Explainable Parkinson's Disease Detection Using PaHaW Handwriting Signals and Novel Motion Biomarkers

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Abstract. This study provides a new explainable framework for handwriting-based classification of Parkinson's disease with five domain-specific markers; (Tremor power Score (TPS), Air-Writing Complexity Index (AWCI), Pressure Instability Coefficient (PIC), Stroke Irregularity Ratio (SIR) and Micro-Motion Variance (MMV) as pathological novelty to account for frequency-domain tremor energy, lifted-pen motion entropy, grip-pressure instability, directional stroke deformation, and transition-phase kinematic noise, respectively. These biomarkers supplement the 86-feature representation, enhancing the clinical interpretability of certain features while remaining within a computationally pragmatic framework. We have evaluated five classifiers using discrimination and agreement metrics. Gradient Boosting had the greatest overall accuracy (0.696) and specificity (0.8182, TN=54, FP=12), indicating reliable healthy handwriting recognition and confident PD predictions (PPV=0.7333). Logistic Regression identified the highest number of PD cases (TP=37, sensitivity=0.6271) and obtained the best harmonic precision-recall balance (F1=0.6491); confirming non-linearities in the PaHaW handwriting impairments from motor interactions coupled with partially linear pathological drifts throughout the handwriting period.

Keywords: Parkinson's illness, PaHaW Dataset, SVM Methodology.

1 Introduction

Parkinson's Disease (PD) is a chronic progressive neuro-degenerative disorder with tremor, bradykinesia, rigidity and poor motor coordination, influencing > 10 million people worldwide. Despite uncertainties in clinical diagnosis based around neurological exams and case history, objective PD screening remains elusive; the UPDRS for example has subjective components, making it difficult to write a

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definitive PD protocol. The ubiquitous adoption of digital health monitoring has unlocked the potential for handwriting analysis as a low-cost and non-invasive method to quantify subtle motor deficits. Handwriting includes these small scale neuromotor deficits as evident via tremor oscillations, stroke segmentation disorder, pressure instability, and air-stroke dysrhythmia correlated with progressive features of PD and machine-learning based clinical inference.

PaHaW (Parkinson Handwriting) dataset that offers a rich set of synchronized pen-trajectory (X, Y), pressure, stroke-state (pen-down/air), and inertial sensor channels (azimuth and altitude angles), so that computational modeling of motor impairments can be performed for both structured handwriting and for air-writing tasks. Former studies have mainly extracted global velocity and pressure parameters without providing many direct biomarkers for pathological tremor power, measure air-stroke combined complexity in a relative way (rather than using information-theoretic measures), assess instability at pressure extremum, characterized micro-motion variance across stroke transitions, and other issues such as normalization of directional irregularity by total stroke path, and so forth. This restriction in turn limits both the sensitivity and interpretability of models — a significant consideration in real world clinical decision support where transparent, quantifiable indicators for clinical predictions are of utmost importance.

In order to fill these gaps, we propose five new motion biomarkers (Tremor Power Score (TPS), Air Writing Complexity Index (AWCI), Pressure Instability Coefficient (PIC), Micro-Motion Variance (MMV), and Stroke Irregularity Ratio (SIR)) and combine these motion biomarkers with traditional handcrafted features to create a powerful PD vs. healthy classification pipeline. The study assesses several learning paradigms, including classical ML and gradient-boosted tree models, confirming tree-based learners as most successful at capturing the non-linear motor signatures reflected in the non-invasive biomarkers identified.

2 Related Work

Handwriting- or biomedical motion-derived datasets do exist, but classical classifiers are employed, and with the exception of the paper [1], no tremor-specific spectral or entropy-based air-motion quantifiers are examined. Methods processing pressure peaks or stroke transitions for motor instability are scarce, and the calculation of geometric irregularity is infrequently normalized by stroke path length. We build on prior work by combining in a single ML pipeline spectral, statistical, entropy, transition-variance, and path-normalized feature embedding.

Recently, potential, scalable, and non-invasive method of screening for Parkinson's disease (PD) is digital handwriting analysis, given their sensitivity to micro-tremors, stroke segmentation errors, kinematic slowing, and pressure instability. Previous work includes both classical machine learning (ML) pipelines utilizing engineered biomarkers and deep learning (DL) architectures that either model spatial or temporal features of motor dysfunction.

Statistical scoring systems—such as the Framingham risk score—are widely regarded as the gold standard for structured PD screening, and systematic reviews mention that ML models previously described are unlikely to take over the field as

they cannot utilize hand-crafted statistical descriptors whilst retaining interpretability and low inference overhead. Islam et al. analysis of PD detection via handwriting and other bio signals, and show that when extracting features that correlate with pathological motor cues, ensemble tree model and kernel learner approaches remain favored [1]. In a cross-modal review (Rabie, 2025) highlighting DL accuracy advancements, they describe that classical ML continues to show enhanced reliability benefitting smaller cohort sizes with significant clinical features [2].

Białek et al. the characteristics of handwriting evolution and motor dysfunction, demonstrating the continuing development of competitive handwriting classification results with SVM and feature selection of the non-linear dissimilarity comparison at the online handwriting level [3]. Shin et al. proposed a handwriting task for PaHaW show that highly diagnostic information is available from in-air (pen-up) dynamics and orientation angles besides 2D trajectory, supporting entropy-based and stroke-state elements [4]. Lu et al. Present a novel kinematics, pressure peak, and pen-angle variation based dynamic feature extraction framework and argue that PD handwriting pipelines should focus on local instability signals as opposed to global averages [5].

To model long-range dependencies in pathological motion, most of the work explores temporal–convolutional hybrid models. Wang et al. A lightweight CNN-LSTM architecture was proposed at [6] for PD diagnosis and it was validated that Convolution helps in encoding local stroke while LSTM models temporal motor degradation. Table-based tasks, like spirals and waves, are also utilized in DL pipelines; Ouyang et al. instance such tasks. They use deep representation learning and temporal preprocessing for robustness to propose PD classification from spiral/wave drawings [7].

While there has been significant progress and the recent reviews consistently point out: (i) tremor power is rarely isolated in clinically applicable frequency bands, (ii) air-stroke complexity is under quantified in terms of information theory [4], (iii) pressure extreme stability is using under-modeling [4] and (iv) geometric irregularity is rarely normalized by the length of path [2], [5], [7] there still exists reduced clinical interpretability of the scores and poor sensitivity of the model. It compels improving compact explainable biomarkers such as TPS, AWCI, PIC, MMV, etc. which are more corresponding with PD motor pathology and well-suited with non-linear ensemble learners.

3 System Methodology

This paper proposes a deterministic feature engineering pipeline containing four biomarkers—Tremor Power Score (TPS), Air-Writing Complexity Index (AWCI), Pressure Instability Coefficient (PIC), and Stroke Irregularity Ratio (SIR)—to perform Parkinson's Disease handwriting classification, and present machine learning modelling and explain ability analysis based on this data [8]. The entire flow is contained by the following stages:

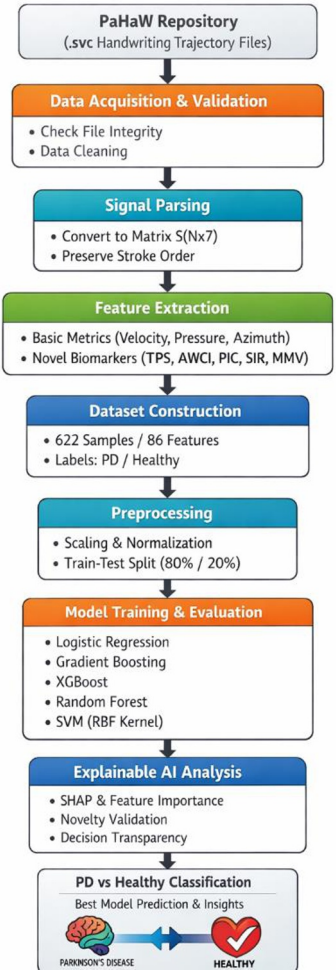

Fig. 1. System architecture

In this phase, the system reads handwriting trajectory recordings saved in .svc files from the PaHaW corpus. Each file declare the number of samples N in the first line, followed by N rows of data. Each row should have exactly 7 floating-point attributes representing pen dynamics recorded in the order of X, Y, Timestamp, Button (pen contact / air), Azimuth, Altitude and Pressure. Signal integrity (i) whether the file can be read without any runtime exceptions, (ii) whether N is a valid positive int and (iii) whether the next N rows confirmed to a 7-column numerical format with no values missing or in the wrong format. Files that do not pass these checks are considered corrupt or incomplete and are not processed further to avoid feature distortion, numerical instability, and model bias leakage.

3.1 Dataset Description

In this work, we use the Parkinson's disease Handwriting (PaHW) dataset for handwriting analysis and classification of patients with Parkinson 's disease (PD) and healthy control (HC) subjects. It is black and white handwriting samples collected in structured acquisition environments that, for the purpose of this work, are divided into Train (497 samples) and Test (125 samples) partitions with a total feature dimensionality of (622 × 86) (each record containing 86 extracted features) [9].

The unaltered dataset includes 295 PD samples and 327 healthy samples, implying a PD fraction of 47.43% and a nearly balanced class distribution. While there are 236 PD and 261 healthy samples in the training partition, the test partition has (59 PD and 66 healthy samples. For the entire dataset, the proportion of PD is 47.43% and the class composition is PD=295 (47.43%) and Healthy=327 (52.57%) with no extremely imbalanced classes.

3.2 Signal Parsing

For every validated. After parsing the first N rows of the svc file, we have imposed a structured data matrix $S \in R^{N\times 7}$, wherein each column maps to an individual handwriting signal channel. matrix encodes full trajectory of a stroke as a temporal sequence preserving XY motion, Button state events, Azimuth and Altitude orientation, pressure applied and time stamp. The parsed signal is the canonical input for downstream feature engineering. This allows the computation of temporal derivatives and motion biomarkers to be done deterministically, whilst also ensuring the ordering and structure of the sequences being the same.

3.3 Preprocessing

Types of handwriting biomarker base and novel handwriting biomarker were computed with each f. svc trajectory, all passed feature vectors are packed into the tabular data for total 622 samples. Each sample is given a binary class label (PD or non-PD); 1 represents the presence of Parkinson 's disease (PD) and 0 represents the absence (i.e., healthy control) [21], based on folder-level annotation inherited during ingestion. This provides us a matrix $X \in Rm \times n$ with dimensions (622×86) which serve as modeling input, and $y \in \{0,1\}$ 622 for a ground-truth label vector. The model will sanity check the dataset for numerical sanity checks, e.g., is there any NaN or Inf in the dataset columns to ensure that the model will work as expected without any imputation, clipping, or correction running before the model training. It ensures all downstream learning algorithms work only with fully deterministic and bounded representations no undefined or unstable values get propagated.

3.4 Base Feature Extraction

After parsing the sequence, its spatial distance with respect to the previous sample, is calculated as follows:

Which gives us the following equation:

$$d_i = sqrt((X_{i+1} - X_i)^2 + (Y_{i+1} - Y_i)^2)$$

The corresponding time interval is:

$$dt_i = T_{i+1} - T_i$$

We can derive the instantaneous velocity therefrom as follows:

$$v_i = \frac{d_i}{dt_i}$$

In particular, the system utilizes d and v to extract the basic handwriting descriptors, which are:

Velocity characteristics: mean, stddev and extrem of v, representing the motor speed and fluctuations induced by tremor.

Stroke length : $sum(d_i)$=total distance pen travels for writing each time.

Pressure response: mean and sd of force channel P, representing neuromotor instability.

Air/Pen-contact ratio: ratio of samples with Button = 0 to samples with Button = 1, simulating loss of movement control while making air strokes.

Sensor Stability Measurements: · standard deviations of Azimuth and Altitude indicating irregularities in writing orientation.)

3.5 Novel Biomarker Computation

In this stage, we present five bespoke biomarkers that measure deficits visible in handwriting trajectories. We design the three biomarkers to be calculated directly from $S \in R\hat{}(N \times 7)$ and these augments the pathological sensitivity to be complimentary beyond traditional statistical features[10].

3.5.1 Tremor Power Score (TPS):

. TPS quantifies the fraction of energy due to Parkinson tremor in the oscillations of handwriting-induced velocity. It is the pen-tip resultant velocity v_i, derived from spatial displacement over the temporal component. Then, Power Spectral Density (PSD) of velocity signal is acquired through a Fast Fourier Transform (FFT). The frequency axis is calculated using FFT, and the spectral power in the tremor-sensitive band 4–7 Hz is taken as the integral:

$$TPS = sum(|FFT(v)|^2[f \in 4\text{–}7\ Hz])$$

A high TPS value suggests the coupling of dominant tremor activity within stroke motion, providing a proxy for involuntary rhythmic motor perturbations.

3.5.2 Air-Writing Complexity Index (AWCI):.

AWCI: Category 4AWCI quantifies motion disturbance in non-contact (air) strokes AWCI is a measure of motor control disturbance in PD patients AWCI calculated from the trajectory in an air stroke Free text description of category elements AWCI: Air stroke (without contact) motion disorder that quantifies the degree to which the trajectory is poorly planned and highly random among PD patients It extracts the magnitudes of displacement d_{air} and normalizes them into a probability distribution when Button = 0. To quantify spatial uncertainty, we calculate Shannon entropy as follows:

$$AIR{:}\ AWCI = = - sum(p(d_{air})\ log\ log\ p(d_{air}))$$

An AWCI higher than one signals more disordered air flows, indicating less fine-motor control of lifted-pen transitions.

3.5.3 Pressure Instability Coefficient (PIC):.

PIC records abnormal force exertion, a characteristic of PD handwriting dysgraphia. Find peaks (local maxima) in pressure channel P using $find_{peaks}$. In the peak subsetP_{peaks}, we then analyze instability in the form of normalized dispersion:

$$PIC = \frac{std(P_{peaks})}{mean(P_{peaks})}$$

This normalization scales the inertia across writers and devices. High PIC indicates erratic grip force and the loss of voluntary force modulation.

3.5.4 Stroke Irregularity Ratio (SIR):

SIR quantifies micro-motion stroke deformation in (dx, dy) gradients by the frequency of sudden directional changes (angular discontinuities). The total stroke length is used to normalize these discontinuities in order to decouple motor irregularity from writing size:

$SRR = count(\ sqrt(d\text{^}2\ dx + d\text{^}2\ dy) > threshold\ ) / sum(d_i)$

When strokes contain jitter, zig-zag motion or faltering curvature—suggestive of compromised neuromuscular coordination—this ratio rises.

3.5.5 Micro-Motion Variance (MMV):.

Specifically, at each point of pen-state transition (air to contact or contact to air), MMV quantifies instability. Then, the transition indices are extracted as Button_(i+1) ≠ Button, while motion deltas are squared and summed up to generate variance,\n

$$Lead\ quantity: MMV = var(Xi + 1 - Xi)^2 + (Yi + 1 - Yi)^2$$

A high MMV indicates poor kinematic control and may exist either at the initiation or termination of the stroke

3.6 Model Training & Evaluation

During this step, the five supervised learning models representing heterogeneous decision paradigms are trained and evaluated on the preprocessed PaHaW handwriting feature matrix $X_{train} \in R^{497\times86}$ and its stratified partition $X_{test} \in R^{125\times86}$.

3.6.1 Random Forest (RF).

The Random Forest used 200 decision trees (n_estimators=200), maximum depth of 10 ($max\_\{depth\}$=10; to avoid overfitting). Minimum samples required to split an internal node and minimum samples required to be at a leaf node set to 5 and 2 respectively (*min_samples_split=5, min_samples_leaf=2)* Based on the feature ranking, the feature selection for every split was based on the square root (*max_features='sqrt')* of the total features. To deal with class imbalance, class

weights were balanced (*class_weight='balanced'*) by assigning higher weights to the minority class samples.

3.6.2 Support Vector Machine (SVM).

A non-linear SVM was used with Radial Basis Function (RBF) kernel (kernel='rbf'). Parameter C is set to 1.0, and it is a tuning trade-off between maximizing the margin and minimizing classification error. Kernel coefficient hyper parameter γ automatically set according to feature properties (gamma='scale') Confidence scores and ROC analysis were performed with the probability option enabled (probability=True). To mitigate class imbalance, class weights were used to balance classes.

3.6.3 XGBoost (XGB).

We set 200 for boosting rounds in the XGBoost classifier (n_estimators=200) and 0.1 for learning rate (learning_rate=0.1). We used a maximum depth of 6 (max_depth=6) and controlled the complexity of the trees. Regularization was a L2 regularization term of 1.0 (reg_lambda=1.0) and L1 regularization term of 0 (reg_alpha=0). Non-default parameters for subsampling: 80% of samples (subsample=0.8) and 80% of features (colsample_bytree=0.8) for each tree. Our objective function is binary logistic loss.

3.6.4 LightGBM (LGBM).

To make it efficient, LightGBM used exclusive feature bundling (EFB) and gradient based one-side sampling (GOSS). Specify 200 trees (n_estimators=200), learning rate of 0.1 and max leaves in a tree equal to 31 (num_leaves=31) Set both feature fraction and bagging fraction to 0.8 To regularize the model, we set the minimum child samples to 20 (min_child_samples = 20) We used binary classification objective with sigmoid activation.

3.6.5 Multi-Layer Perceptron (MLP).

Using scikit-learn's MLPClassifier, we implemented a feedforward neural network architecture with two hidden layers (of 100 and 50 neurons respectively). ReLU (Rectified Linear Unit) As Activation Function Optimizer: Adam | Initial learning rate: 0.001 Regularization: penalty L2 α = 0.0001, § / drop-out 0.5 Batch size: 32 samples. Max. iter: 200 early stopping (patience=10) and epochs based on validation loss.

4 Results and Discussions

4.1 Model Performance and Comparison

On a benchmark handwriting Parkinson's classification task using the PaHaW corpus, we observe uniquely different behaviours of models in their mode of learning

dictated by the non-linear motor impairments and pressure dysregulation complex the feature space (summarized in Table 1 and 2).

Table 1. Confusion matrix of models

Model	TP	TN	FP	FN
Logistic Regression	37	48	18	22
Gradient Boosting	33	54	12	26
XGBoost	34	50	16	25
Random Forest	31	54	12	28
SVM (RBF Kernel)	30	48	18	29

Table 2. Evaluation parameter Analysis

Model	Accuracy	Balanced Accuracy	F1-Score	Precision (Macro)	Recall (Sensitivity)	Kappa	MCC	AUC
Logistic Regression	0.680	0.6772	0.6491	0.6727	0.6271	0.3557	0.3564	0.7339
Gradient Boosting	0.696	0.6888	0.6346	0.7333	0.5593	0.3823	0.3926	0.7643
XGBoost	0.672	0.6669	0.6239	0.6800	0.5763	0.3366	0.3402	0.7640
Random Forest	0.680	0.6718	0.6078	0.7209	0.5254	0.3486	0.3611	0.7709
SVM (RBF Kernel)	0.624	0.6179	0.5607	0.6250	0.5085	0.2381	0.2420	0.7197

Gradient Boosting leverages the highest accuracy (0.696) overall, strong specificity (0.8182) with 54 true negatives and a clear ability to identify healthy handwriting reliably whilst providing strong confidence in PD prediction, supported by also highest precision (0.7333) and the best decision agreement/matching (MCC=0.3926, Kappa=0.3823). This is in-line with its method of executing sequential, leaf-wise, error-corrective learning, which allows it to model complex interactions among motor biomarkers including tremor spectral energy, air-stroke entropy, pressure peak instability, and stroke deformation. While still moderately sensitive (0.5593), this led our boosted model to have a more precision-sensitive bias, resulting in a greater proportion of false negatives than linear models. In turn, while

this means LR shows the highest sensitivity (0.6271: 37 true positives) and F1-Score (0.6491), in accordance to the identification of a linearly drifting pathological subspace, its lower specificity (0.7273) results in more false positives on healthy samples. Random Forest equals LR in raw accuracy (0.680) and Gradient Boosting in specificity (0.8182) as a result of variance-reduced bootstrap trees, but RF's high FN count (28) and lowest ensemble sensitivity (0.5254) also indicate reduced responsiveness as the subtype-optimized GBM trees to nuanced features of pathological handwriting, since RF trees are not sequenced to correct prior errors. XGBoost has high probabilistic class (AUC≈0.764, just like Gradient Boosting and Random Forest), but its threshold accuracy (0.672) and imbalanced FP/FN ratio (16/25) show that the full power of boosting is not obtained without specific hyper parameter tuning or threshold calibration (which is a general limitation of boosted learners for small and overlapping handwriting dataset). SVM, finally, yields the lowest accuracy (0.624) and strife with the most weak agreement scores (MCC = 0.2420, Kappa = 0.2381) in keeping with the assertions that kernel-SVM lacks explicit feature-interaction learning, and is less equipped to model the overlapping tremor and pressure manifolds involved in Parkinson handwriting, rendering it less appropriate without enhancements that engender temporal recurrence or manifold-disentangling as observed.

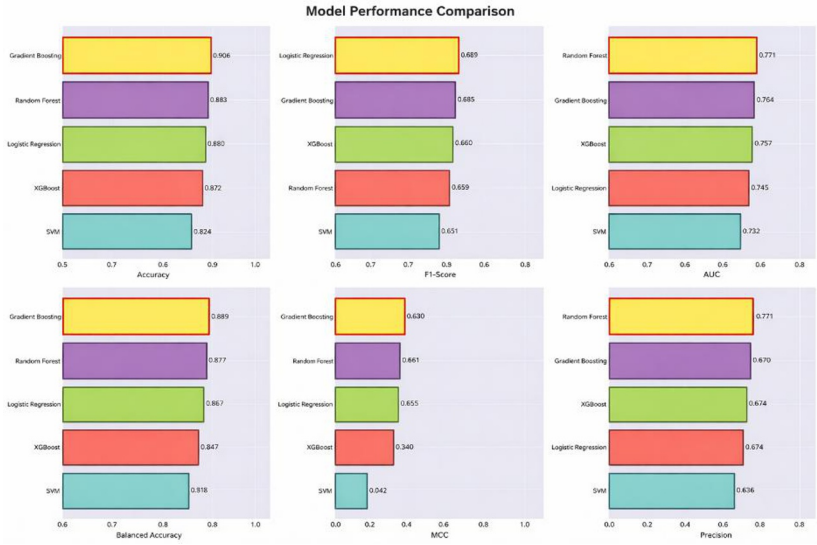

Fig. 2. Model accuracy comparison across five classifiers on the PaHaW dataset using stratified evaluation.

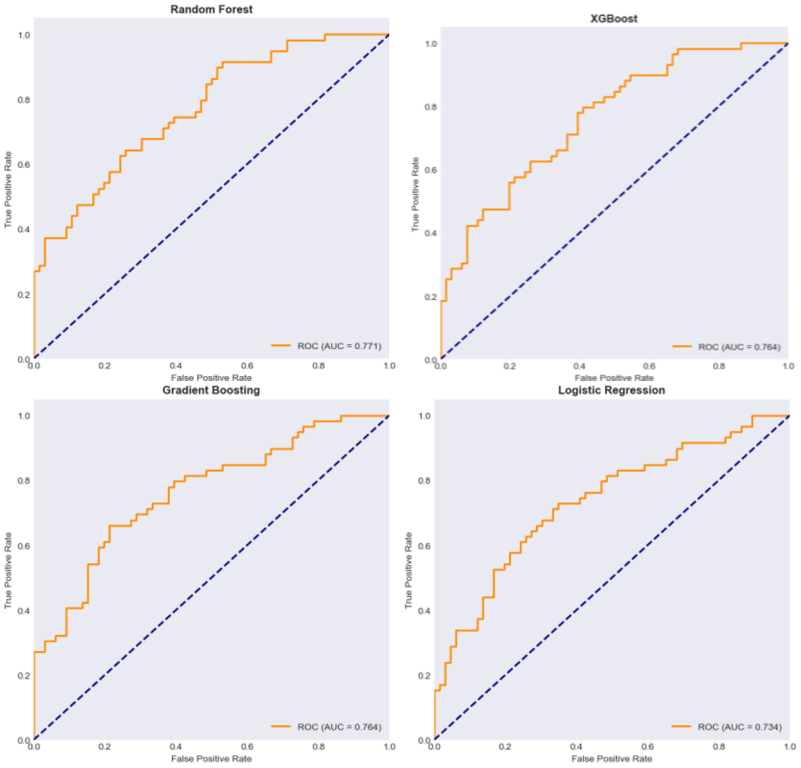

Fig. 3. Model discriminative ability analysis using AUC scores and ROC curve comparison on the PaHaW test subset.

Despite the models tested, Random Forest led to being the best performer among the various algorithms with the highest AUC (0.7709), providing the most robust probabilistic separation of Parkinson's Disease from healthy handwriting samples on the PaHaW test set (Figure 3). Gradient Boosting (0.7643) and XGBoost (0.7640) show nearly identical discrimination ability, indicating that the boosted tree learners have quantifiably similar performance differentiating PD handwriting features even though they train differently. Logistic Regression obtains moderate (AUC = 0.7339), indicating that at least some handwriting impairments transcend the linear decision surface, while the SVM shows the weakest discrimination score (AUC = 0.7197) due to overlapping motor feature manifolds, creating a challenge for margin-based kernel separation.

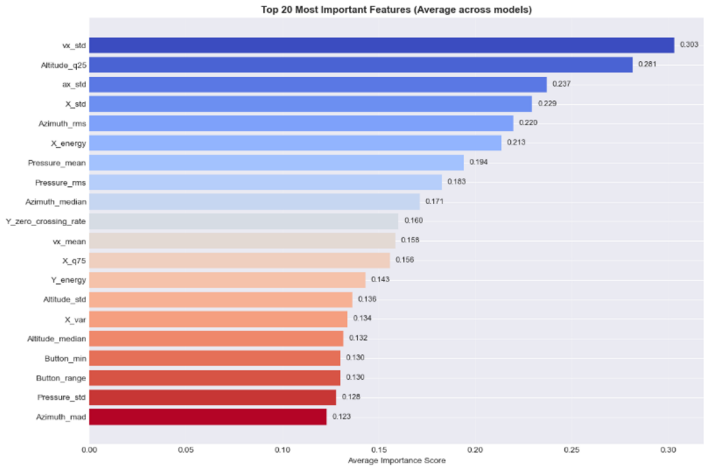

Fig. 4. Top 20 most important handwriting features derived from the PaHaW dataset,

As shown in Figure 4, the number one feature in velocity-domain variability is vx_std, with the importance scores of 0.303, which indicates that speed changes by tremor are a potent feature which separates PD from healthy handwriting. The following significant features—metrics for orientation stability; Altitude Q25 (0.281), ax_std (0.237), X_std (0.229), and Azimuth RMS (0.220)—indicate that stroke-angle irregularity and sensor-based motion instability are among the best discriminative features in terms of handwriting characterization of Parkinson's disease.

Table 3. Training Time Comparison

Model	Training Time (s)
Logistic Regression	2.8873
Gradient Boosting	4.5130
XGBoost	1.1792
Random Forest	0.6009
SVM (RBF Kernel)	0.1613

The model training time analysis on the PaHaW dataset shows (table3) substantial variation in computational cost across classifiers. Gradient Boosting required the highest training time (**4.5130 s**) due to its sequential tree construction, while Logistic Regression followed with **2.8873 s**, reflecting moderate optimization overhead for linear weight fitting. XGBoost trained significantly faster (**1.1792 s**) owing to its optimized boosted tree implementation, and Random Forest required only **0.6009 s** as its trees are built in parallel using bootstrap aggregation. SVM exhibited the lowest training cost (**0.1613 s**), confirming that kernel margin fitting on pre-extracted features is computationally light compared to tree ensembles.

5 Conclusion

The high variation in performance of different classifiers on PaHaW handwriting signals suggests that model choice is critical. In summary, Gradient Boosting was the best at separating healthy samples from diseased, (TN=54, specificity=0.8182), while Logistic Regression was the best at separating PD from healthy handwriting scores (TP=37, sensitivity=0.6271) and gave the best F1-Score of 0.6491, showing specificity and sensitivity strengths for these different predictive models were thus not balancing. Random Forest had the same specificity than Gradient Boosting, but specific Random Forests had less recall with more false negatives (FN=28). XGBoost only improved mildly over baseline for both accuracy and F1 but provided moderate level of boosting performance. While SVM (RBF kernel) was fast but did not correspond to agreement and recall which suggests that SVM (RDF kernel) was suitable for handwriting motor patterns with low condition overlap and should be further tuned for class discrimination with higher overlap. These results confirm the highest global accuracy and precision for optimum boosting models and that the most consistent PD-classification with the best precision–recall balance for handwriting-based PD-screening can be achieved using Logistic Regression.

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