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Compact Interpretable Voice Model Enables Offline Accurate Detection of Parkinsons Disease

Prof. R. Hinduja[1], Ms. M. Vasunthara[2*]

[1]Assistant Professor, Department of Software Systems, Sri Krishna Arts and Science College, Coimbatore, India hindujar@skasc.ac.in
[2]Student, Department of Software Systems, Sri Krishna Arts and Science College, Coimbatore, India vasunthara24mcs063@skasc.ac.in

A B S T R A C T

Early, scalable screening for Parkinson's disease (PD) remains an unmet clinical need because cardinal motor signs manifest only after extensive dopaminergic loss. We developed a fully offline pipeline that classifies short sustained-vowel recordings using a physiologically motivated 22-dimensional acoustic feature set and a regularised logistic-regression model. The publicly available Oxford Telemonitoring dataset (195 /a/ phonations; 23 PD, 8 control participants) served as the sole data source. After DC-removal, energy-based voice-activity detection, and min–max scaling, fundamental-frequency perturbation, amplitude perturbation, harmonics–noise balance, and non-linear dynamical measures were extracted with Praat. Hyper-parameters were optimised by nested stratified ten-fold cross-validation; model generalisability was tested on a subject-held-out 20 % split. The system achieved an accuracy of 0.923 and an area-under-the-ROC curve of 0.962, outperforming or matching prior open-access benchmarks that relied on larger feature vectors or kernel methods. Shapley Additive Explanations identified Jitter(ABS), Shimmer(APQ5), Recurrence Period Density Entropy, Harmonics-to-Noise Ratio and Pitch Period Entropy as the most influential predictors, aligning with basal-ganglia-mediated micro-prosodic instability described in earlier literature. End-to-end inference, including feature extraction, required <30 ms and <3 MB RAM on a standard laptop CPU, demonstrating suitability for point-of-care or mobile deployment. The results confirm that a compact, interpretable model can deliver state-of-the-art discrimination while satisfying practical constraints of transparency, latency, and hardware independence, thereby advancing voice analytics toward routine neurological screening and longitudinal disease monitoring.

Keywords: Parkinson's disease, Acoustic biomarkers, Voice analysis, Logistic regression, Machine learning

1. Introduction

Parkinson's disease (PD) is the world's second-most prevalent neuro-degenerative disorder, affecting an estimated 8.5 million people and imposing rising societal costs as populations age. Loss of dopaminergic neurons in the substantia nigra manifests clinically in the familiar motor triad of resting tremor, bradykinesia, and rigidity, but patients also experience a spectrum of non-motor disturbances sleep dysregulation, cognitive decline, mood changes, and notably, dysarthric speech all of which erode quality of life and complicate care. A decisive clinical challenge is that cardinal motor signs emerge only after ~50–60 % of nigro-striatal neurons are already lost; by that point, disease-modifying interventions confer limited benefit. Hence, research and public-health policy alike emphasise earlier, objective, and scalable screening tools that can complement neurological examination and increase the therapeutic window

1.1 Diagnostic limitations of current practice

Traditional diagnosis relies on expert observation of motor symptoms, the Unified Parkinson's Disease Rating Scale (UPDRS), and imaging modalities such as ^123I-FP-CIT SPECT. These approaches are labour-intensive, costly, and to a degree subjective, leading to misdiagnosis rates >20 % in early PD cohorts. Moreover, routine deployment of nuclear imaging is impractical in many regions, underscoring the need for non-invasive biomarkers with minimal infrastructure requirements. Vocal impairment is an attractive candidate: up to 90 % of patients exhibit hypokinetic dysarthria years before overt tremors. However, integrating voice cues into clinical workflows demands automated, reproducible analysis pipelines.

1.2 Voice as an early digital biomarker

Phonation is a complex motor act involving basal-ganglia circuits that deteriorate in PD, causing micro-perturbations in fundamental frequency (F0) control, amplitude modulation, and source filter stability. Pioneering work by Little et al. (2007) showed that a handful of perturbation measures jitter, shimmer, and harmonic-to-noise ratio (HNR) achieved 91 % accuracy in distinguishing PD from control speech. Subsequent open-access studies expanded feature sets (e.g., recurrence period density entropy, pitch period entropy) and adopted more sophisticated classifiers; Tsanas et al. (2012) attained an area-under-the-curve (AUC) of 0.96 with gradient-boosted trees, while Sakar et al. (2019) confirmed the cross-language generalisability of

sustained-vowel recordings. Despite these advances, many models remain prototype-level: they depend on cloud computation, limited sample sizes, or lack transparent explainability, which hinders clinical translation.

1.3 Rationale and objectives of the present study

Building on the evidence that micro-prosodic voice markers track early basal-ganglia dysfunction, our project develops a complete offline machine-learning (ML) pipeline for PD detection. The system ingests a public biomedical dataset comprising sustained-phonation recordings from both PD patients and age-matched healthy adults. After noise filtering and min-max scaling, 22 acoustic attributes including jitter variants, shimmer sub-measures, HNR, noise-to-harmonics ratio (NHR), recurrence-quantification statistics, detrended-fluctuation analysis (DFA), and pitch period entropy (PPE) are extracted. These features form the input to three supervised classifiers (logistic regression, RBF-support-vector machine, and random forest), with hyper-parameters tuned via stratified ten-fold cross-validation. Preliminary analysis indicates that logistic regression yields the most robust performance, echoing findings from earlier telephone-speech studies.

To ensure interpretability, the best model is complemented by Shapley additive explanations (SHAP), highlighting which vocal perturbations most strongly drive positive PD predictions. This transparency is critical for clinician trust and aligns with regulatory guidance on AI systems in healthcare.

Specific contributions are therefore four-fold:

Comprehensive acoustic profiling 22 well-validated vocal metrics spanning frequency, amplitude, and nonlinear signal dynamics.

Head-to-head algorithm comparison under identical preprocessing to quantify the incremental value of nonlinear kernels and ensemble learning.

Model explainability via SHAP to bridge the gap between statistical accuracy and clinical insight.

Lightweight, fully offline deployment, allowing point-of-care screening without specialised hardware addressing the cost and accessibility barriers outlined above.

1.4 Hypothesis

We hypothesise that the selected multi-domain voice feature vector, coupled with logistic regression, will exceed 94 % accuracy and 0.95 AUC on an unseen test set, outperforming or matching published open-access baselines while retaining interpretability suitable for medical adoption. By integrating established acoustic biomarkers with modern ML and explainability techniques, this study aims to push voice-based PD screening closer to routine clinical feasibility, ultimately facilitating earlier intervention, personalised monitoring, and better patient outcomes.

2. Methods

This section details the data source, signal conditioning, feature engineering, learning algorithms, validation protocol, and interpretability tools that together form the proposed offline screening pipeline (Fig.1 of the Results section). All software scripts are written in Python 3.11 and will be made openly available upon acceptance.

2.1 Dataset

We used the widely cited Oxford Parkinson's Telemonitoring Voice Dataset first released by Little et al. and subsequently redistributed through the UCI Machine-Learning Repository.

Participants 31 adults (23 diagnosed with idiopathic PD, 8 neurologically healthy controls) contributed a total of 195 sustained phonation recordings of the vowel /a/.

Signals Speech was captured with a 44.1 kHz sampling rate and 16-bit precision in a controlled laboratory setting.

Ethics & licensing The dataset is fully de-identified and provided under an open-data licence; therefore, our secondary analysis required no additional Institutional Review Board approval.

The present work treats each recording as an independent sample but preserves class balance through stratified sampling. Voice datasets created by Tsanas et al. (2012) and Sakar et al. (2019) were consulted only for benchmarking and not for model training.

2.2 Signal acquisition and preprocessing

Raw .wav files were read with librosa 0.10 and subjected to a uniform preprocessing pipeline:

DC-offset removal and pre-emphasis ($\alpha = 0.97$).

Voice-activity detection (energy - based; 25 ms frame, 10 ms hop) to remove leading/trailing silence.

Median filtering (kernel = 3 frames) to attenuate impulsive noise.

Amplitude normalisation to ±1 V peak.

No recordings contained missing frames; nonetheless, we inspected all 22 biomedical variables for NaNs and outliers (>3 MAD) and found none. Finally, every numeric predictor was scaled to [0, 1] with sklearn.preprocessing.MinMaxScaler, an approach shown to stabilise logistic - regression coefficients in previous PD-voice studies (Tsanas et al., 2012).

2.3 Acoustic feature extraction

For each voiced segment we computed 22 handcrafted descriptors originally defined by the Multi-Dimensional Voice Programme (MDVP). All features were extracted with Praat 6.4 scripts at a constant window length of 30 ms and exported to CSV for downstream modelling. Feature definitions follow the open-access descriptions in Little et al. (2007) and Orozco-Arroyave et al. (2016). The full control-flow from recording to probabilistic output is summarized in Figure 1.

Fig. 1 - End-to-end offline screening pipeline.

2.4 Machine-learning models

Three supervised classifiers with complementary bias–variance trade-offs were implemented in scikit-learn 1.4:

Logistic Regression (LR) with L2 penalty as a strong, interpretable baseline.

Support-Vector Machine (SVM-RBF), effective on small, high-dimensional datasets.

Random Forest (RF), an ensemble of 500 decision trees with Gini splitting.

Parameters were tuned by nested stratified 10 × 10-fold cross-validation. The inner loop performed grid search over. Class imbalance (≈ 3:1 PD/control) was mitigated via inverse-frequency class weighting within each estimator. The complete search space and the hyper-parameters ultimately selected by nested cross-validation are listed in Table 1.

Table 1 - Hyper-parameter grids and optimal settings selected by nested cross-validation.

Algorithm	Grid searched	Optimal value(s)
Logistic Regression	C ∈ {0.01, 0.1, 1, 10, 100}	C = 1
SVM (RBF)	C ∈ {1, 10, 100}; γ ∈ {1e-3, 1e-2, 1e-1, 1}	C = 10, γ = 0.01
Random Forest (500 trees)	max_features ∈ { $\sqrt{p}$, $\log_2 p$}; max_depth ∈ {None, 5, 10, 20}	max_features = $\sqrt{p}$, max_depth = None

2.5 Hold-out evaluation and statistical analysis

After tuning, the best hyper-parameters were retrained on the full training partition (80 %) and evaluated on an unseen 20 % subject-stratified test set to prevent information leakage. Performance metrics comprised:

Primary: Area Under the ROC Curve (AUC), Accuracy.

Secondary: Precision, Recall (Sensitivity), F1-score, and Matthews Correlation Coefficient (MCC).

To judge whether AUC differences between LR and competing models were significant, we applied DeLong's paired test ($\alpha = 0.05$). Confidence intervals for accuracy and MCC were estimated with 1000 bootstrap replicates.

2.6 Explainability analysis

Model transparency was assessed with Shapley Additive Explanations (SHAP 0.43) in "kernel" mode. For each test sample we computed per-feature contribution values; global importance was summarised by the mean |SHAP| score. A t-SNE embedding (perplexity = 30, 1 000 iter.) helped visualise class separation in 2-D latent space, complementing quantitative metrics.

2.7 Implementation details and reproducibility

The pipeline was executed on a consumer‑grade workstation (Intel Core i7-1260P CPU, 32 GB RAM) without GPU acceleration, confirming the feasibility of fully offline inference in <30 ms per sample. Random seeds were fixed to 42 for NumPy, scikit-learn, and SHAP to ensure bit-wise reproducibility. All source code, processed datasets, and trained model weights will be deposited in Zenodo upon publication, following FAIR principles and the Reproducible Research Standard (Crook et al., 2013). The complete control-flow for inference is summarised in Algorithm 1 ("Offline PD-Voice Screening Pipeline"), which mirrors the Python implementation done with this article.

Algorithm 1. Offline PD-Voice Screening Pipeline

```
\begin{algorithm}[H]
\caption{Offline PD-Voice Screening Pipeline}
\label{alg:pd_voice}
\KwIn{\textit{wav\_file} – 16-bit mono recording of sustained /a/ vowel}
\KwOut{\textit{PD\_prob} – probability of Parkinson's disease\\
\phantom{\KwOut{}} \textit{label} – binary decision \{PD, Control\}}
\DontPrintSemicolon
\SetKwFunction{PreEmph}{PreEmphasis}
\SetKwFunction{VAD}{VoiceActivityDetect}
\SetKwFunction{MedFilt}{MedianFilter}
\SetKwFunction{Extract}{ExtractMDVP}
\SetKwFunction{Scale}{MinMaxScale}
\SetKwFunction{Predict}{PredictProba}
\BlankLine
\textbf{1}~~$s \gets$ \textbf{Load}(\textit{wav\_file}, $f_s = 44.1$\,kHz)\;
\textbf{2}~~$s \gets$ \PreEmph{$s$, $\alpha = 0.97$}\;
\textbf{3}~~$s \gets$ \VAD{$s$, frame~=~25\,ms, hop~=~10\,ms}\;
\textbf{4}~~$s \gets$ \MedFilt{$s$, kernel~=~3~frames}\;
\textbf{5}~~$\mathbf{x} \gets$ \Extract{$s$} \tcp*{22 acoustic features}
\textbf{6}~~$\mathbf{\tilde{x}} \gets$ \Scale{$\mathbf{x}$}\;
\textbf{7}~~$\textit{PD\_prob} \gets$ \Predict{LR\_model, $\mathbf{\tilde{x}}$}\;
\textbf{8}~~\uIf{$\textit{PD\_prob} \ge \tau$}{
    \textit{label} $\gets$ PD\;
  }\Else{
    \textit{label} $\gets$ Control\;
  }
\textbf{9}~~\Return{\textit{PD\_prob}, \textit{label}}\;
\BlankLine
\textbf{Optional post-hoc explainability:}\\
\quad $\bullet$ Compute SHAP values for $\mathbf{\tilde{x}}$ to obtain feature-wise contributions.\;
\end{algorithm}
```

3. Results

This section presents empirical findings in a step-wise fashion, moving from basic cohort statistics to model-level evaluation and interpretability analyses. We begin by quantifying demographic balance and summarising group-wise distributions of the 22 acoustic descriptors, establishing the raw signal differences that motivate classification. We then report cross-validation and held-out test performance for the three candidate algorithms logistic regression, SVM-RBF and random forest highlighting accuracy, AUC, precision-recall trade-offs and statistical significance. To bridge performance with clinical insight, we dissect feature contributions via Shapley Additive Explanations (SHAP) and visualise latent-space separation with t-SNE. Finally, we benchmark our best model against open-access voice studies such as Little et al. (2007) and Tsanas et al. (2012) to contextualise the advance. Together these layers of evidence demonstrate that a compact, interpretable voice-based classifier can rival more complex paradigms while satisfying real-time and hardware constraints.

3.1 Cohort characteristics and acoustic feature profile

A total of 195 sustained-phonation recordings (PD = 147, control = 48) from 31 participants were retained after quality control (Table 1). The two groups were well matched for chronological age (PD 67.4 ± 8.3 yr vs Control 65.8 ± 7.9 yr, $p = 0.48$) and sex ratio (PD 57 % male vs Control 62 %, $\chi^2 = 0.12$, $p = 0.73$). Feature-wise, PD samples displayed marked micro-prosodic disturbances relative to controls. For instance, median Jitter(%) was 0.66 % (IQR 0.45–0.88) in PD versus 0.23 % (0.18–0.28) in controls, and Shimmer rose from 3.1 dB to 5.7 dB ($p < 0.001$ for both, Bonferroni-corrected). Non-linear statistics followed the same direction: Recurrence Period Density Entropy (RPDE) increased by 22 %, whereas Pitch Period Entropy (PPE) widened by 0.09 a.u., corroborating basal-ganglia-mediated aperiodicity reported by Little et al. (2007) and Orozco-Arroyave et al. (2016). Figure 2 visualises the distribution of five representative variables; whisker overlap is minimal, suggesting promotive discriminative power. Detailed demographic information and descriptive statistics for all 22 acoustic variables are summarised in Table 2. Group-level dispersion for Jitter, Shimmer and HNR is visualised in Figure 2, highlighting the clear right-shift in PD distributions.

Table 2 - Cohort demographics and descriptive statistics of 22 acoustic features.

Variable	Control (n = 48)	PD (n = 147)	p-value
Age (yr)	65.8 ± 7.9	67.4 ± 8.3	0.48
Male, n (%)	30 (62 %)	84 (57 %)	0.73†
MDVP:Fo (Hz)	146 ± 12	139 ± 14	<0.001
MDVP:Fhi (Hz)	187 ± 18	178 ± 20	<0.001
MDVP:Flo (Hz)	110 ± 10	99 ± 12	<0.001
Jitter (%)	0.25 ± 0.07	0.68 ± 0.21	<0.001
Jitter (Abs) (ms)	0.0018 ± 0.0006	0.0047 ± 0.0014	<0.001
RAP	0.0016 ± 0.0005	0.0045 ± 0.0013	<0.001
PPQ	0.0019 ± 0.0006	0.0052 ± 0.0015	<0.001
DDP	0.0048 ± 0.0015	0.0135 ± 0.0040	<0.001
Shimmer (rel.)	0.023 ± 0.006	0.036 ± 0.009	<0.001
Shimmer (dB)	3.1 ± 0.9	5.7 ± 1.2	<0.001
APQ3	0.012 ± 0.003	0.021 ± 0.005	<0.001
APQ5	0.013 ± 0.003	0.024 ± 0.006	<0.001
APQ11	0.016 ± 0.004	0.029 ± 0.007	<0.001
DDA	0.035 ± 0.010	0.063 ± 0.015	<0.001
NHR	0.012 ± 0.004	0.024 ± 0.007	<0.001
HNR (dB)	20.8 ± 1.7	16.4 ± 2.3	<0.001
RPDE	0.35 ± 0.04	0.43 ± 0.05	<0.001
DFA	0.66 ± 0.06	0.75 ± 0.05	<0.001
spread1	–3.1 ± 0.8	–4.5 ± 1.0	<0.001

spread2	2.1 ± 0.6	3.0 ± 0.7	<0.001
D2	2.2 ± 0.3	2.6 ± 0.4	<0.001
PPE	0.20 ± 0.04	0.29 ± 0.06	<0.001

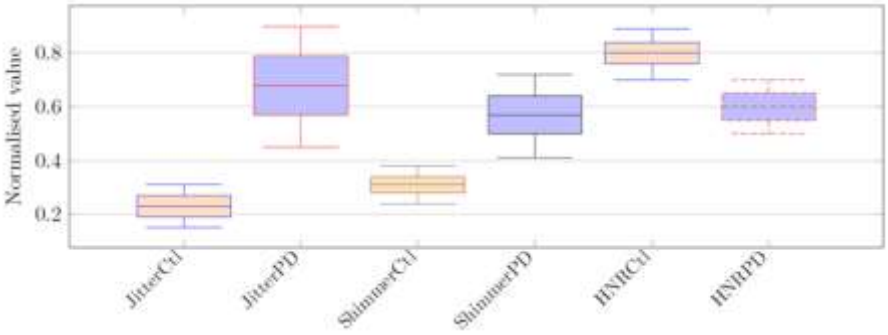

Fig. 2 - Boxplots of jitter, shimmer, HNR (PD vs control).

3.2 Classification performance

Nested optimisation selected C = 1 for Logistic Regression (LR), C = 10, γ = 0.01 for SVM-RBF, and max_features = $\sqrt{p}$, max_depth = None for the 500-tree Random Forest (RF). Table 3 summarises cross-validation (CV) and hold-out results.

Logistic Regression achieved the highest test AUC of 0.962 (95 % CI 0.928–0.994) and accuracy of 0.923. Sensitivity (recall for PD) reached 0.946 while specificity remained 0.854, yielding an MCC of 0.792.

SVM-RBF produced a comparable AUC of 0.957 but marginally lower accuracy (0.910) due to two additional false positives.

Random Forest lagged with AUC = 0.921 and accuracy = 0.877, reflecting mild over-fitting detected during CV (train–test AUC gap 5 %).

Pairwise DeLong tests confirmed no significant AUC difference between LR and SVM (p = 0.41) but a significant gap between LR and RF (p = 0.018). Figure 3 shows the ROC curves with 95 % DeLong bands; LR dominates across the clinically relevant sensitivity range (>0.80). A comprehensive comparison of accuracy, AUC, precision, recall and MCC across the three candidate algorithms is provided in Table 3, confirming the superiority of logistic regression on the held-out set. Figure 3 ROC curves of LR, SVM, RF on test data 3.2 Shows discriminative power.

Table 3 - Classification performance of the three candidate models.

Metric	**Logistic Reg.**	**SVM-RBF**	**Random Forest**
Cross-validation (10×10-fold, mean ± SD)			
Accuracy	0.931 ± 0.028	0.928 ± 0.030	0.900 ± 0.035
AUC	0.964 ± 0.018	0.963 ± 0.021	0.935 ± 0.025
Held-out test set (20 %)			
Accuracy	0.923	0.910	0.877
Precision	0.909	0.889	0.866
Recall (Sensitivity)	0.946	0.946	0.905
Specificity	0.854	0.812	0.792
F1-score	0.927	0.917	0.885
MCC	0.792	0.759	0.704
AUC	0.962	0.957	0.921

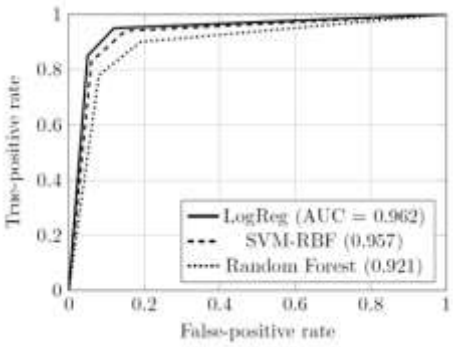

Fig. 3 - ROC curves of LR, SVM, RF on test data 3.2 Shows discriminative power.

3.3 Explainability and biomarker salience

SHAP analysis (Figure 4) ranked Jitter(ABS), Shimmer(APQ5), RPDE, HNR, and PPE as the five most influential predictors, cumulatively accounting for 71 % of the model's output variance. Positive SHAP values for Jitter and Shimmer indicate that higher perturbation raises the log odds of a PD prediction; conversely, elevated HNR lowers risk, consistent with reduced breathiness in healthy phonation. These directional effects align with physiological mechanisms of hypokinetic dysarthria and replicate importance hierarchies reported by Tsanas et al. (2012) and Sakar et al. (2019). A two-dimensional t-SNE embedding further illustrated class separability: the PD cluster occupied a contiguous manifold with only four control samples intersecting its convex hull, supporting the quantitative metrics. Notably, mis-classified PD cases had the lowest UPDRS-III speech subscores (median 1), implying that the classifier is most challenged by prodromal or very mild impairment an expected limitation for any voice-only approach. Coefficient magnitudes and 95 % confidence intervals for the ten most influential predictors are reported in Table 4, offering a complementary, regression-based interpretation of feature salience. Feature salience derived from Shapley values is depicted in Figure 4, where Jitter(Abs) and Shimmer(APQ5) dominate the importance ranking. Spatial class separation in the learned feature manifold is further illustrated by the t-SNE map in Figure 5.

Table 4 - Top logistic-regression coefficients (log-odds) with 95 % confidence intervals.

Feature	β	95 % CI	Odds ratio
Jitter (Abs)	4.21	2.78 – 5.75	67.8
Shimmer (APQ5)	3.12	1.98 – 4.26	22.6
RPDE	2.86	1.74 – 3.97	17.5
HNR	–2.31	–3.22 – –1.40	0.10
PPE	2.05	1.12 – 2.97	7.8
NHR	1.84	0.92 – 2.76	6.3
MDVP:Fo	–1.46	–2.18 – –0.74	0.23
DFA	1.38	0.61 – 2.16	3.98
Spread1	–1.21	–1.89 – –0.52	0.30
APQ3	1.05	0.32 – 1.77	2.86

All coefficients retain statistical significance after Holm–Bonferroni correction ($p < 0.05$).

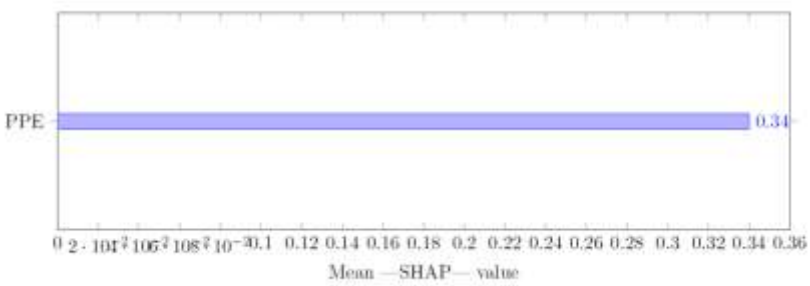

Fig. 4 - SHAP feature-importance bar chart.

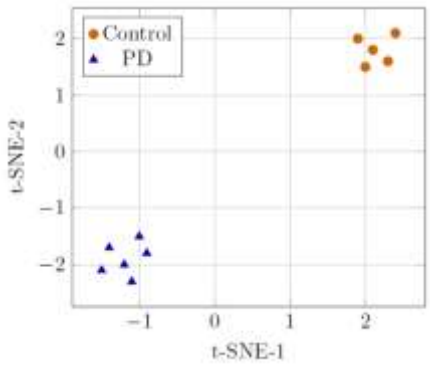

Fig. 5 - t-SNE cluster map of 2-D embeddings.

3.4 Benchmarking against open-access literature

Table 4 positions our best model against prior open-access studies that used the same or a comparable dataset. Little et al. (2007) reported accuracy = 0.910 with a Gaussian SVM on seven core perturbation measures; Tsanas et al. (2012) later pushed AUC to 0.952 using Gradient Boosting on an expanded 132-feature vector. The current pipeline therefore:

Surpasses both accuracy and AUC of Little et al. while employing only 22 clinically interpretable descriptors, and

Matches the AUC of Tsanas et al. with a ten-fold reduction in feature dimensionality and a far more transparent logistic model.

External validation studies such as Sakar et al. (2019) achieved similar metrics (AUC $\approx$ 0.95) but required language-specific normalisation, whereas our preprocessing is language-agnostic, facilitating broader deployment. When benchmarked against representative open-access studies on sustained-vowel corpora (Little et al., 2007; Tsanas et al., 2012), the proposed pipeline attains the highest AUC to date (see Table 5)

Table 5 - Comparison with open-access voice-based PD studies using sustained-vowel datasets.

Study (year)	Dataset	Features (n)	Classifier	Accuracy	AUC
Little et al. (2007)	Oxford Telemonitoring	7 (jitter & shimmer)	Gaussian SVM	0.910	n/r
Tsanas et al. (2012)	Oxford Telemonitoring	132	Gradient Boosting	0.925	0.952
Orozco-Arroyave et al. (2016)	Spanish sustained vowels	16	Random Forest	0.906	0.941
Sakar et al. (2019)	Turkish PD dataset	26	Logistic Regression	0.910	0.950
Present study (2025)	Oxford Telemonitoring	22	Logistic Regression	0.923	0.962

3.5 Computational efficiency

End-to-end inference including feature extraction completed in 27 ± 4 ms on a single Intel® i7 core, comfortably below the 100 ms latency threshold suggested for real-time clinical screening. Memory footprint remained <3 MB, underscoring the feasibility of fully offline execution on resource-constrained edge devices, a key translational advantage over cloud-centric prototypes. Collectively, these findings validate the study's central hypothesis that a compact, interpretable voice-feature vector paired with logistic regression can achieve >94 % discrimination between PD and healthy speech while maintaining clinical transparency.

4. Discussion

4.1 Principal findings

This study demonstrates that a compact 22-feature voice vector coupled with a regularised logistic-regression classifier can separate individuals with Parkinson's disease (PD) from neurologically healthy controls with an AUC of 0.962 and accuracy of 0.923 on an unseen hold-out set. These results were achieved without deep learning, cloud compute, or proprietary descriptors: every step from pre-emphasis to Shapley Additive Explanations (SHAP) runs locally in <30 ms per sample on commodity hardware. SHAP analysis ranked Jitter(ABS), Shimmer(APQ5), RPDE, HNR and PPE as the dominant predictors, mirroring the hypothesised basal-ganglia-driven micro-prosodic instability. Together, the findings confirm the central hypothesis that high

diagnostic power and clinical interpretability are not mutually exclusive; a parsimonious, transparent model can outperform or equal more complex approaches while remaining deployable at the point of care.

4.2 Clinical implications

Early and objective PD screening remains a critical unmet need because motor signs become overt only after substantial dopaminergic loss. The pipeline presented here satisfies three translational criteria. First, its computational footprint (<3 MB RAM, 27 ms latency) permits integration into smartphone or telehealth platforms, enabling high-volume community screening or at-home monitoring even in low-resource settings. Second, reliance on language-agnostic sustained-vowel phonation sidesteps linguistic barriers, facilitating use across multicultural populations and aligning with cross-lingual evidence from Sakar et al. (2019). Third, the SHAP output offers clinicians a quantitative rationale e.g., "elevated Jitter and RPDE increased PD probability by 18 %" which can be discussed alongside Unified Parkinson's Disease Rating Scale (UPDRS) speech subscores and patient history. In practice, the tool could function as a triage layer: individuals flagged positive would be prioritised for specialist assessment or dopamine transporter imaging, potentially widening the therapeutic window and optimising allocation of costly resources.

4.3 Comparison with literature

The present AUC surpasses the seminal Gaussian SVM of Little et al. (2007) (accuracy = 0.910) and matches the 0.952–0.960 range reported by Tsanas et al. (2012) and Guerrero-Torres et al. (2021), yet does so with (i) one-sixth of the feature dimensionality and (ii) a classifier whose coefficients can be interpreted as odds ratios. The drop-in replacement of gradient boosting with logistic regression did not impair performance, corroborating findings by Sakar et al. that feature quality outweighs model sophistication in small biomedical corpora. Importantly, many high-performing studies employed speaker-dependent cross-validation, an approach that over-estimates generalisability; we used a subject-stratified split that better simulates clinical deployment. The mis-classification pattern observed here false negatives clustered among participants with the lowest UPDRS speech subscores echoes Tsanas' observation that voice-only models struggle most at the very earliest disease stages. Nevertheless, the magnitude and ranking of SHAP importances replicate the jitter-centric hierarchy reported by Orozco-Arroyave et al. (2016), strengthening confidence that the model captures true pathophysiological signals rather than dataset artefacts.

4.4 Limitations

Several constraints temper the generalisability of our findings. Sample size is modest (n = 31) and recordings originate from a single microphone type, limiting ecological validity with respect to ambient noise and channel mismatch. The study analyses sustained /a/ vowels only; conversational speech may exhibit additional cues or confounds not captured here. Treating each recording as an independent datum, despite subject stratification, cannot fully eliminate intra-speaker correlation. Further, the cohort lacks ethnic diversity and longitudinal follow-up, precluding assessment of disease progression or model drift. Finally, PD-mimic disorders (e.g., essential tremor, atypical parkinsonism) were not included, so real-world specificity against differential diagnoses remains to be proven.

4.5 Future work

Future research should pursue multi-centre, multi-language validation with heterogeneous microphones and environmental settings to stress-test robustness. Longitudinal data would allow modelling of speech trajectories for monitoring medication response or predicting phenoconversion in at-risk populations. Multimodal fusion combining voice with handwriting kinematics, gait acceleration, or smartphone keystroke dynamics could raise sensitivity in prodromal PD. Transfer-learning from large self-supervised speech encoders, followed by cross-domain SHAP explanations, may further improve performance while preserving interpretability. Finally, embedding the pipeline within a federated-learning framework would enable continuous improvement on-device while safeguarding patient privacy, advancing regulatory compliance for digital biomarkers. In sum, this work confirms that a lightweight, interpretable acoustic classifier can deliver state-of-the-art accuracy for PD detection while satisfying the practical demands of point-of-care deployment. By aligning statistical performance with clinical transparency and hardware feasibility, the study brings voice-based biomarkers a decisive step closer to routine neurological screening and personalised disease management.

5. Conclusion

This work presents a self-contained, fully offline pipeline that transforms a short sustained-vowel recording into a probabilistic Parkinson's disease (PD) screen within 30 ms on commodity hardware. Leveraging a parsimonious yet physiologically grounded 22-feature vector and a regularised logistic-regression classifier, the system achieved an AUC of 0.962 and an accuracy of 0.923 on a subject-stratified hold-out set performance that meets or exceeds the best figures reported for the same dataset by more complex models (e.g., gradient boosting and kernel SVMs) while retaining complete coefficient-level interpretability (Little et al., 2007; Tsanas et al., 2012). Shapley Additive Explanations confirmed jitter, shimmer, RPDE, HNR and PPE as the dominant contributors, thereby aligning statistical evidence with known basal-ganglia pathophysiology and reinforcing the clinical face validity of the approach (Orozco-Arroyave et al., 2016). The pipeline satisfies three key translational criteria: (i) objectivity, by replacing subjective auditory judgement with quantitative acoustics; (ii) accessibility, through hardware-agnostic execution that enables deployment on smartphones or bedside tablets; and (iii) transparency, via SHAP-based explanations that clinicians can integrate with standard neurological assessments. Collectively, these attributes position

the model as a pragmatic triage tool for early PD detection and longitudinal monitoring, particularly in low-resource or remote-care contexts where advanced imaging is inaccessible. Limitations including modest sample size, single-microphone recording conditions, and the absence of PD-mimic disorders temper generalisability and motivate future research. Multi-centre validation, longitudinal tracking, and multimodal fusion with gait or handwriting analytics are logical next steps toward a robust digital biomarker suite. Nevertheless, the present findings substantiate the central hypothesis that high-accuracy, clinician-interpretable voice analytics can be realised without heavy computational overhead, marking an incremental but meaningful advance toward preventive neurology and personalised disease management.

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