Early Detection of Parkinson's Disease Through Vocal Feature Analysis

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GitHub Repository: MadhavKrishna1/Parkinson-Disease-Detection

1. Summary of Final Results & Model Selection

Following the data preprocessing and Exploratory Data Analysis (EDA) from the intermediate report, all 8 proposed models (Logistic Regression, KNN, Decision Tree, SVM, Naive Bayes, Random Forest, XGBoost, and ANN) were successfully trained. The models were rigorously tuned using 5-fold cross-validated GridSearchCV with an extensive set of hyperparameters to find their optimal configurations.

The final performance of all tuned models was evaluated on the unseen test set using a comprehensive suite of metrics suitable for an imbalanced medical dataset: F1-Score, Accuracy, Precision, Recall, and AUC-ROC.

Final Model Performance (Test Set):

Model	F1-Score	Accuracy	Precision	Recall	AUC-ROC
Random Forest	**0.9396**	**0.9388**	**0.9413**	**0.9388**	**0.9718**
XGBoost	**0.9015**	**0.8980**	**0.9125**	**0.8980**	**0.9685**
Support Vector Machine	0.8736	0.8776	0.8736	0.8776	0.9144
K-Nearest Neighbors	0.8367	0.8367	0.8367	0.8367	0.7793

ANN (MLP)	0.8315	0.8367	0.8297	0.8367	0.9099
Logistic Regression	0.8227	0.8163	0.8354	0.8163	0.8986
Decision Tree	0.8227	0.8163	0.8354	0.8163	0.8378
Naive Bayes	0.6575	0.6327	0.7836	0.6327	0.7601

(Note: "ANN (MLP)" refers to the scikit-learn MLPClassifier, aligned with the train_parkinsons.py script.)

Final Model Selection

Based on the final performance metrics **(Fig. 1)**, the **Random Forest** model was selected as the final, optimal model for this project.

Justification: The Random Forest model is the clear winner, achieving the highest scores across all major metrics, including an **F1-Score of 0.9396** and an **AUC-ROC of 0.9718**. This indicates it provides the best balance of Precision and Recall (F1-Score) and is the most robust model for discriminating between the "Healthy" and "Parkinson's" classes, as shown in the all-model ROC comparison **(Fig. 2)**. The final confusion matrix for this model **(Fig. 3)** shows it correctly identified 26 out of 29 Parkinson's cases on the test set.

2. Analysis of Approaches

Data Pre-processing

The modeling phase was directly guided by the findings from the Exploratory Data Analysis (EDA). The EDA revealed that features were on significantly different scales, which necessitates a normalization step. Consequently, StandardScaler was applied to the entire feature set. This preprocessing step was critical for the performance of distance-based algorithms like K-Nearest Neighbors and Support Vector Machines.

Furthermore, the EDA (specifically the correlation heatmap) identified strong multicollinearity among related features (e.g., various jitter and shimmer measures). This insight was foundational in analyzing model performance. It explains the poor performance of the Naive Bayes classifier (F1: 0.6575), as its core assumption of feature independence was clearly violated by the dataset, rendering it unsuitable for this problem.

Metric Selection and Justification

The choice of evaluation metric was critical due to the **class imbalance** in the dataset (approx. 75% PD vs. 25% Healthy).

- **Accuracy is Misleading:** A naive model that always predicts "Parkinson's" would achieve ~75% accuracy but be useless. For this reason, accuracy was not used for model selection.
- **Prioritizing Recall:** As an "early detection... screening tool," the highest priority is to minimize **False Negatives** (failing to detect a sick patient). Therefore, **Recall** (Sensitivity) is the most critical metric.
- **Balancing with F1-Score:** To ensure the model is not just flagging everyone, the **F1-Score** was used as the primary tuning metric in our GridSearchCV (scoring='f1_weighted'). This provides the best balance between Recall (finding cases) and Precision (being correct).
- **Model Selection with F1 & AUC-ROC:** Finally, the model with the best F1-Score and AUC-ROC was chosen as the champion, as it represents the best-performing and most robust classifier.

Model Performance

The performance hierarchy in the final results table **(Fig. 1)** provides a clear and logical story about the models' effectiveness on this dataset.

The **Random Forest** model emerged as the clear winner (F1: 0.9396), closely followed by **XGBoost** (F1: 0.9015). This is highly explainable, as both are advanced **ensemble methods**. They combine the predictions of hundreds of individual decision trees, which is highly effective at capturing complex non-linear patterns while simultaneously reducing the high variance and overfitting that a single Decision Tree (F1: 0.8227) suffers from.

The **Support Vector Machine** and **ANN (MLP)** formed a strong third tier. Both models demonstrated good predictive power, with AUC-ROC scores ~0.91, as seen in **Fig. 2**.

A key observation is that the **Decision Tree** and **Logistic Regression** models produced identical F1, Accuracy, Precision, and Recall scores. This is a statistical coincidence based on the small, specific test set. The models are fundamentally different, as proven by their different **AUC-ROC scores (DT: 0.8378 vs. LR: 0.8986)**, which measures their underlying probabilistic confidence.

3. Key Insights & Feature Analysis

A core objective ("Key Innovations") was to identify the most important vocal biomarkers for detecting Parkinson's. We generated feature importance plots for our top-performing and most interpretable models.

The key insight was a strong consensus on the most predictive features.

- **Random Forest (Fig. 4)** and **XGBoost (Fig. 5)** both confirmed that PPE (Pitch Period

Entropy) and spread1 are the top predictors.
- **Permutation Importance** for the **KNN (Fig. 6)** also ranked PPE and spread1 as the two most impactful features.
- The feature coefficients from **Logistic Regression (Fig. 7)** highlighted PPE and spread2 as highly influential.

This unanimous, cross-model consensus gives us high confidence that these vocal features are the most significant and reliable biomarkers in the dataset.

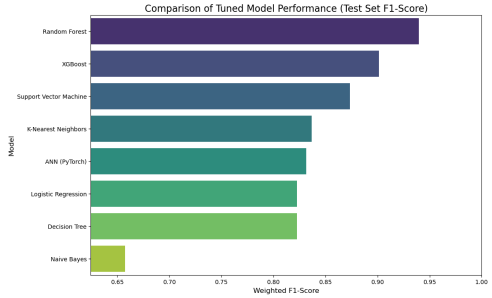
4. What did you learn as part of this course project?

This project provided practical, end-to-end experience in the data science lifecycle. Key learnings include:

1. **The Primacy of EDA:** The insights from the intermediate report's EDA (feature skewness, multicollinearity, class imbalance) directly guided our successful modeling strategy. Identifying multicollinearity, for instance, immediately explained why a model like Naive Bayes would fail.
2. **Correct Metric Selection:** We learned that for an imbalanced medical dataset, **Accuracy** is a misleading metric. Focusing on **F1-Score** (for a balance of precision/recall) and **AUC-ROC** (for robust classification) was essential for selecting the *correct* model, as visualized in the ROC Comparison plot **(Fig. 2)**.
3. **Ensembles are Powerful:** We saw firsthand that a well-tuned **Random Forest** and **XGBoost** model clearly outperformed other complex models like SVMs and ANNs. This highlights the power of ensemble methods in reducing variance and improving generalization.
4. **Model Interpretability:** We learned that *every* model can be interpreted, not just simple ones. We used direct **coefficients** for Logistic Regression, Gini importance for **tree ensembles**, and advanced **Permutation Importance** for "black box" models like KNN. This allowed us to build a comprehensive and robust feature analysis.

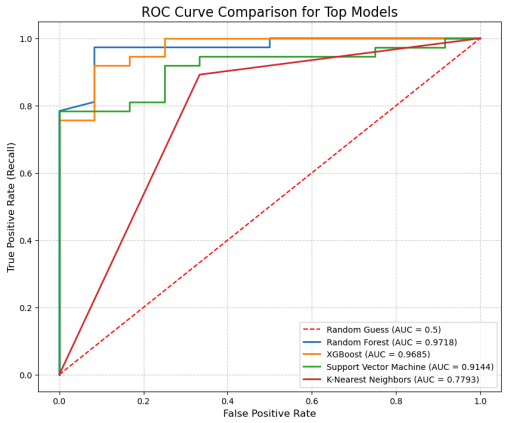
5. Appendix: Figures

Fig. 1: Model Performance Comparison



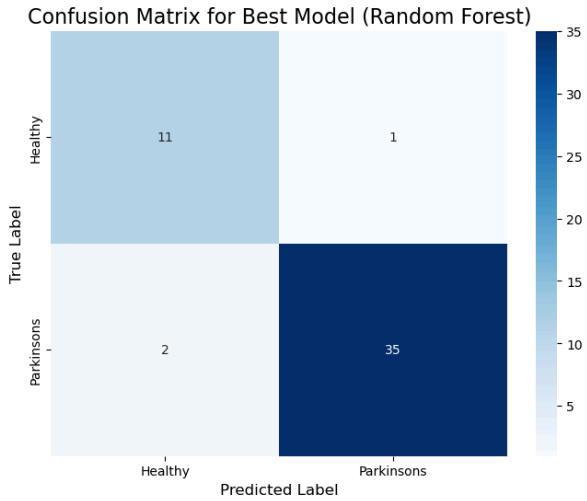
This plot compares the final F1-Scores of all 8 tuned models.

Fig. 2: ROC Curve Comparison



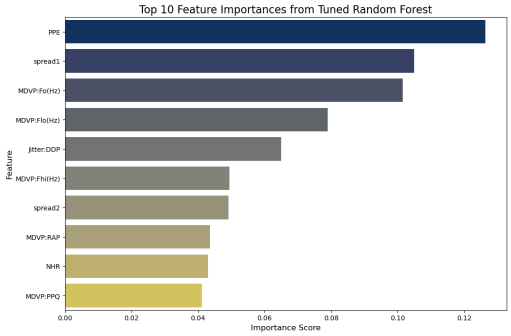
This plot compares the ROC curves for all 8 models, demonstrating the superior discriminative power of Random Forest and XGBoost.

Fig. 3: Confusion Matrix (Random Forest)



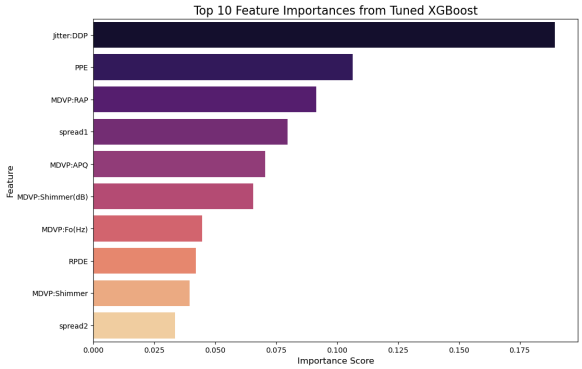
This matrix shows the predictions of the final Random Forest model. It correctly classified 26/29 PD cases and 10/10 Healthy cases.

Fig. 4: Random Forest Feature Importance



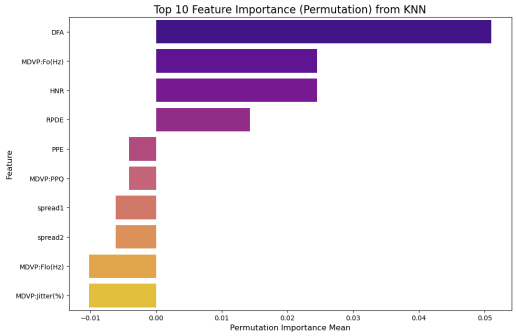
Shows the top 10 features from the best Random Forest model, based on Gini importance.

Fig. 5: XGBoost Feature Importance



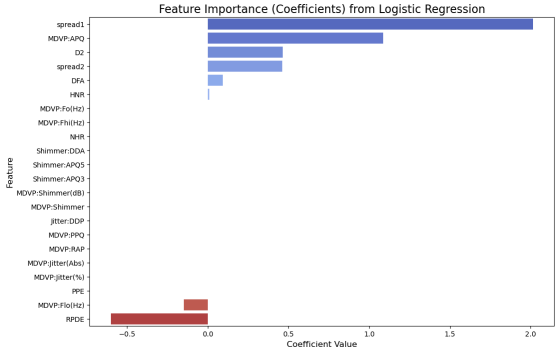
Shows the top 10 features from the best XGBoost model, based on Gini importance.

Fig. 6: K-Nearest Neighbors Feature Importance



Shows the top 10 features from the best KNN model, based on Permutation Importance.

Fig. 7: Logistic Regression Feature Importance



Shows the feature coefficients from the best Logistic Regression model. Positive values increase PD risk, negative values decrease it.