column=0, sticky=tk.W)

```

```

all_features_entry = tk.Entry(root, width=50)

all_features_entry.grid(row=0, column=1)

# Create a button to set individual feature values

def set_input_features():

    all_features = all_features_entry.get().split()

    for i, val in enumerate(all_features):

        feature_entries[i].delete(0, tk.END)

        feature_entries[i].insert(0, val)

    set_features_button = tk.Button(root, text="Set Features",
                                    command=set_input_features)

    set_features_button.grid(row=0, column=2)

# Create labels and entry fields for feature values

feature_entries = []

for i, feature in enumerate(features):

    tk.Label(root, text=feature).grid(row=i+1, column=0, sticky=tk.W)

    entry = tk.Entry(root)

    entry.grid(row=i+1, column=1)

    feature_entries.append(entry)

# Function to get feature values from the entry fields

def get_feature_values():

    return [float(entry.get()) for entry in feature_entries]

# Function to predict Parkinson's disease

def predict_parkinsons():

    feature_values = get_feature_values()

```

```
prediction = rf_classifier.predict([feature_values])

result_label.config(text="The prediction indicates Parkinson's disease." if
prediction[0] == 1 else "The prediction indicates no Parkinson's disease.")

# Button to trigger prediction

predict_button = tk.Button(root, text="Predict", command=predict_parkinsons)

predict_button.grid(row=len(features)+1, column=0, columnspan=2)

# Label to display prediction result

result_label = tk.Label(root, text="")

result_label.grid(row=len(features)+2, column=0, columnspan=2)

root.mainloop()
```

## CHAPTER 4

### SNAPSHOTS

#### 4.1 GUI:

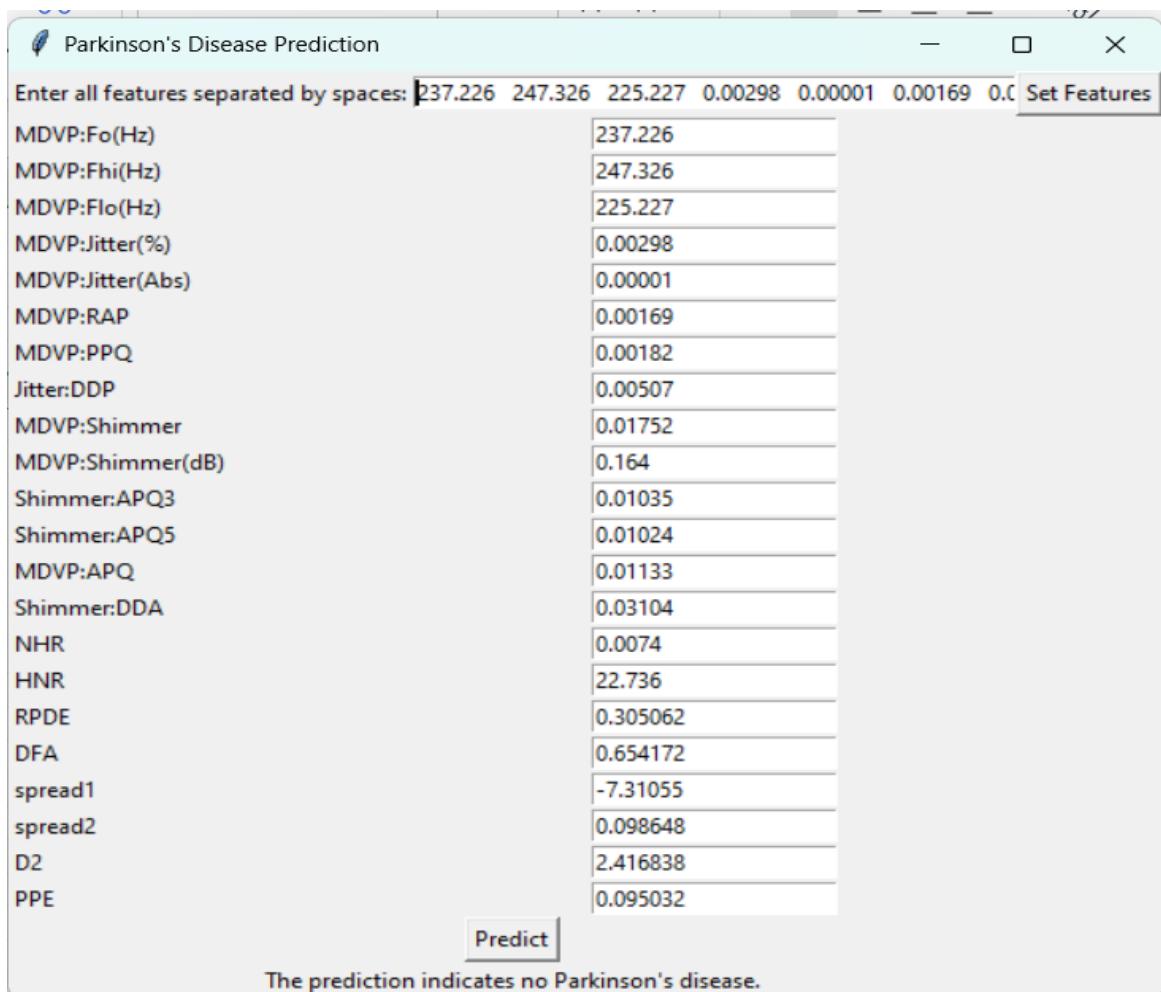


Figure 4.1 Feature selection from Dataset

Parkinson's Disease Prediction

Enter all features separated by spaces: 184.055 196.537 166.977 0.00258 0.00001 0.00134 0.01573 Set Features

MDVP:Fo(Hz)	184.055
MDVP:Fhi(Hz)	196.537
MDVP:Flo(Hz)	166.977
MDVP:Jitter(%)	0.00258
MDVP:Jitter(Abs)	0.00001
MDVP:RAP	0.00134
MDVP:PPQ	0.00147
Jitter:DDP	0.00403
MDVP:Shimmer	0.01463
MDVP:Shimmer(dB)	0.132
Shimmer:APQ3	0.00742
Shimmer:APQ5	0.00901
MDVP:APQ	0.01234
Shimmer:DDA	0.02226
NHR	0.00257
HNR	26.453
RPDE	0.306443
DFA	0.759203
spread1	-7.044105
spread2	0.063412
D2	2.361532
PPE	0.11573

**Predict**

The prediction indicates Parkinson's disease.

Detecting Disease from dataset

#### 4.3 Performance and Model Comparison:

Fig. 4.1.Accuracy and precision ,recall,F1 score of the of SUPPORT VECTOR MACHINE ALGORITHM

```
[13] from sklearn.metrics import classification_report
```

```
[14] # classification report for test set
    print("\nClassification Report for Test Set:")
    print(classification_report(y_test, y_pred_test))
```

Classification Report for Test Set:				
	precision	recall	f1-score	support
0	0.67	0.57	0.62	7
1	0.91	0.94	0.92	32
accuracy			0.87	39
macro avg	0.79	0.75	0.77	39
weighted avg	0.87	0.87	0.87	39

Fig. 4.2 Accuracy and precision ,recall,F1 score of the of SUPPORT VECTOR MACHINE ALGORITHM in a graph

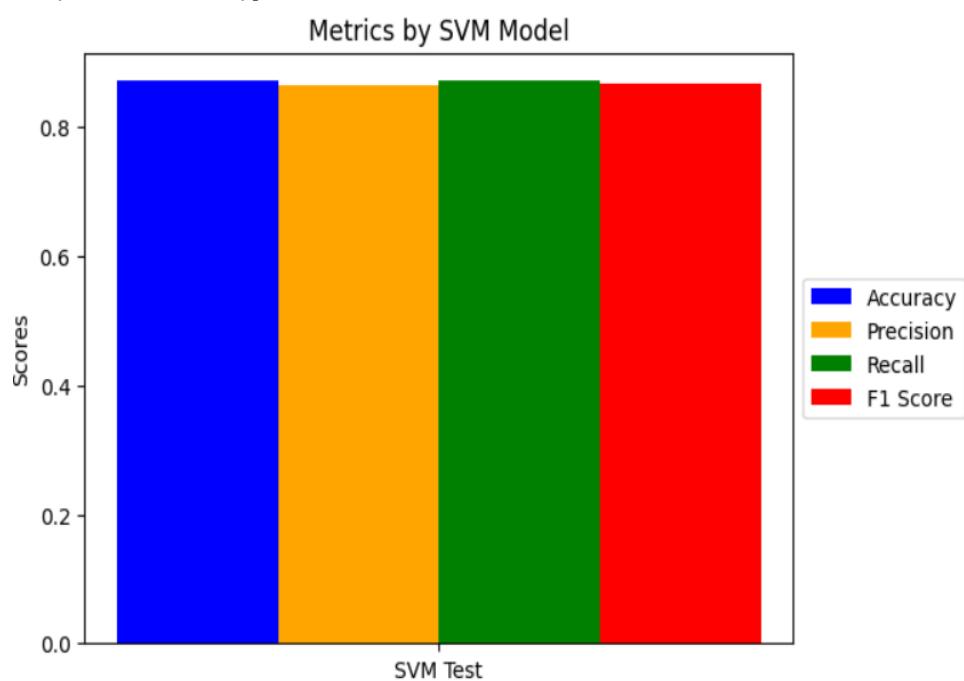


Figure Performance metrics comparison for SVM

Fig. 4.3. Accuracy and precision ,recall,F1 score of the of RANDOM FOREST

```
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import classification_report

rf_model = RandomForestClassifier()
rf_model.fit(X_train, y_train)
y_pred_rf_test = rf_model.predict(X_test)

# Print classification report
print("Classification Report for Random Forest:")
print(classification_report(y_test, y_pred_rf_test))
✓ 0.3s
```

	precision	recall	f1-score	support
0	1.00	0.71	0.83	7
1	0.94	1.00	0.97	32
accuracy			0.95	39
macro avg	0.97	0.86	0.90	39
weighted avg	0.95	0.95	0.95	39

Fig.4.4 Accuracy and precision ,recall,F1 score of the of RANDOM FOREST in a graph

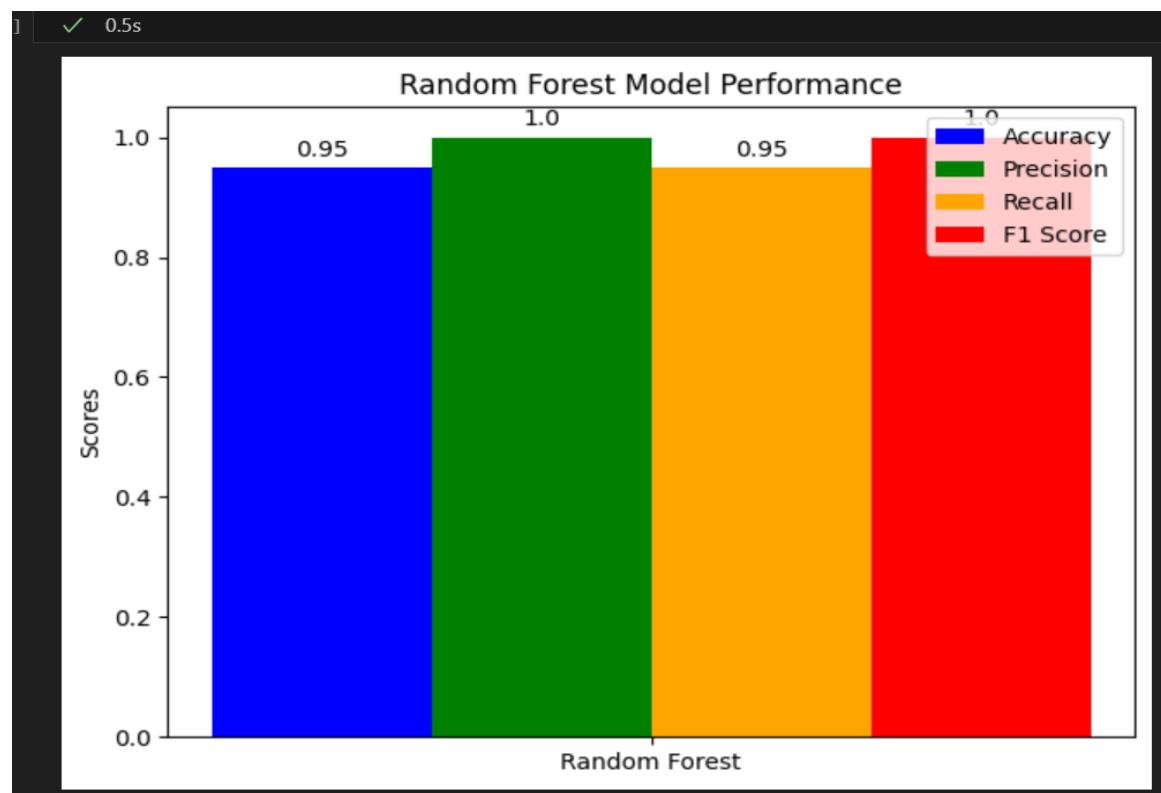


Fig.4.5 Compariosn between Random Forest and Support Vector Algorithm  
(Accuracy,Precision,Recall,F1 Score)

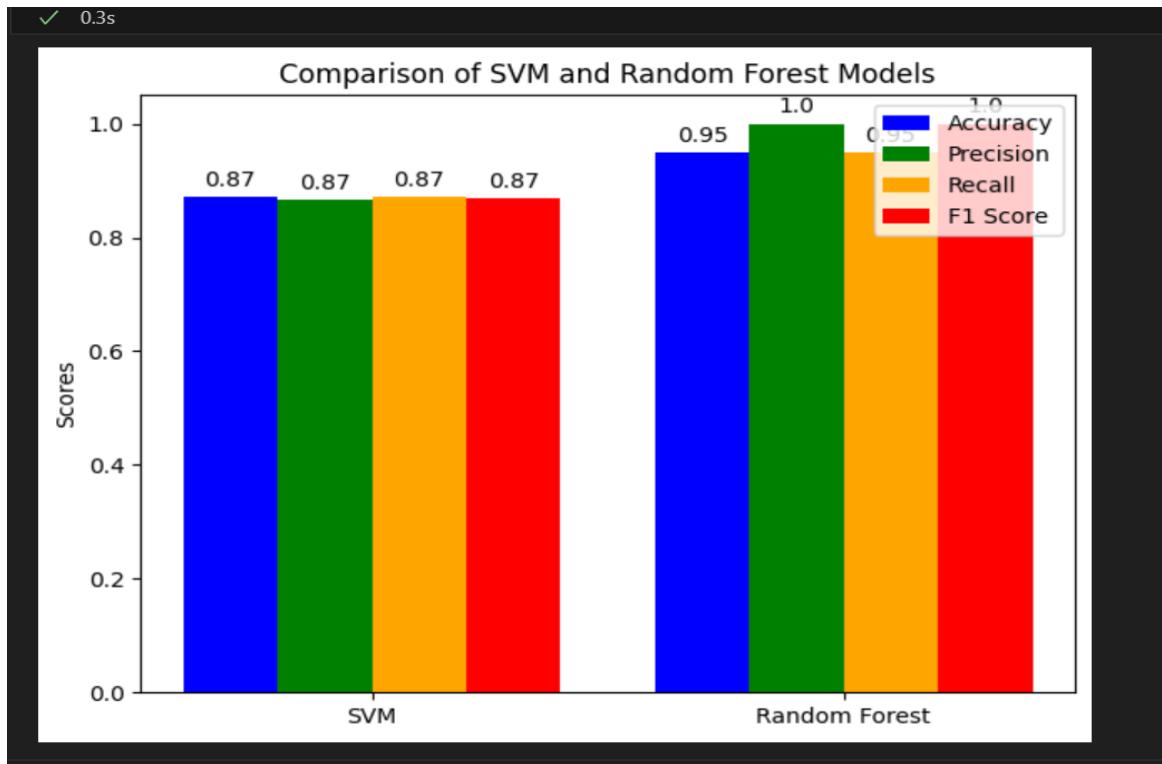


Figure comparison between SVM and RF

## **CHAPTER 5**

### **CONCLUSION AND FUTURE PLANS**

Detection of Parkinson disease prediction by the taking input from speech signals and this prediction we done by the machine learning algorithms Random Forest and Support Machine Vector Algorithm and we taken the dataset from Kaggle website and we finded out the accuracy for the both algorithms and we taken and considered a RF is a best algorithm by the checking the accuracy between both and next we finded Accuracy,Recall,Precision for the both algorithms .At last we compared both the algorithms and we plotted in a graph and maked prediction by the User Interface and last predicted the person have the disease or not .

In future, we plan to extend this proposed RF and SVM and over a comprehensive range of datasets. We also plan to investigate the efficiency of the approach by using more set of features and to integrate alternative algorithms which may be adaptable to real time applications.

## **CHAPTER 6**

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# CHAPTER 7

## APPENDIX – BASE PAPER



### Proposing a new approach based on convolutional neural networks and random forest for the diagnosis of Parkinson's disease from speech signals



Gaffari Celik\*, Erdal Başaran

Department of Computer Technology, Agri Ibrahim Cecen University, Agri 04200, Turkey

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#### ABSTRACT

Parkinson which occurs because of affected motor system by central nervous system is a neurodegenerative disease which is often seen in community. This disease, which is frequently seen especially in the elderly, brings problems such as speech disorders in patients. It is seen that with the rapidly developing deep learning and machine learning methods in recent years, it is possible to distinguish speech disorders in PD patients at a high rate and quickly. In this study, PD diagnosis was performed using datasets containing voice signals of healthy individuals and PD patients (PD\_Dataset and PDO\_Dataset). Current convolutional neural networks (CNN) and machine learning (ML) algorithms for PD diagnosis have been examined and a comparative performance analysis has been made. In addition, a different method called SkipConNet + RF based on CNN and random forest (RF) has been proposed for PD diagnosis. With the proposed SkipConNet, important features were obtained from the speech signals; then, the estimation process was performed using the RF algorithm. The proposed method provided an improvement between 3% and 17.19% in the performance of RF algorithms. In addition, the SkipConNet + RF method showed the highest success with 99.11% accuracy in the PD\_Dataset dataset and 98.30% in the PDO\_Dataset dataset.

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#### 1. Introduction

Parkinson's disease (PD) results from damage to dopamine-producing cells in the substantia nigra region of the brain (see Fig. 1), and it is the second most common neurodegenerative disease after Alzheimer's disease. PD, which is an age-related chronic disease, also affects people's lives in the following years, and it is seen that it especially affects 1–2% of people over the age of 65 [1–4]. According to recent studies, approximately one million people in the United States have Parkinson's disease, and approximately 60,000 people are diagnosed with this disease each year. In addition, PD affects approximately 10 million people worldwide per year [3,5]. As the proportion of the elderly population in the world increases, an increase in personal, social, and economic burden is expected due to PD [3]. This disease is predicted to double between 2005 and 2030 [6].

Symptoms such as slowed movement, tremors, sleep disturbances, autonomic dysfunction, and cognitive impairment are frequently observed in people with PD [3]. In addition, PD affects the speed and length of speech expressions [7], causes the problem of

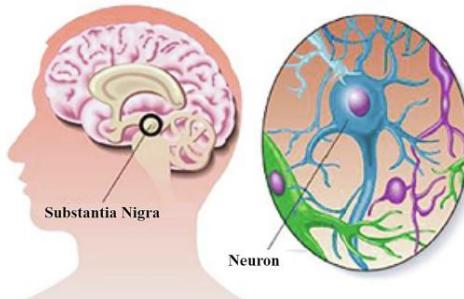
communication problems (dysarthria) [8,9], and causes abnormal disturbances in the functioning of the voice system known as dysphonia [10–11].

There are six stages of Parkinson's disease. In the first two stages, symptoms of olfactory and voice disorders are observed. In the third and fourth stages, motor symptoms show signs, while in the fifth and sixth stages, a large part of the brain is severely affected and the disease manifests itself with all its effects [12].

Speech signals can provide specific information about the speaker, such as age, gender, identity, mood, and the presence of diseases [13]. Speech signals can be measured by acoustic instruments by speech clinicians [14]. These instruments can objectively provide sound function measurements by recording changes in acoustic pressure inside the vocal tract. In the early stages of Parkinson's disease, 90% of the patients have speech disorders [15,16], which is an effective method for the early diagnosis of PD with voice analysis methods. This method is cheap and easy to do [10]. With various signal processing techniques, speech features are extracted and artificial learning techniques provide classification. In this way, PD can be detected in the early stages, preventing the progression of the disease and improving the quality of life of patients [17,18].

\* Corresponding author.

E-mail address: [gcelik@agri.edu.tr](mailto:gcelik@agri.edu.tr) (G. Celik).



**Fig. 1.** Substantia nigra region in the brain [5].

In the literature, there is an increasing interest in speech-based DL and ML techniques for detecting Parkinson's disease. There are many studies conducted with ML methods such as SVM [15,17,19–24], K-nearest neighbors (KNN) [20,22–25], decision trees [24], and genetic algorithms [26]. At the same time, PD detection is made by using existing CNN architectures (AlexNet, DenseNet, LSTM SqueezeNet, VGG19, etc.) or with CNN architectures created by the authors in deep learning studies [27–29]. CNN architectures seem to perform better in feature extraction [29].

In addition, CNN techniques have been successfully applied to many studies such as ocean noise detection [30], COVID-19 detection from X-ray images [31–34], mammography images segmentation and classification [35], environmental sound classification [36], lymph node metastases [16], detection of Alzheimer's disease [37], skin cancer [38], cartilage lesions [39], fatigue diagnosis based on heart sounds [40], joint disorder diagnosis [41], premature retinopathy [42], and diagnosis of idiopathic Parkinson's disease [43].

A new diagnostic model based on SkipConNet and RF has been proposed for early diagnosis of Parkinson's disease. The contributions of the study can be summarized as follows:

- Performances of current CNN and ML algorithms for PD diagnosis from speech signals are examined.
- A new architecture has been proposed with the name SkipConNet + RF based on CNN and RF.
- SkipConNet is designed to extract important feature maps from audio signals.
- A significant improvement has been made in the performance of the RF algorithm by using the SkipConNet architecture and the RF algorithm together.
- The study highlights the importance of feature extraction from speech signals in the diagnosis of Parkinson's disease.

## 2. Related works

Tsanas et al. [17] used a dataset containing 263 sound samples from 43 subjects to detect Parkinson's disease from sound signals. In this study, in which random forest and support vector machines (SVM) algorithms were used, 99% success was achieved. Yaman et al. [20] used a publicly available dataset from the UCI dataset platform. This dataset contains 240 voice samples from 40 healthy individuals and 40 Parkinson's patients. In the proposed method, the properties of the data set were increased by the statistical pooling method, and then weighted features were obtained by using the ReliefF method. Obtained weighted feature vectors were classified by SVM and KNN methods. The authors achieved a success rate

of 91.25% with the SVM method and 91.23% with the KNN algorithm. Sakar et al. [15] used sound samples from 40 subjects, 20 healthy and 20 Parkinson's patients. By using K-NN and SVM algorithms in their studies, the authors reached 82.50% accuracy with the K-NN algorithm and 85% accuracy with the SVM algorithm. Benba et al. [44] performed PD detection using sound samples from 20 Parkinson's patients and 20 healthy subjects. Effective features were obtained by reducing the size of the time-frequency properties obtained from the sound database with linear and non-linear principal component analysis (PCA and NPPCA) methods. Then, they achieved 87.5% success with the SVM method.

Chen et al. [45] used an architecture based on Hilbert-huang transform (HHT) and KNN algorithms. A total of 21 features were obtained, 12 for each sound sample with the HHT algorithm and 9 with the linear prediction coefficients (LPCC) algorithm. Then, the obtained features were classified separately with the help of KNN, RF, and decision tree (DT) algorithms. The authors achieved the highest performance in the KNN algorithm with an accuracy rate of 93.3%. Yucelbas et al. [46] diagnosed PD using a dataset containing recorded sound signals from a total of 252 individuals (64 healthy, 188 Parkinson's patients). Three different methods, namely reconstruction ICA (RICA), max-kurtosis ICA (KICA), and fast ICA (FICA) were used for size reduction in the dataset. Then the obtained features were classified by the RF algorithm. The RICA method showed the highest performance with 82.01% classification accuracy. Karan et al. [47] used two different datasets for a total of 90 subjects (40 normal, 50 Parkinson's patients). Significant features were obtained from the sound samples with the proposed intrinsic mode function cepstral coefficient (IMFCC, Mel-frequency cepstral coefficient (MFCC)) algorithm. Then, the obtained features were estimated by the SVM algorithm.

When other current studies in the literature for the detection of Parkinson's disease from sound signals are examined, it is seen that deep neural networks (DNN) and convolutional neural networks (CNN) contribute greatly. Trinh and Darragh [48] proposed a CNN-based method. They achieved 96.7% accuracy in the study using two different PD datasets. Arias-Vergara et al. [49] used two different datasets, training and testing. The training dataset includes voice recordings of 68 PD patients and 50 healthy individuals. All of the people whose voice recordings were taken are Colombian Spanish native speakers. The test dataset includes voice recordings of 25 individuals, 8 healthy and 17 PD patients, via the Apkinson mobile application. First, they transformed each sound recording into the time-frequency domain via the short-time Fourier transform (STFT). Then, they performed the prediction process with CNN architecture. Nagasubramanian and Sankayya [50] obtained spectral features from sound recordings to predict individuals with and without Parkinson's disease. They have designed many architectures such as acoustic deep recurrent neural network (ADRNNA), deep multi-variate vocal data analysis (MVDA) system, acoustic deep convolutional neural network (ADCNN), and acoustic deep neural network (ADNN) to handle the resulting features. They also did performance evaluations of existing architectures such as CNN and RNN. With the proposed architectures, they achieved a performance increase of 3% compared to the existing architectures.

Another Parkinson's disease study relies on the DNN architecture developed by Wroge et al [51]. In this study, a dataset containing voice recordings (PD and non-PD) collected using a mobile application was used. By applying the minimum redundancy maximum relevance (mRMR) method to this dataset, the authors ensured that the redundant features were removed and the most important features belonging to the relevant class were selected. In addition, the second feature dataset was created by selecting the feature using the MFCC method. Then, the obtained feature dataset was classified with DNN and an accuracy of 85% was obtained. In another CNN study by Quan et al. [52], a new

end-to-end deep learning model was developed. In the developed model, time series features were obtained by using 2D-CNN. The obtained features were classified using a one-dimensional CNN (1D-CNN). They used two databases named Database-1 and Database-2. The authors validated the performance of their proposed model in both databases. 75.3% accuracy was obtained from Database-1 obtained from Chinese conversations. Database-2 contains sounds in texts containing simple/complex sentences in Spanish. The authors achieved a success rate of approximately 92% from this dataset as well.

In another CNN study for detecting PD disease from audio signals [29], firstly, by removing noise from audio signals with variational mode decomposition (VMD), mel-spectrograms of audio signals were obtained. In the next step, features were extracted from the mel-spectrograms obtained by using trained deep neural networks (ResNet-18, ResNet-50, and ResNet-101). Finally, the obtained features were classified using the Long short-term memory (LSTM) architecture and 98.61% accuracy was achieved.

### 3. Material

In this study, two different datasets were used to diagnose Parkinson's disease from speech signals. The first dataset (PDO\_Dataset) was created by Little et al. [14] in collaboration with the University of Colorado National Center for Voice and Speech and the University of Oxford. The PDO\_Dataset dataset contains 195 speech recording signals from 31 individuals, 8 healthy, and 23 Parkinson's patients. A dataset was obtained by extracting 23 features from each sound recording.

The other dataset (PD\_Dataset) includes sound data collected at Istanbul University Cerrahpaşa Faculty of Medicine, Department of Neurology [53]. The dataset includes voice information from a total of 252 individuals, 64 of whom are healthy and 188 with Parkinson's disease. The ages of healthy individuals (23 males and 41 females) vary between 41 and 82, while those of sick individuals (107 males and 81 females) vary between 33 and 87 years. The data were obtained by repeating the vowel 'a' three times in each individual using a microphone tuned to 44.1 KHz under the supervision of a physician. In this way, a dataset containing a total of 756 sound recordings was created. Each recording is set to 220 sec. Recording times are divided into frames of 25 ms. 754 features were obtained from each frame using six different signal processing techniques (baseline feature, time-frequency features, MFCCs, wavelet transform-based features, vocal fold features, and TWQT features). The overall feature vector of a signal is found by averaging the feature vectors of all its signal frames. Detailed information about these datasets used in the experimental applications in this study is given in Table 1.

### 4. Method

In this study, an architecture consisting of a combination of deep learning-based CNN model and ML learning-based RF algorithm is proposed for Parkinson's disease detection from speech signals. The methodology of the proposed architecture is given in Fig. 2. CNN architectures have few parameters and are used to

obtain multidimensional feature extraction layers. Multidimensional features are obtained by the convolution operation with different filter sizes [54,55]. In the first stage, training of the SkipConNet module is carried out with speech signals. In the second step, important feature vectors are obtained from the trained SkipConNet module. The feature vectors obtained in the last stage are trained with the RF method and then the estimation process is performed.

#### 4.1. Random forest (RF)

Random Forest (RF) algorithm is an ML algorithm that consists of multiple decision trees (DT) independent of each other. DT is a supervised learning algorithm used in classification and regression problems. DT is a hierarchical model consisting of root node, branches (internal nodes), and leaves (end nodes), which iteratively categorizes arguments and positions important features according to decision rules from root to end nodes. The root node is the starting point of the tree that expands into various branches. Internal nodes are decision nodes used to make decisions, while leaves are final result nodes with no branches and outputs of decision nodes. In decision trees, each node is divided into at least two branches. Branching ends when no new questions arrive. This process is repeated recursively and ends when all samples are assigned to a classification [56–58]. The Gini method given in Eq. (1) is widely used to create nodes in the tree structure and determine the threshold value [57,59].

$$Gini(P) = \left( \sum_{i=1}^n p_i(1-p_i) \right) = 1 - \sum_i^n (p_i)^2 \quad (1)$$

Here  $p_i$ ,  $i$ . While  $n$  indicates the probability of finding the class, the value of  $n$  represents the total number of classes.

RF uses multiple independent decision trees to model the algorithm  $\times$  samples selected in the sample dataset. In the estimation process, classification is made by deciding on the most appropriate estimation value by voting according to the estimation result of the individual decision trees. The RF algorithm consists of four steps [60–62]:

Step 1: Random samples are generated from the training dataset ( $N = 1, 2, \dots, n$ ) with the bootstrap sampling method ( $D_N$ ). The probability distribution of  $D_N$  is given in Eq. (2) and entropy information in Eq. (3):

$$P(D_N) = P_j, j = 1, 2, \dots, n \quad (2)$$

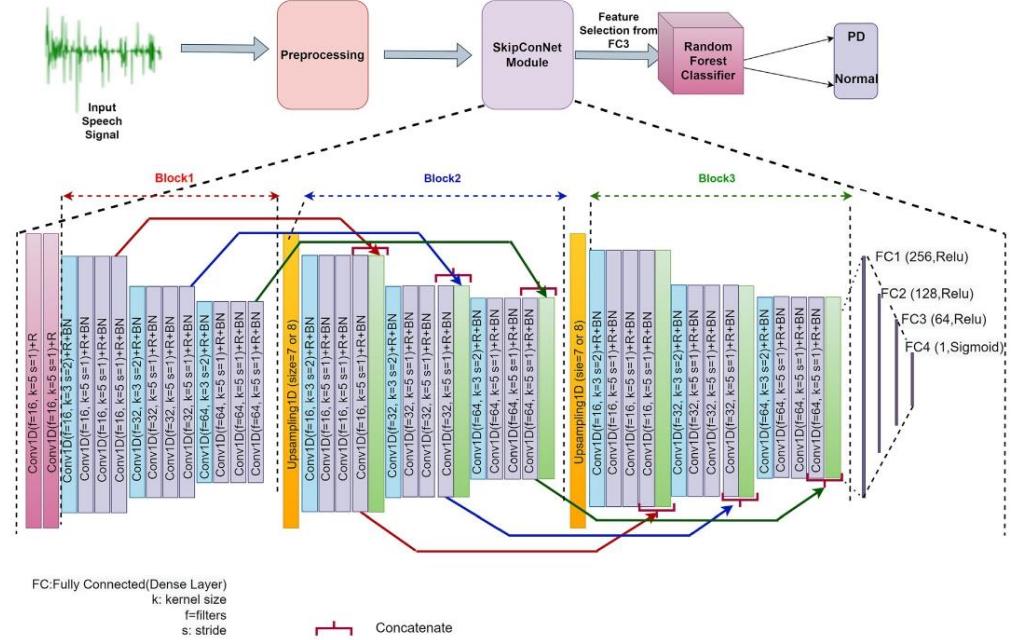
$$H(D_N) = - \sum_{j=1}^n p_j \log_2 p_j \quad (3)$$

Step 2: Creates a decision tree for each instance created. Then, the information gain entropy in randomly selected feature factors is calculated according to Eq. (4). If the  $D_N$  feature factor  $A$  contains  $M$  values, then  $D_N$  can be divided by these values. In this case, the new information entropy can be calculated as follows:

$$Gain(D_N, A) = H(D_N) - \sum_{M=1}^M \frac{|D_N^M|}{D_N} H(D_N^M) \quad (4)$$

**Table 1**  
Number of samples for training and testing of datasets.

Dataset	Class	Training(%70)	Testing(%30)	Total
PDO_Dataset	PD	100	47	147
	Normal	36	12	48
PD_Dataset	PD	390	174	564
	Normal	139	53	192



**Fig. 2.** The methodology of the proposed architecture. In the Upsampling1D operation, the size parameter is 8 for PD\_Dataset and size = 7 for PDO\_Dataset.

Step 3. After the information gain entropy is found according to Step 2, it is divided by the best candidate feature factor among them, and the information gain entropy is calculated again according to Eq. (2). The above operations are repeated until the information gain entropy is lower than the specified value.

Step 4: Finally, to classify the data, decision trees in the forest estimate the classification with the most votes by voting.

#### 4.2. Proposed SkipConNet module

The SkipConNet module is based on the convolution operation and the reuse of properties. This module consists of three consecutive Blocks linked to each other. More than one Block is used to obtain more detailed important features. In the proposed module, the speech signal given as input is subjected to two successive convolutions, and Relu activation is applied after each convolution operation. If the model is trained for PD\_Dataset to solve the problem caused by the data size difference in the datasets, ZeroPadding (padding = 3) is applied after these operations. Then, size reduction is performed by giving two to the step number parameter in the convolution process. With the size reduction process, unnecessary data is eliminated and important features are obtained. After the size reduction process, three consecutive convolutions are applied. The result of the last convolution operation is kept to be combined with the same level convolution operation in the next Block. These operations are repeated three times for each block. Combining features enables the reuse of important features and at the same time prevents the loss of significant features. After these operations are performed for each block, the features obtained are averaged with the GlobalAveragePooling method and the features are combined. In

this way, the model can be learned better. Then, after the obtained feature map is given to three fully connected layers, the classification process is performed with the sigmoid function. Binary cross entropy is used as the cost function of the SkipConNet module given in Eq. (5).

$$L_{BCE} = -\frac{1}{n} \sum_i ((y_i \log(\hat{y}_i)) + (1 - y_i) \log(1 - \hat{y}_i)) \quad (5)$$

Here  $n$  is the number of samples.  $y$  represents the actual value and  $\hat{y}$  the predicted value.

The mathematical expression of the convolution operation is given in Eq. (6).

$$Conv = (I * K)(i, j) = \sum_m \sum_n I(i + m, j + n)K(m, n) \quad (6)$$

where  $I$  denotes the input matrix.  $K$  represents the filter and  $m \times n$  filter size.

The Relu and Sigmoid activation functions used in the SkipConNet module are given in Eqs. (7) and (8) [63].

$$f(x)_{Relu} = \max\{0, x\} \quad (7)$$

$$f(x)_{Sigmoid} = \frac{1}{1 + e^{-x}} \quad (8)$$

Here  $x$  represents input information.

The block for reusing the features that make up the basic structure of the SkipConNet module is expressed as follows.

$$y_i = F(x_{i+1}, w_i)x_i \quad (9)$$

where  $w_i$  is the weights,  $x$  is the input,  $y_i$  is the output of the  $i^{\text{th}}$  block, and  $\text{x}$  is the concatenation.

**Algorithm:** Pseudocode of the proposed architecture:

1. **Input:** (speech signal ( $x_1, x_2, \dots, x_n$ ))
2. **Output:** PD estimate (0,1)
3. Load PD\_Dataset
4. Normalize data using minimum maximum normalization
5. **For** number of epochs **do**
6. Get input data ( $x_i$ ) up to batch\_size
7. Start the training process of the SkipConNet module ( $\text{SkipConNet}(x_i)$ )
8. Class probabilities are found according to Eq. (8)
9. Calculate the cost function ( $L_{BCE}$ ) according to Eq. (5)
10. SkipConNet weights ( $W$ ) are updated
11. **end for**
12. The parameters and weights of the SkipConNet module are saved
13. Retrieve eigenvectors from FC3 in the trained SkipConNet module
14. RF is trained according to the received eigenvectors.
15. Prediction results are obtained with RF

Different metrics are used to evaluate the performance of architectures. Although accuracy is the most frequently used metric in the literature, results can be misleading in datasets with imbalance problems between classes. Therefore, using different metrics to make a healthy evaluation is necessary. Accuracy, Precision, Recall, F1-Score, Specificity, and AUC metrics were used to evaluate the performance of the architectures. These metrics are mathematically defined as follows.

**Table 2**  
Confusion matrix for classification of two-class problems.

Actual	Predicted	
	Negative	Positive
Negative	True Negative ( $TN$ )	False Negative ( $FN$ )
Positive	False Positive ( $FP$ )	True Positive ( $TP$ )

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN} \quad (10)$$

$$\text{Precision} = \frac{TP}{TP + FP} \quad (11)$$

$$\text{Recall} = \frac{TP}{TP + FN} \quad (12)$$

$$\text{F1-Score} = \frac{2 * \text{Precision} * \text{Recall}}{\text{Precision} + \text{Recall}} \quad (13)$$

$$\text{Specificity} = \frac{TN}{TN + FP} \quad (14)$$

where patients with  $TP$  (True Positives) predicted correctly,  $TN$  (True Negatives) predicted non-patients,  $FP$  (False Positives) incorrectly predicted, and  $FN$  (False Negatives) incorrectly predicted healthy individuals [28,32,62,64]. The receiver operating characteristic (ROC) curve is used in classification problems to evaluate the performance of models by plotting the true positive rate (TPR) versus the false positive rate (FPR). The area Under the ROC Curve (AUC) indicates the area under the ROC [65,66].

$$\frac{FP}{FP + TN} \quad (15)$$

$$\frac{TP}{TP + FN} \quad (16)$$

$$AUC = \int_{-\infty}^{+\infty} TP_{rate}(t)FP_{rate}(t)dt \quad (17)$$

Here  $t$  is a parameter that takes a value in the range of [0,1].  $TP_{rate}$  stands for true positive rate, and  $FP_{rate}$  stands for false positive rate.

Confusion matrix was also used to evaluate the performances of the architectures per class. **Table 2** shows the number of  $TP$  (true positive),  $TN$  (true negative),  $FP$  (false positive), and  $FN$  (false negative) in the confusion matrix for binary classes [27].

**Table 3**  
Performances of architectures using PD\_Dataset for the detection of Parkinson's disease.

Method	Accuracy (%)	Precision	Recall	F1-Score	Specificity(%)	AUC (%)
EfficientNet-B0	90.75	0.89	0.85	0.86	84.78	84.78
VGG19	76.65	0.38	0.50	0.43	50.00	50.00
InceptionV3	92.95	0.91	0.89	0.90	89.50	89.50
LSTM	83.70	0.79	0.72	0.75	72.31	72.31
DenseNet	87.22	0.88	0.75	0.79	74.61	74.61
AlexNet	88.99	0.85	0.84	0.84	83.63	83.63
SVM	87.22	0.86	0.77	0.80	76.58	76.58
DT	79.73	0.73	0.76	0.74	76.28	76.28
RF	89.86	0.89	0.82	0.84	81.58	81.58
SkipConNet + RF	<b>99.11</b>	<b>0.99</b>	<b>0.99</b>	<b>0.99</b>	<b>98.77</b>	<b>98.77</b>

**Table 4**  
Success rates of algorithms for detecting Parkinson's disease using PDO\_Dataset.

Method	Accuracy (%)	Precision	Recall	F1-Score	Specificity(%)	AUC (%)
EfficientNet-B0	94.92	0.97	0.88	0.91	87.50	87.50
VGG19	79.66	0.40	0.50	0.44	50.00	50.00
InceptionV3	94.92	0.97	0.88	0.91	87.50	87.50
LSTM	93.22	0.96	0.83	0.88	83.33	83.33
DenseNet	91.53	0.90	0.82	0.86	82.27	82.27
AlexNet	93.22	0.96	0.83	0.88	83.33	83.33
SVM	86.44	0.93	0.67	0.71	66.67	66.67
DT	91.52	0.90	0.82	0.86	82.27	82.27
RF	93.22	0.96	0.83	0.88	83.33	83.33
SkipConNet + RF	<b>98.30</b>	<b>0.99</b>	<b>0.96</b>	<b>0.97</b>	<b>95.83</b>	<b>95.83</b>

## 5. Results

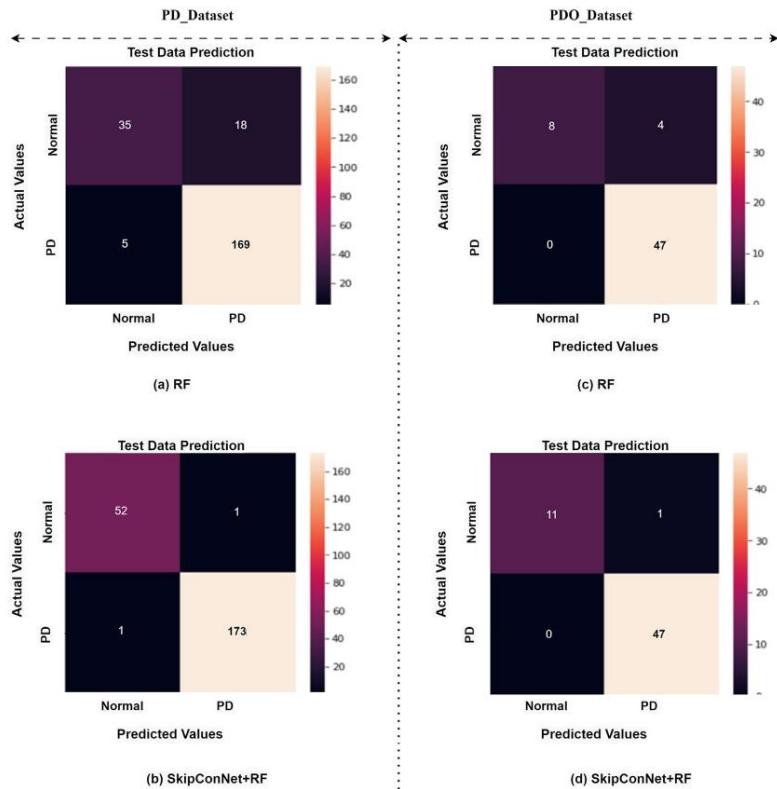
In this study, various experimental studies were carried out to detect Parkinson's disease from sound signals. To emphasize the importance of the proposed architecture, performance evaluation was made with current CNN architectures (EfficientNet-B0, VGG19, InceptionV3, LSTM, DenseNet, and AlexNet) and ML (SVM, DT, and RF) algorithms. 70% of the data sets used in the studies were reserved for training and 30% for testing. The training batch\_size value of each CNN architecture is set to 16, the learning coefficient is 0.001, and the epoch value is 100.

In the first experimental application, the PD\_Dataset dataset was used and the findings are presented in Table 3. When the results are examined, we can say that the proposed model shows the highest performance according to all metrics with 99.11% accuracy, 0.99 precision, 0.99 recall, 0.99 F1-Score, 98.77% specificity, and 98.77% AUC. In addition, it is possible to say that the architecture consisting of SkipConNet and RF combination improves the success of the RF algorithm between 9.25% and 17.19% according to different metrics.

In another application for PD detection, PDO\_Dataset is used. Experimental application results are given in Table 4. When the results are examined, it is seen that the recommended architec-

ture, accuracy, precision, recall, F1-Score, specificity, and AUC metrics show the highest performance with 98.30%, 0.99, 0.96, 0.97, 95.83%, and 95.83% success rates, respectively. In addition, it is possible to say that our model, which is formed by the combination of SkipConNet and RF algorithm algorithms, increases the performance of the RF algorithm between 3% and 13% according to different metrics.

The confusion matrix results showing the class performance of the proposed method and the RF algorithm are given in Fig. 3. The PD\_Dataset test dataset contains sample speech signals from 53 normal and 174 Parkinson's patients. When the estimation results of the RF algorithm in Fig. 3-(a) are examined, we can say that it predicted 169 PD and 35 normal samples correctly, while 23 people misclassified the voice data. However, when the SkipConNet + RF results in Fig. 3-(b) are examined, it can be seen that only 2 (1 Normal and 1 PD) recordings were misclassified. Similarly, the classification results on the PDO\_Dataset dataset are given in Fig. 3 (c-d). When the results are examined, it is seen that the RF algorithm misclassifies 4 voice samples (4 normal), while the SkipConNet + RF method misclassifies only 1 sound samples (1 normal). It is possible to say that the proposed method has shown great success and provides a significant increase in the performance of the RF algorithm.



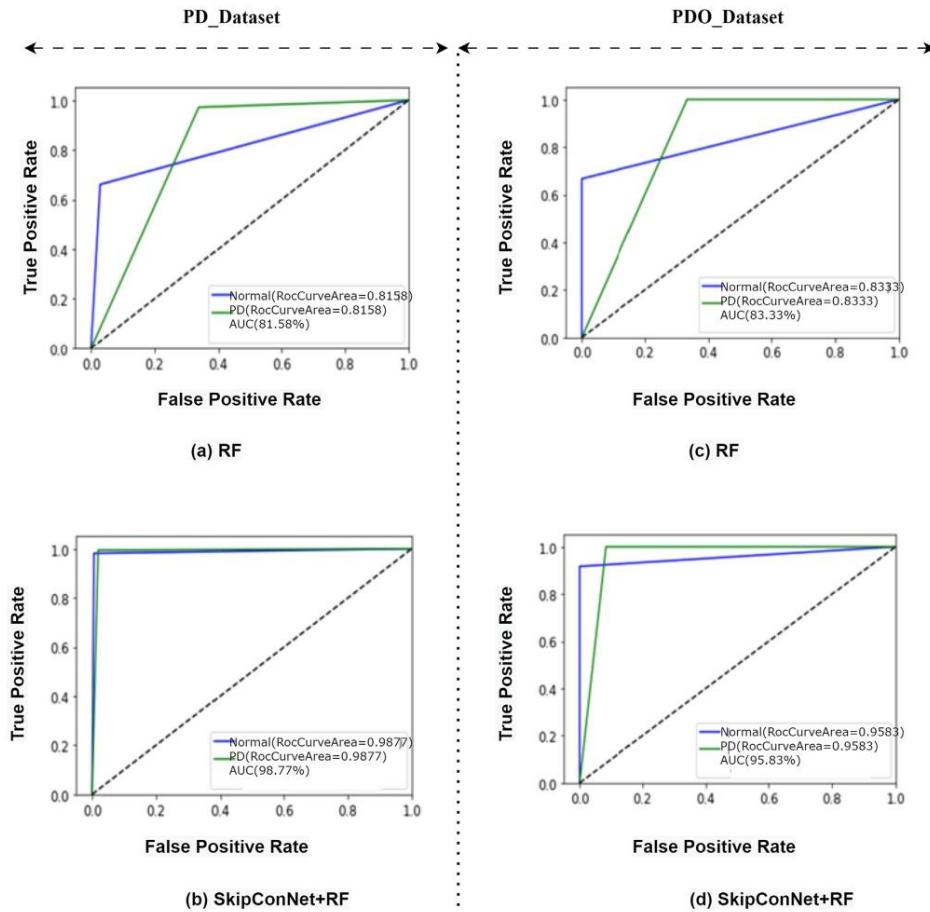
**Fig. 3.** Confusion matrix results were obtained using the test dataset. (a) and (b) according to the PD\_Dataset dataset; (c) and (d) show the results based on the PDO\_Dataset dataset.

In addition, the ROC curves of the architectures are given in Fig. 4 (a-b for PD\_Dataset and c-d for PDO\_Dataset) using test samples in the PD\_Dataset and PDO\_Dataset datasets. The RF algorithm in (a) showed a performance of 81.58% AUC and in (b) the SkipConNet + RF method showed a performance of 98.77% AUC. The obtained findings contributed 17.19% to the RF performance with the proposed method. At the same time, when the ROC curves obtained by using test samples in the PDO\_Dataset dataset in Fig. 4 (c-d) were examined, RF showed a performance of 83.33%, while the SkipConNet + RF method showed a performance increase of 12.5% and achieved a success of 95.83%. As in the previous experimental applications, we can say that the confusion matrix and ROC curve results, the feature vectors obtained from the SkipConNet method show a significant improvement in the classification performance of the RF algorithm.

## 6. Discussion

Parkinson's disease occurs as a result of the deterioration of cells in the brain that produce a substance called dopamine, which enables brain cells to communicate with each other. Diagnosing this disease at an early stage is extremely important for the course of the disease. In this study, a deep learning and machine learning-based model (SkipConNet + RF) is proposed for PD detection from speech signals. Important features were obtained with the proposed SkipConNet architecture, and then the prediction process was performed with the RF algorithm. The studies and success rates on the same and different datasets for the detection of Parkinson's disease from speech signals are given in Table 5.

In studies using the Pe-Gita dataset, Er et al. [29] show the highest success with 98.61% accuracy. Er et al. [29], feature vectors



**Fig. 4.** ROC curves are relative to the test dataset. (a) and (b) PD\_Dataset; (c) and (d) show the results based on the PDO\_Dataset dataset.

**Table 5**  
Recent studies on the same and different datasets as ours for the detection of Parkinson's disease from speech signals.

Study	Dataset	Method	Accuracy (%)	Precision	Recall	F1-Score	Specificity (%)	AUC (%)
<b>Studies Using Different Data Sets</b>								
Er et al. [29]	Pc-Gita	ResNet-101 + LSTM	98.61	96.11	–	–	–	–
Rueda et al. [67]	Pc-Gita	RF, SVM	70.00	–	–	–	–	–
Despotovic et al. [68]	23 PD and 8 HC, 195 samples in total	Gaussian Process	96.92	–	–	–	99.29	–
Narendra et al. [21]	Pc-Gita	CNN-MLP	67.93	–	–	–	66.14	–
Fujita et al. [69]	30 PD and 22 HC, 156 samples in total	RNN-SH	70.28	–	–	0.696	–	–
Vásquez-Correa et al. [70]	Three databases in Spanish, German, and Czech	CNN	89.00	–	–	–	–	–
Karan et al. [71]	Pc-Gita	MLP	91.00	–	–	0.90	0.90	–
Karan et al. [47]	Pc-Gita	RF, SVM	96.00	–	–	–	–	–
Trinh and Briën [48]	SPDD	CNN	96.70	–	–	–	–	–
<b>Studies Using the Same Data Set</b>								
Das [72]	PDO_Dataset	ANN	92.90	–	–	–	–	–
Shahbaba and Neal [73]	PDO_Dataset	Dirichlet process mixtures	87.70	–	–	82.6	–	–
Sakar and Kursun [74]	PDO_Dataset	Mutual information + Support vector machine	92.75	–	–	–	–	–
Luukka [75]	PDO_Dataset	Fuzzy entropy measures + Similarity classifier	85.03	–	–	–	–	–
Polat [76]	PDO_Dataset	kNN + FCMFW	97.93	–	–	95.6	97.37	–
<b>Proposed</b>	PDO_Dataset	SkipConNet + RF	<b>98.30</b>	<b>0.99</b>	<b>0.96</b>	<b>0.97</b>	<b>95.83</b>	<b>95.83</b>
Sakar et al. [53]	PD_Dataset	SVM	86.00	–	–	0.84	–	–
Polat [77]	PD_Dataset	RF	94.89	0.894	0.951	0.949	–	99.1
Xiong et al. [78]	PD_Dataset	LDA	91.00	–	–	–	0.92	–
El-Hasnoni et al. [79]	PD_Dataset	ANFIS + PSOGWO	87.50	–	–	–	–	–
Gündüz [19]	PD_Dataset	SVM	91.60	–	–	0.945	–	–
Gündüz [27]	PD_Dataset	CNN	86.90	–	–	0.917	–	–
Yucelbas et al. [46]	PD_Dataset	RF	82.10	–	–	–	–	–
Liu et al. [7]	PD_Dataset	SHAP-gcForest	91.78	–	–	0.945	–	–
Solana-Lavalle [10]	PD_Dataset	KNN	95.05	0.94	–	–	94.27	–
Tuncer et al. [25]	PD_Dataset	KNN	96.83	0.9677	0.9478	0.957	–	–
<b>Proposed</b>	PD_Dataset	SkipConNet + RF	<b>99.11</b>	<b>0.99</b>	<b>0.99</b>	<b>0.99</b>	<b>98.77</b>	<b>98.77</b>

were obtained using various CNN models (ResNet-18, ResNet-50, and ResNet-101). Then, the estimation process was carried out using the feature vectors obtained by the LSTM method. The highest accuracy (98.61%) was obtained from the combination of ResNet-101 and LSTM architectures. When the studies using the PDO\_Dataset dataset are examined, the proposed method has the highest success with 98.30% accuracy, 0.99 precision, 0.96 recall, 0.97 F1-Score, 95.83% specificity, and 95.83% AUC. Similarly, when the studies on PD\_Dataset are examined, the proposed method showed the highest performance in accuracy, precision, recall, F1-Score, specificity, and AUC metrics with 99.11%, 0.99, 0.99, 0.99, 98.77%, and 98.77%, respectively. Er et al. [29] showed that the feature maps obtained by using CNN models in this study significantly increased the classification performance. In addition, when all the studies in Table 5 are examined, we can say that the proposed SkipConNet + RF method shows the highest success in all metrics.

Er et al. [29], the properties of the spectrogram images were extracted and classified with LSTM. However, the results of the classification of CNN models, which are directly in the model, of the spectrogram images are not included. The classification results with direct CNN could be compared with the proposed model's. Removing features from CNN models with spectrogram images positively affected the model performance. Karan et al. [47] empirical mode decomposition (EMD)-based attributes are shown to capture speech characteristics. He proposed a new feature selection, the IMFCC model, to efficiently represent the features of Parkinson's speech. The most suitable hyperparameters were determined with the grid search algorithm and experimental studies were tested on two data sets. However, the size of the dataset used in the study is small, and there is a difference in acoustic status and

language between PD patients and normal people, which may affect the classification result. Sakar and Kursun [74] used a mutual information-based mRMR feature selection method to distinguish PD disease from sound signals. This algorithm performs feature ranking by measuring the relevance of features to the target. All data are used in mutual information calculations (for mRMR). Here, since mutual information works between two variables simultaneously, the common effects of these variables are not included in the score. In the model proposed in this study, another feature selection method other than the mRMR feature selection method could be tried. Polat [77] balanced the data set by using the SMOTE method to classify the unbalanced data set. The balanced distribution of the data set in machine learning problems reduces the bias error of machine learning problems. Making the data set balanced is one of the advantageous aspects of the proposed model. However, in recent years, CNN models have achieved very good results on many problems and a high accuracy rate. In this study, the model performance could be improved if the data set was classified with the CNN model after it was balanced.

In this study, training the data set with CNN architectures and extracting the features in the proposed model for diagnosing PD disease contributed positively to the model performance. Very detailed information is obtained about the data set given as an input to CNN models [80]. The limitation of this study is that the success rate could be increased if the model was trained on a larger set.

## 7. Conclusion

Parkinson's disease is a difficult-to-treat disease that limits the human quality of life. More common PD especially in the elderly, is

the second most common neurodegenerative disease after Alzheimer's disease. Parkinson's patients may experience many symptoms such as speech and smell. Speech signals in people with this disease seem to differ greatly from normal people. It is seen that this change in sound signals is made with high performance in disease detection without the need for any clinical test with deep learning and machine learning methods.

In this study, a deep learning and machine learning-based model called SkipConNet + RF is proposed for PD diagnosis from speech signals. It is designed to extract key features from speech signals with SkipConNet. The RF algorithm, on the other hand, is used to predict the features obtained from the SkipConNet architecture. Two different datasets, PD\_Dataset and PDO\_Dataset, were used as datasets. In addition, the performances of current deep learning models and machine learning architectures are analyzed comparatively.

In the first application using the PD\_Dataset, it has the highest success rate of 99.11% according to the accuracy metric and 0.99 according to the precision, recall, and F1-Score metrics. Similarly, it was seen that it showed the best success with 98.77% success according to the specificity and AUC metrics. Furthermore, the proposed architecture has shown a high performance by only mispredicting 2 out of a total of 227 audio signals, consisting of 53 normal and 174 PD, indicating a remarkable success rate. Similarly, in another application using the PDO\_Dataset dataset, we can say that the recommended method provides the highest performance compared to other methods with 98.30% accuracy, 0.99 precision, 0.96 recall, 0.97 F1-Score, 95.83% specificity, and 95.83% AUC. Additionally, it can be said that the proposed architecture has achieved a high success by incorrectly predicting only 1 out of 59 sound recording examples of Normal and PD patients. When we consider the results of both studies in a general way, it has been seen that the proposed method provides an improvement between 3% and 17.19% in the performance of the RF algorithm compared to different metrics.

Future studies on the diagnosis of PD disease are planned to use different neural network models and feature selection algorithms on a larger data set.

#### CRediT authorship contribution statement

**Gaffari Celik:** Conceptualization, Methodology, Software, Formal analysis, Data curation, Writing – original draft, Writing – review & editing, Visualization, Investigation, Validation. **Erdal Başaran:** Methodology, Formal analysis, Writing – review & editing, Visualization, Investigation, Validation.

#### Data availability

No data was used for the research described in the article.

#### Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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