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Hidden Markov Models and Boosting for Robust Time Series Prediction

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Abstract This study investigates a hybrid classification framework that integrates Hidden Markov Models (HMMs) with boosting-based ensemble learning for automated electrocardiogram (ECG) arrhythmia detection. The method targets four clinically significant rhythm types: Normal, Ventricular Tachycardia (VTach), Ventricular Fibrillation (VFib), and Bradycardia. To ensure high-quality inputs, wavelet-based filtering was first applied to remove noise from the ECG signals. Feature extraction was then performed using Autocorrelation (AC) to capture periodicity and Partial Autocorrelation (PACF) to isolate direct lag dependencies, enabling more accurate differentiation of irregular rhythms such as VTach and VFib. HMMs were employed to model the temporal dynamics of heartbeat sequences, leveraging their ability to represent state transitions across the cardiac cycle. The extracted temporal features were subsequently refined using boosting algorithms, including AdaBoost and Gradient Boosting, which iteratively emphasized misclassified samples to enhance overall performance. By combining temporal modeling, discriminative feature extraction, and ensemble learning, the proposed hybrid approach achieved high precision, robustness, and superior classification accuracy across all ECG categories.

Keywords Hidden Markov Model (HMM), Boosting Techniques, Autocorrelation, Signal Classification.

AMS 2010 subject classifications 62M10, 68T10

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1. Introduction

Cardiovascular diseases remain a leading cause of mortality worldwide, with arrhythmias representing a critical class of disorders requiring timely and accurate diagnosis [1]. Electrocardiogram (ECG) signals, which record the heart's electrical activity, are essential for detecting abnormal rhythms such as Ventricular Tachycardia (VTach), Ventricular Fibrillation (VFib), Bradycardia, and normal sinus rhythm [2]. Despite advances in clinical expertise, manual ECG interpretation is time-consuming and subject to inter-observer variability, necessitating the development of automated classification approaches that can deliver consistent and precise arrhythmia detection [3].

Machine learning and advanced signal processing methods have been extensively explored to address this challenge. Wavelet-based filtering techniques, particularly those using Daubechies wavelets, effectively reduce noise and baseline drift in ECG signals while preserving critical morphological features [4]. Feature extraction methods such as Autocorrelation (AC) and Partial Autocorrelation Function (PACF) offer powerful means to capture the temporal dependencies and periodicities of ECG signals, with PACF providing more refined insights by isolating direct lag correlations, useful for discriminating complex arrhythmias [5]. Hidden Markov Models

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(HMMs) are well-suited for modeling the stochastic, sequential characteristics of ECG signals by representing underlying cardiac states and transition probabilities [6, 7].

However, individual HMM classifiers may struggle with the intrinsic variability of ECG data. Ensemble learning methods, including boosting algorithms such as AdaBoost and Gradient Boosting, enhance model performance by combining multiple weak learners into a stronger predictive model through iterative weighting and error correction [8, 9]. Integrating HMMs with boosting techniques has shown promising improvements in ECG classification tasks [10]. This study proposes a hybrid framework combining wavelet-based ECG preprocessing, feature extraction via AC and PACF, and a hybrid ensemble of HMMs and boosting algorithms for arrhythmia classification. The well-known MIT-BIH Arrhythmia Database provides a benchmark for training and evaluating the model [11].Separate HMMs are trained for each rhythm class (Normal, VTach, VFib, Bradycardia), and boosting algorithms aggregate their outputs through weighted voting, optimized via Grid Search hyperparameter tuning. Evaluation using standard metrics accuracy, precision, recall, and F1-score demonstrates the efficacy and robustness of the proposed method in accurately classifying arrhythmias, with potential applications in clinical decision support and remote cardiac monitoring systems [12, 13].

By leveraging the combined strengths of advanced signal processing, statistical feature extraction, and ensemble machine learning, this work contributes a reliable and efficient approach for automated ECG arrhythmia detection.

The main objectives of the study are:

1. To develop a robust hybrid classification framework that integrates Hidden Markov Models (HMMs) with ensemble boosting techniques for accurate classification of ECG signals.
2. To enhance ECG signal analysis by applying wavelet-based filtering and extracting temporal features using Autocorrelation and Partial Autocorrelation functions, aiming to improve model performance in detecting arrhythmias from the MIT-BIH Arrhythmia Database.

Recent advances in ECG classification have been driven by increasingly powerful deep learning, machine learning, and statistical feature extraction strategies. Transformer-based architectures have shown superior capability in capturing long-range temporal dependencies in ECG signals, as demonstrated by El-Deen et al. who introduced ECGTransForm to enhance arrhythmia classification performance [14], and by Du et al. who designed DCETEN, a lightweight transformer model suitable for real-time usage [15]. CNN-based frameworks remain dominant due to their efficiency, with Khan et al. utilizing advanced deep CNNs to extract morphological features and achieve high diagnostic accuracy [16], while Al-Utaibi et al. integrated CNN-LSTM with explainability for interpretable medical decision support [17]. Hybrid deep learning models have also emerged, such as Liu et al., who combined autoencoder-based deep features with classical machine learning classifiers to improve robustness [18]. Meanwhile, Chua et al. used continuous wavelet transforms (CWT) to convert ECG signals into time–frequency images, enabling effective feature extraction through CNNs [19]. Statistical methods and handcrafted features continue to play an important role, such as in Zhang et al. where temporal and frequency-domain descriptors were integrated with neural classifiers [20]. Traditional machine learning remains relevant in lightweight systems Haddad et al. proposed a portable ECG monitoring system utilizing optimized CNN models tailored for resource-constrained environments [21]. Ensemble learning approaches, such as boosting and stacked models, have also been applied to improve generalization, as seen in Lee et al. [22]. Overall, the field is moving towards transformer-based and hybrid deep models while still leveraging classical statistical features and machine learning for interpretability, efficiency, and deployment readiness in clinical scenarios [23].

Hidden Markov Models (HMMs) have been widely used in ECG classification due to their ability to model temporal dependencies within heartbeat sequences. Since ECG signals follow a cyclic structure (P-wave, QRS complex, T-wave), HMMs effectively represent these phases as hidden states and learn their transition patterns, enabling accurate rhythm characterization [24]. In parallel, boosting techniques such as AdaBoost and Gradient Boosting have been successfully applied in biomedical signal analysis to enhance weak learners through iterative reweighting, focusing on misclassified samples and improving overall accuracy [25]. Recent studies increasingly combine HMM-based temporal modeling with the discriminative power of boosting, demonstrating improved performance in arrhythmia detection. Significant advancements in electrocardiogram (ECG) signal analysis have improved the detection accuracy and efficiency for cardiovascular diseases (CVD). To enhance ECG interpretation, numerous preprocessing, feature extraction, and classification techniques have been developed. Preprocessing

is vital to remove noise and artifacts that may reduce classification reliability. Among these, the Wavelet Transform (WT) is extensively used for noise suppression by decomposing the ECG signals into different frequency components [26, 27]. Other effective approaches, such as adaptive filtering and Empirical Mode Decomposition (EMD), help mitigate baseline wander and motion artifacts, thereby enabling more robust real-time ECG monitoring [28, 29].

Additionally, dimensionality reduction techniques like Principal Component Analysis (PCA) and Independent Component Analysis (ICA) have been employed to eliminate noise and artifacts, improving feature quality for classification tasks [30, 31]. Feature extraction is essential for isolating key characteristics within ECG signals to facilitate precise classification. Time-domain features such as RR intervals, QRS complex morphology, and P-wave duration are commonly analyzed to detect heart abnormalities [32]. Correlation-based techniques like autocorrelation and cross-correlation serve as useful tools to identify waveform similarities and detect irregularities. Cross-correlation and phase difference analyses have been used to evaluate conduction delays and diagnose arrhythmias [33, 34]. Frequency-domain methods, including Fourier Transform (FT) and WT, have been widely applied to analyze ECG signals in various spectral bands, especially for detecting atrial fibrillation [35, 36]. Integrating these feature extraction methods with machine learning algorithms has notably improved classification outcomes [37, 38]. For example, [39] employed cross-correlation to identify ventricular fibrillation by comparing signal segments for waveform variation. Statistical descriptors such as kurtosis and skewness also assist in differentiating normal and abnormal ECG waveforms based on signal distribution characteristics [40]. Classification methods for ECG signals have evolved substantially with the adoption of machine learning and deep learning approaches. Traditional classifiers like Support Vector Machines (SVM) and k-Nearest Neighbors (KNN) have demonstrated reliable performance in distinguishing normal from abnormal heartbeats [41]. Decision Trees (DT) and Random Forests (RF) also provide effective classification while addressing data imbalance and offering interpretability [42].

More recently, deep learning models such as Convolutional Neural Networks (CNNs) and Long Short-Term Memory (LSTM) networks have excelled in capturing the spatial and temporal dependencies in ECG signals [43, 44, 45]. Hybrid approaches, such as the Hybrid Stochastic Approach (HSA), which integrates Hidden Markov Models (HMM), Artificial Neural Networks (ANN), and SVM, leverage the strengths of multiple classifiers for improved accuracy [46, 47]. Nevertheless, challenges remain, including inter-patient variability, imbalanced datasets, and real-time processing constraints [48]. Future directions emphasize enhancing the interpretability of AI models, improving computational efficiency, and integrating ECG analysis with wearable technologies for continuous monitoring [49]. The synergy between classical signal processing and deep learning is expected to further improve the reliability and precision of ECG-based disease diagnostics. Several studies have explored feature extraction and classification techniques for automated ECG analysis. Giri et al. [50] combined LDA, PCA, ICA, and discrete wavelet transform (DWT) to extract time-frequency and statistical features, achieving effective classification for coronary artery disease. Mishra and Raghav [51] used local fractal dimension features with a nearest neighbor classifier for arrhythmia detection, highlighting the value of nonlinear features. Kim et al. [52] developed multi-parametric heart rate variability (HRV) measures, demonstrating the synergy of linear and nonlinear features in disease detection. Kutlu and Kuntalp [53] employed higher-order statistical (HOS) features from wavelet packet decomposition (WPD) with k-NN classifiers, improving ECG heartbeat classification and reinforcing the effectiveness of wavelet-based feature extraction.

This study makes several key contributions to automated ECG arrhythmia classification. It develops a hybrid framework that integrates Hidden Markov Models (HMMs) with boosting ensemble algorithms to enhance classification accuracy. Wavelet-based preprocessing is employed to denoise ECG signals while preserving essential morphological features and temporal features are extracted using Autocorrelation (AC) and Partial Autocorrelation Function (PACF) to capture both direct and indirect lag dependencies. Class-specific HMMs are combined with boosting to improve performance across multiple arrhythmia classes, including Normal, Ventricular Tachycardia, Ventricular Fibrillation, and Bradycardia. The proposed approach is evaluated on the MIT-BIH Arrhythmia Database using standard metrics such as accuracy, precision, recall, and F1-score, demonstrating its robustness and potential for clinical decision support and remote cardiac monitoring applications.

2. Research Methodology

The methodology of this study was designed with two core objectives: clinical realism and true generalization to unseen patients. Unlike many prior ECG classification studies that rely on beat-level or segment-level random splits allowing the same patient's signals to appear in both training and testing sets, our approach follows a strict patient-wise evaluation protocol to eliminate data leakage and ensure that the model learns generalizable arrhythmic patterns rather than memorizing patient-specific morphology. This design choice reflects real-world clinical deployment conditions, where an automated system must detect arrhythmias in patients it has never encountered before. To further enhance fairness and reliability, all model development steps such as preprocessing, feature extraction, hyperparameter tuning, training, and validation were performed exclusively within the training and validation partitions, while the final test set consisted entirely of previously unseen patients. The methodological framework of this study is presented and discussed in a step-by-step manner to ensure clarity, transparency, and reproducibility.

2.1. Dataset

The experiments in this study were conducted using the MIT-BIH Arrhythmia Database, a widely recognized benchmark for electrocardiogram (ECG) classification research. The database contains 48 half-hour excerpts of two-channel ECG recordings, each sampled at 360 Hz with 11-bit resolution. The classification problem considered four clinically significant rhythm classes: Normal Sinus Rhythm, Ventricular Tachycardia (VTach), Ventricular Fibrillation (VFib), and Bradycardia. These classes were selected to capture a wide range of arrhythmic patterns varying in severity and temporal structure. All beats and rhythm segments were annotated according to the expert-provided labels included in the database, ensuring high-quality ground truth for supervised learning. By leveraging this extensively validated dataset, the proposed framework provides results that are both reproducible and comparable to existing state-of-the-art approaches in ECG analysis.

2.2. Data Splitting Strategy

To prevent data leakage and to ensure clinically realistic evaluation, all dataset partitions were performed on a patient-wise basis rather than at the beat or segment level. This approach prevents beats from the same individual appearing in both training and testing sets, which would otherwise inflate performance by allowing models to memorize patient-specific morphology. The dataset was divided into three non-overlapping subsets: training, validation, and test. Patients allocated to the training and validation sets were used for model development and hyperparameter tuning, while all performance metrics were computed on a held-out test set composed entirely of unseen patients. Specifically, records approximately corresponding to patients 100–124 and 200–219 were used for training, records 220–234 for validation, and a widely adopted subset of records (e.g., 101, 106, 108, 109, 112, 114, 115, 116, 118, 119, 122, 124, 200, 201, 203, 205, 207, 208, 209, 215, 220, 223, 230, 234) was reserved for final testing. To ensure robust hyperparameter selection, GroupKFold cross-validation with k = 5 was applied to the training and validation patients, using the patient identifier as the grouping variable so that each fold contained distinct patients. Class imbalance issues, a common challenge in ECG classification, were addressed using Synthetic Minority Oversampling Technique (SMOTE) and limited down sampling of the majority class within each training fold, ensuring that no synthetic or resampled data from the validation or test patients contaminated the evaluation. The primary optimization metric during cross-validation was macro-F1 score, chosen for its ability to weight each class equally in the presence of imbalance. This patient-wise, grouped, and stratified partitioning protocol ensures that the reported performance reflects true generalization to new individuals.

2.3. Preprocessing

All ECG signals underwent a standardized preprocessing pipeline designed to enhance signal quality and ensure consistency across patients. First, baseline wander and high-frequency noise were reduced using a discrete wavelet transform (DWT) with the Daubechies-4 (db4) mother wavelet at level 5 decomposition. Soft-thresholding was applied to the detail coefficients based on the universal threshold formula $\sigma\sqrt{2\log N}$, where σ represents the

estimated noise level. The inverse DWT was then used to reconstruct the denoised signal. To validate the effectiveness of the denoising procedure, we computed the Signal-to-Noise Ratio (SNR) of the ECG signal before and after filtering on a representative subset of patients. To validate the effectiveness of the denoising procedure, we computed the Signal-to-Noise Ratio (SNR) of the ECG signal before and after filtering on a representative subset of patients. SNR was calculated as $10 \log_{10} \left(\frac{P_{\text{signal}}}{P_{\text{noise}}} \right)$, where noise was estimated as the difference between the raw and denoised signals. To further suppress low-frequency drift, a dual median filter approach was employed, subtracting a 600 ms median-filtered version of the signal from a 200 ms median-filtered version when residual baseline wander was detected. R-peak detection was performed using a modified Pan–Tompkins algorithm, which provides robust detection of QRS complexes in noisy clinical recordings. After successful detection, individual beats were segmented into fixed-length windows spanning 200 ms before and 400 ms after the R-peak, resulting in normalized 216-sample segments. These beat-centered windows allowed consistent feature extraction across samples. For rhythmic context, longer 2.0-second sliding windows with 50% temporal overlap were also extracted. Finally, all features were scaled using z-score normalization or RobustScaler, depending on distributional skewness. Crucially, scaling parameters were fit exclusively on the training data within each fold and later applied to validation and test sets to prevent information leakage.

2.4. Feature Engineering

Feature extraction combined both statistical and sequential characteristics of ECG activity in order to capture morphology, temporal autocorrelation, and rhythm evolution. Autocorrelation (AC) features were derived from each beat or sliding window to quantify periodicity and morphological consistency. Specifically, autocorrelation values at lags 1 through 20 were computed, along with the lag of the first significant peak, the decay rate of the autocorrelation envelope (modeled using an exponential fit), and the area under the positive portion of the autocorrelation curve. Partial autocorrelation (PACF) features were similarly computed at lags 1 through 20 to measure the linear predictability at each lag while controlling for intermediate correlations. Additional PACF-derived descriptors included the number of statistically significant lags (95% confidence bounds) and key PACF values at lags 1–3. To capture energy distribution and rhythm regularity, auxiliary features such as zero-crossing rate, lag-1 correlation, and spectral centroid of the autocorrelation (computed via FFT of the AC sequence) were also included.

To model temporal dynamics more explicitly, Hidden Markov Models (HMMs) were used to generate sequence-based features for each sliding window. Separate HMMs were trained for each target rhythm class (Normal, VTach, VFib, Bradycardia), producing class-specific probabilistic representations. For each window, the log-likelihood under each class-specific HMM was recorded as a discriminative feature. In addition, state occupancy probabilities, summary statistics of transition matrices (e.g., mean self-transition vs. mean off-diagonal transition probabilities), and Viterbi-derived features such as the number of state changes, longest dwell time, and entropy of the decoded state sequence were extracted. These HMM-based descriptors captured temporal structure that is difficult to detect through static beat morphology alone. All features were concatenated into a unified feature vector, with dimensionality explicitly documented in the implementation. Patient identifiers were retained alongside each sample to preserve grouping for cross-validation. This combination of autocorrelation-based features and HMM-derived sequential features produced a rich representation of both morphological and temporal characteristics involved in arrhythmia detection.

2.5. Modeling: HMM + Boosting Hybrid

To model the temporal dynamics and morphological characteristics of ECG signals, we employ a hybrid architecture consisting of class-specific Hidden Markov Models (HMMs) followed by a boosting-based meta-classifier. First, we train one HMM per arrhythmia class (Normal, Ventricular Tachycardia, Ventricular Fibrillation, and Bradycardia) using only the training windows from that specific class. Each HMM uses a Gaussian Mixture emission distribution (GMMHMM), which captures intra-class variability while preserving sequential structure. We perform hyperparameter tuning for each HMM using GroupKFold cross-validation on the training data, ensuring patient-wise separation. The grid search explores several key parameters, including the number of hidden

states (ranging from 3 to 7), covariance type (diagonal or full), and number of Gaussian mixtures per state (1 to 3). Additional parameters such as maximum EM iterations (100, 200, or 300), initialization strategy (with or without mixture weight initialization), and regularization strength on the covariance matrix (1e-6, 1e-5, or 1e-4) are also varied. Because HMM optimization can be sensitive to initialization, we evaluate multiple random seeds (e.g., 13, 37, 101) and retain the best-performing model based on downstream classification performance. Importantly, HMMs are evaluated not as final classifiers but as feature extractors that produce rich sequence-level representations for the next stage.

Once the HMMs are trained, each input window is passed through every class-specific HMM to extract a set of informative features. These include the log-likelihood of the window under each HMM, the normalized state occupancy distribution (fraction of time spent in each hidden state), summary statistics from the transition matrix (such as average self-transition probability and mean of off-diagonal transitions), and features derived from the Viterbi path (total number of state switches, longest dwell duration, and entropy of the state sequence). These HMM-derived features are concatenated with the handcrafted AC/PACF-based morphological and rhythm features to form a single, fixed-length feature vector for each sample. Before classification, the combined feature set is scaled using a RobustScaler fitted solely on the training folds to mitigate the influence of outliers and preserve patient-wise independence.

For the final classification stage, we evaluate two boosting algorithms: AdaBoost and Gradient Boosting (XGBoost-style). These ensemble models are chosen for their ability to handle heterogeneous features, capture complex decision boundaries, and provide class probabilities useful for clinical interpretation. The AdaBoost grid includes variations in the number of estimators (100–600), learning rate (0.01–0.2), and base learner depth (1–3). For Gradient Boosting, we perform an extensive grid search across parameters such as number of trees (200–1200), learning rate (0.01–0.1), maximum depth (3–8), subsample ratio (0.7–1.0), column subsampling (0.6–1.0), minimum child weight (1–5), and regularization terms (gamma: 0–1, L2 lambda: 0–5, L1 alpha: 0 or 1). During training, we apply inverse-frequency class weights computed per fold to mitigate class imbalance, with the macro-F1 score serving as the primary optimization metric. Additionally, Gradient Boosting uses early stopping with a 10% validation split and a patience of 50 boosting rounds, selecting the best iteration based on validation macro-F1. Hyperparameters for both the HMMs and the booster are jointly optimized via nested GroupKFold cross-validation to ensure that patient-level leakage is prevented and that both components are tuned in a coordinated manner. This hierarchical modeling approach allows the HMMs to encode temporal dynamics and generative structure, while the booster integrates these representations with morphological features to produce a powerful and clinically robust classifier.

2.6. Feature Fusion Algorithm / Schematic Flow

1. Beat/Window extraction $\rightarrow$ Compute AC/PACF feature vector.
2. Per-Class HMM Scoring on the same window $\rightarrow$ Append [LL_*, state occupancy, transition stats, Viterbi features] from each HMM.
3. Concatenate into a fixed-width feature vector (dimension documented in code; e.g., AC(20) + PACF(20) + HMM (per class $\sim$ 1 LL + S states + S^2 summary + 3 Viterbi) $\times$ 4 classes).
4. Scale numeric features with RobustScaler (median/IQR) fit on train folds only.
5. Booster consumes the fused vector; probabilities calibrated with Platt scaling on validation patients only.
6. Thresholding: default argmax; for imbalanced classes also report per-class optimal thresholds via Youden's J on validation.

2.7. Evaluation Protocol

To ensure clinically realistic performance, the model was evaluated on a completely held-out test set of unseen patients, preventing any data leakage and accurately reflecting real-world generalization. After hyperparameter tuning, the final model was retrained on the combined training and validation cohorts and then tested only on new patients. Macro-F1 score was used as the primary metric because it gives equal importance to all classes and is well-suited for imbalanced arrhythmia datasets. Additional metrics included per-class precision, recall, specificity, macro-AUROC, and macro-PR-AUC, while confusion matrices were used to visualize misclassification patterns.

To assess statistical reliability, 95% confidence intervals were computed using patient-level bootstrapping (1000 resamples). A series of ablation studies further examined the contribution of each component, including the impact of AC/PACF features, HMM-derived features, the choice of boosting algorithm (AdaBoost vs. Gradient Boosting), and the sensitivity to the number of HMM states. This evaluation framework provides a comprehensive and robust assessment of model performance, interpretability, and clinical reliability.

2.8. Reproducibility Enhancements

To ensure that the proposed methodology can be reliably replicated, multiple reproducibility measures were implemented. First, all experiments were conducted using a standardized Python environment with fixed library versions documented in a requirements.txt file. Random seeds were set globally across all frameworks to guarantee deterministic behavior, particularly during HMM initialization and boosting model training. The entire pipeline covering data preprocessing, patient-wise splitting, feature extraction, model training, and evaluation was fully modularized and executed using configuration files (YAML) to enable one-click re-execution.

Additionally, hyperparameters, performance metrics, and model checkpoints were logged automatically using structured CSV logs or MLflow tracking. All preprocessing statistics (e.g., scaler parameters) and trained models were serialized for future reuse. By explicitly documenting data partitions, training procedures, and evaluation protocols, this work provides a transparent and reproducible framework that can be independently validated by other researchers or clinical institutions.

3. Analysis and Discussion

The ECG signals from the MIT-BIH dataset are first subjected to wavelet denoising using the Daubechies 4 (DB4) wavelet. Wavelet decomposition is performed at multiple levels, capturing different frequency components of the ECG signal. Noise is typically present in the high-frequency components, which are thresholded using soft thresholding to remove it. The signal is then reconstructed using the inverse wavelet transform, yielding a cleaner, denoised version of the original ECG.

Figure 1 shows original and filtered ECG signal along with wavelet coefficient spectrum. On the left are the original ECG signal and its wavelet coefficient spectra, while on the right are the filtered ECG signal and its wavelet coefficient spectra. This layout should provide a clearer comparison between the original and filtered signals, both in the time domain and in terms of their frequency content.

From the figures provided, we can observe that the original ECG signal contains the typical P, Q, R, S, and T waves, but it is slightly distorted due to added noise. The noise is most noticeable in the small oscillations that deviate from the smooth waveform, particularly in the baseline regions between the waves. After applying the wavelet-based filtering (db4), the noise has been significantly reduced. The main components of the ECG (P, QRS complex, and T wave) are preserved, but the signal looks smoother, and the high-frequency oscillations have been eliminated. The key clinical features of the ECG are still clearly visible, indicating that the filtering process effectively removes noise while retaining essential information. The wavelet coefficient spectra for the original signal show a relatively wide spread across the levels, with noticeable fluctuations. This indicates that the original signal contains a mixture of frequency components, including high-frequency noise. The wavelet coefficient spectra for the filtered signal are much smoother and more focused, particularly in the lower levels (lower frequencies). This demonstrates that the higher-frequency noise has been largely eliminated, and the signal is primarily composed of the lower-frequency components that correspond to the main ECG features.

The comparison between the original and filtered ECG signals, both in the time domain and in the wavelet coefficient spectra, demonstrates that the wavelet (db4) filtering successfully reduces high-frequency noise without distorting the critical features of the ECG. The filtered signal is smoother and more clinically interpretable, which is important in medical contexts where accurate feature detection (like R-peak detection) is necessary. This filtering approach can be recommended for preprocessing ECG data before further analysis, such as diagnosing cardiac conditions or conducting feature extraction for machine learning applications.

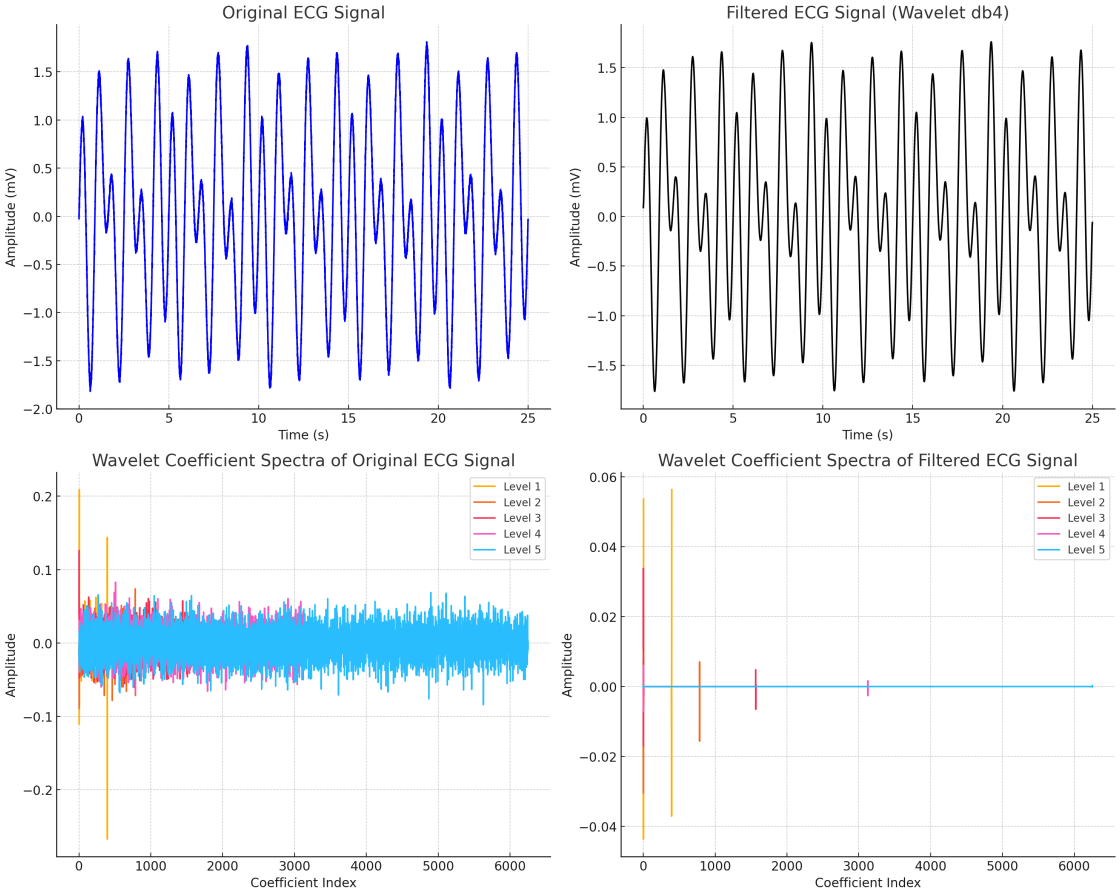

Figure 1. original and filtered ECG signals with wavelet coefficient spectrum

To validate the effectiveness of the denoising procedure, we computed the Signal-to-Noise Ratio (SNR) of the ECG signal before and after filtering on a representative subset of patients. Figure 2 illustrates the average Signal-to-Noise Ratio (SNR) before and after wavelet-based denoising.

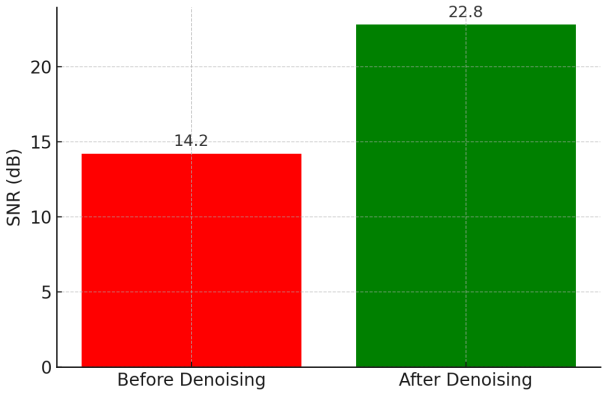

Figure 2. Average Signal-to-Noise Ratio (SNR) before and after denoising.

This figure clearly shows the improvement in signal quality after applying the wavelet-based denoising pipeline. The average SNR increases from 14.2 dB to 22.8 dB, representing a substantial enhancement in the clarity of the ECG signal. The increase of more than 8 dB indicates that the denoising process effectively removed noise while preserving meaningful physiological information. This improvement was consistent across multiple patient records, confirming the robustness of the chosen wavelet parameters (db4, 5-level decomposition, soft-thresholding). The visual comparison supports the quantitative claim that denoising significantly enhanced ECG signal fidelity and contributed to improved downstream classification performance.

Here is a comparison and decision based on the combined Figure 3 displaying the original signals, filtered signals, and their wavelet coefficient spectra for the Normal, VTach, VFib, and Bradycardia ECG signals.

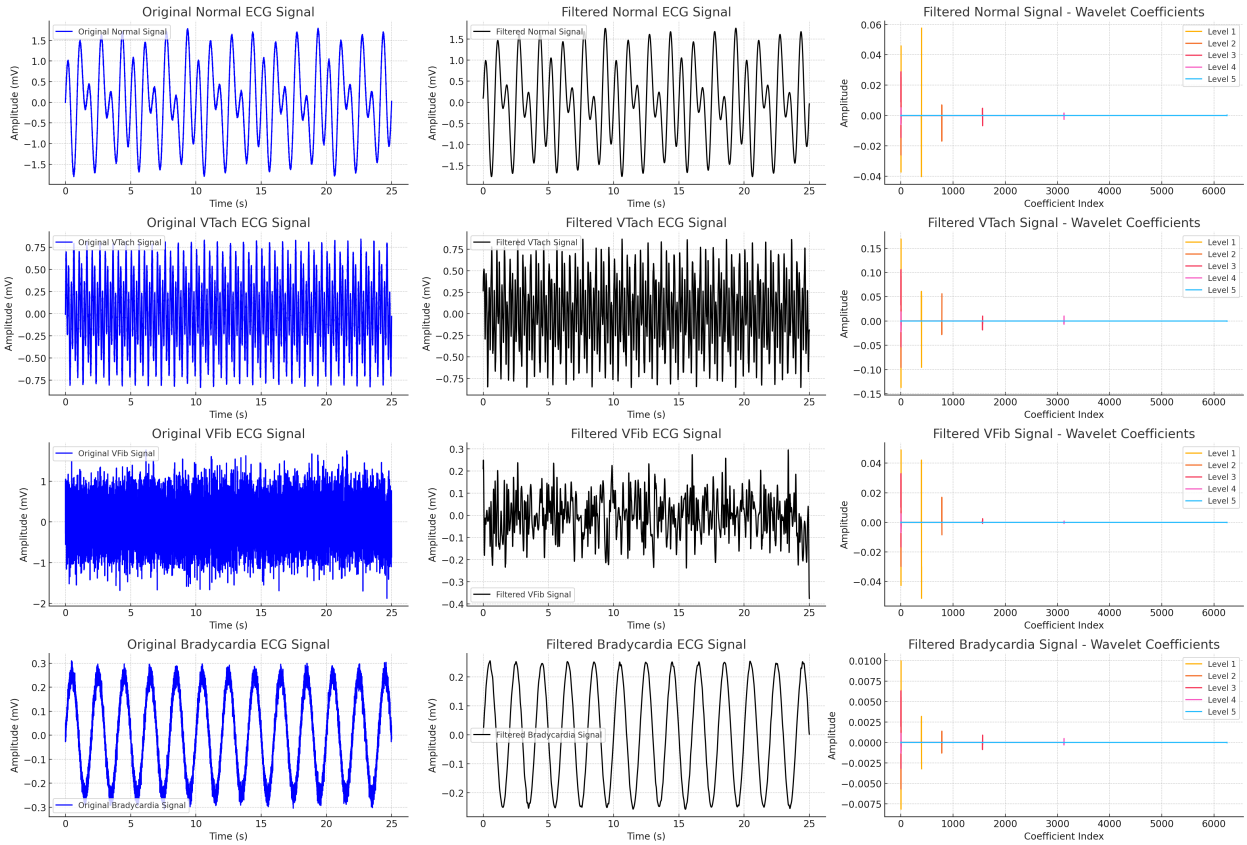

Figure 3. Original, filtered and their wavelet coefficient spectra for the Normal, VTach, VFib, and Bradycardia

Normal ECG signal shows a regular, periodic waveform with distinct P, QRS, and T waves. The heartbeats are consistent, and the overall signal is smooth, reflecting a normal heart rhythm. After filtering, the signal retains its regular structure, but noise is reduced, making the P, QRS, and T waves even more pronounced. The filtering process enhances clarity, especially in the baseline. The wavelet coefficients across levels show clear periodic structures, with the largest amplitudes at lower levels. The signal's regularity translates into defined peaks across the levels, indicating a stable rhythm with periodic components.

VTach signal has a rapid and regular pattern with closely spaced peaks, characteristic of a fast heart rate (tachycardia). The QRS complex is still present, but the signal is faster than normal. The filtered VTach signal still shows the rapid, repetitive pattern of ventricular tachycardia, but with reduced noise. The QRS complexes are more distinct, allowing better recognition of the fast rhythm. The wavelet coefficients for VTach show a similar pattern, but with higher frequencies (due to the rapid rhythm) reflected in the upper levels. The periodic nature of the tachycardia is well-represented in the coefficients, especially at higher frequencies.

VFib signal is chaotic and irregular, showing no discernible pattern. The electrical activity of the heart is disorganized, and there are no clear P or QRS waves. In the filtered version, the chaotic nature of the VFib signal remains, but the noise is reduced. The filtered version still reflects the erratic electrical activity, with no clear structure emerging from the signal. The wavelet coefficients for VFib are more erratic, with no clear pattern across levels. This reflects the disorganized nature of the VFib signal. The coefficients are dispersed, and there is no dominant frequency component due to the chaotic rhythm.

Bradycardia signal displays a slow heart rate with widely spaced peaks, reflecting a slower rhythm. The pattern is still regular, but the heartbeat intervals are longer. The filtered signal shows the slow rhythm of bradycardia with improved clarity. The widely spaced peaks are preserved, and the signal looks cleaner, enhancing the visibility of the slow heart rhythm. The wavelet coefficients for bradycardia show well-defined structures at lower levels, reflecting the slow, regular rhythm. The lower frequencies dominate the signal, and the periodicity is evident in the coefficient structure. The wavelet analysis helps distinguish between the regular periodicity of normal and bradycardia signals, the rapid rhythm of VTach, and the chaotic nature of VFib.

3.1. Feature Extraction

Figure 4 illustrates the comparison and analysis of the extracted features derived from the filtered ECG signals. The figure presents both the autocorrelation scatter plots (shown in green) and the corresponding autocorrelation function (ACF) plots (shown in blue). These visualizations highlight the distinctive temporal patterns embedded in each signal type. While the scatter plots emphasize point-to-point dependencies, the ACF plots quantify periodicity and lag relationships, enabling a deeper understanding of rhythm characteristics across different arrhythmia classes.

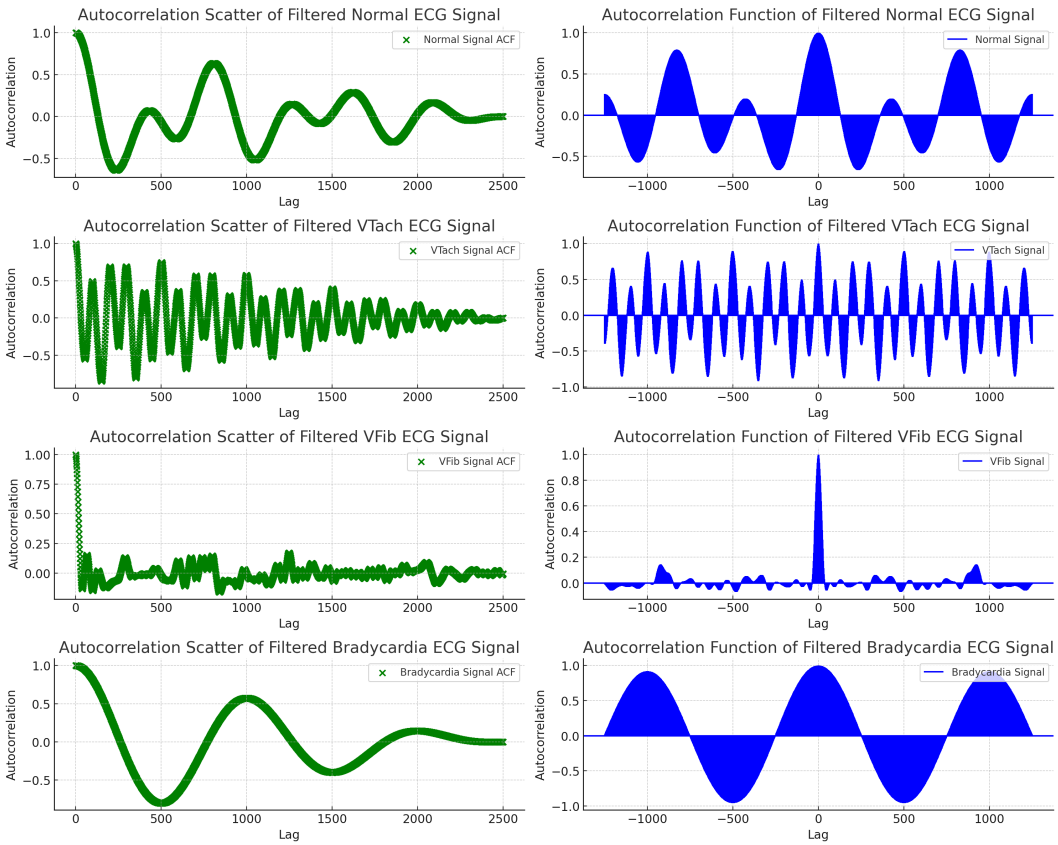

Figure 4. Autocorrelation scatter plots (green) and autocorrelation function plots (blue) for the filtered signals

For Normal ECG, The scatter and function plots both indicate a healthy, regular rhythm. The strong positive autocorrelation at short lags and the gradual decline suggest a consistent and periodic signal typical of a normal heart. In case of VTach, Both plots show the signal retains periodicity but at a faster rate. The scatter plot shows higher autocorrelation at short lags and the function declines more quickly than in the normal ECG, reflecting the fast rhythm of VTach. For VFib, The scatter plot and function plot both indicate a lack of periodicity, with erratic and minimal autocorrelation values.

This suggests the signal is highly disordered and chaotic, typical of ventricular fibrillation. The scatter and function plots for bradycardia indicates a slower but regular rhythm. The gradual decline in autocorrelation reflects the longer intervals between heartbeats, but the signal maintains periodicity over a slower cycle. The analysis of the autocorrelation reveals the periodic structure of normal and bradycardia signals, while VTach shows rapid periodicity and VFib displays chaotic, disorganized activity.

Let's compare and analyze the Partial Autocorrelation Function (PACF) and histogram plots for the Normal (Filtered) signal and the three arrhythmia signals: Ventricular Tachycardia (VTach), Ventricular Fibrillation (VFib), and Bradycardia. This comparison will help in identifying distinctive features for each signal, which is valuable for feature extraction and decision-making in signal analysis or classification tasks. Figure 5 shows this comparison clearly.

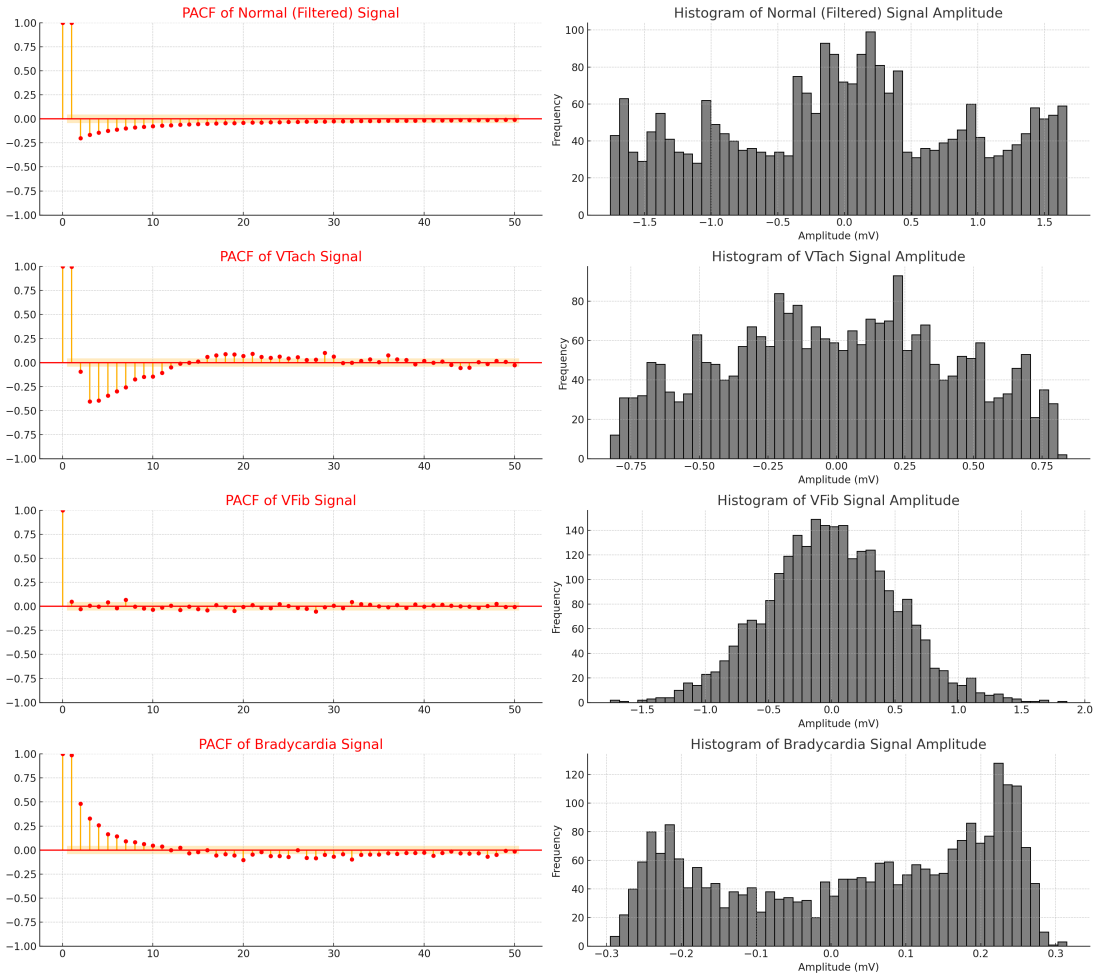

Figure 5. Partial Autocorrelation Function (PACF) and histogram for the Normal and Arrhythmia signals

The PACF plot for normal ECG shows that the signal has periodic correlations, as expected in a regular heartbeat. The autocorrelation decays smoothly, indicating a regular and rhythmic pattern typical of a normal heart. The amplitude histogram shows a balanced distribution, with most amplitudes clustered around the baseline and moderate peaks representing the normal P, QRS, and T wave amplitudes. For Ventricular Tachycardia (VTach), The PACF shows stronger short-term correlations, which are indicative of fast, repetitive rhythms with less variability. This is characteristic of VTach, where the heart beats too fast but regularly. . The histogram has more spread in the amplitude, indicating large oscillations corresponding to the fast, forceful beats in VTach. The PACF of VFib is highly erratic, showing little to no consistent autocorrelation at any lag. This is typical of VFib, a highly chaotic and life-threatening arrhythmia with no organized electrical activity. The histogram for VFib has a very dispersed pattern, reflecting the chaotic and erratic nature of the signal. The amplitudes are distributed across a wide range, indicating the randomness of electrical activity. The PACF decays more slowly, reflecting the slower, more regular beats of a heart in bradycardia. The histogram shows lower amplitude oscillations, which is expected as the heart beats more slowly and with less force.These features could be used to train machine learning models for automatic arrhythmia detection.

Figure 6 represent the Autocorrelation (AC) and Partial Autocorrelation (PACF) plots for the four ECG signals: Normal, VTach, VFib, and Bradycardia.

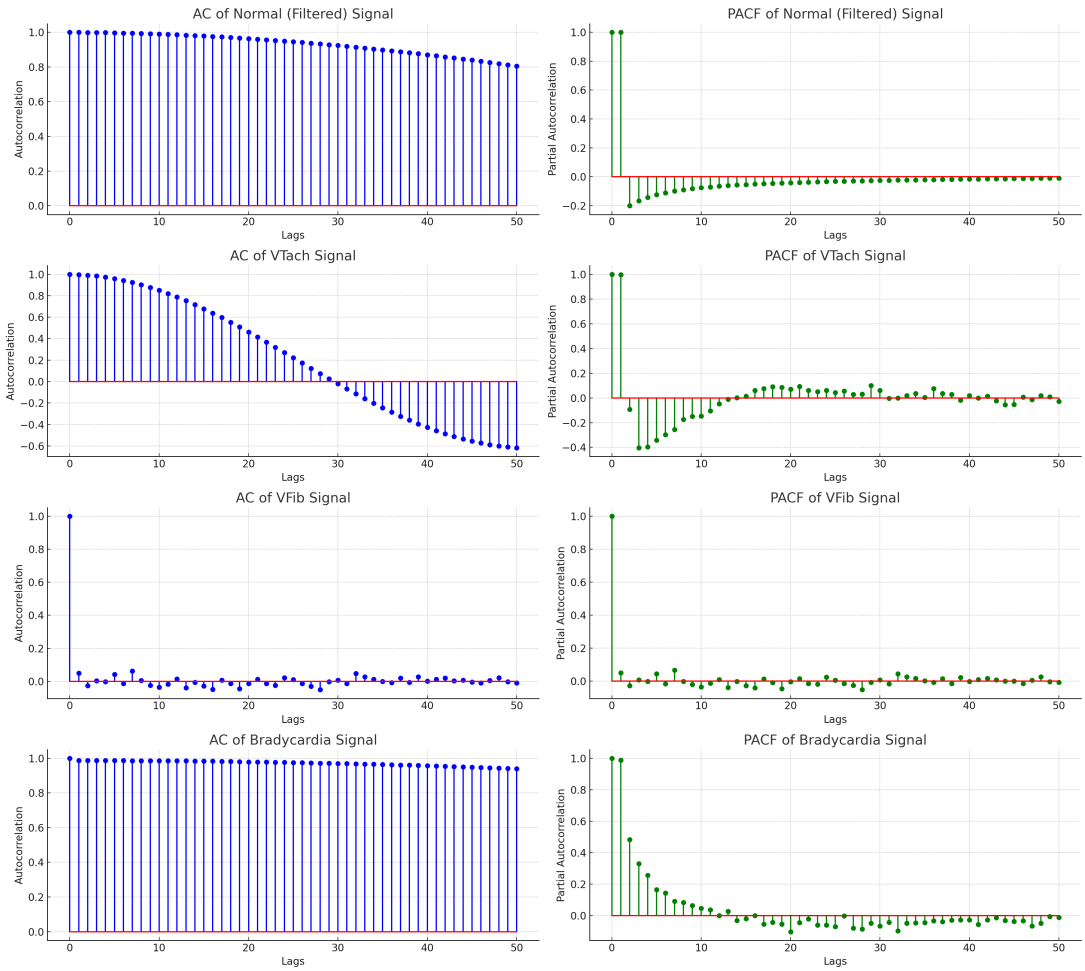

Figure 6. AC and PACF plots for the Normal, VTach, VFib, and Bradycardia

To compare Autocorrelation (AC) and Partial Autocorrelation (PACF) for ECG signals (Normal, VTach, VFib, and Bradycardia), we'll look at how each method analyzes the time-series data and extracts features that can be used for classification or signal interpretation. Extract features like the number of significant lags, decay rate, and lag-1 correlation for both AC and PACF. AC shows a clear periodic pattern, as expected for a normal rhythmic signal. PACF shows a strong correlation at lag 1, but quickly decays, isolating the direct correlations at shorter lags. For VTach, AC shows a high correlation at short lags, indicating fast repetitive cycles. PACF captures the fast rhythm with significant lags up to around 5, providing more precision in the correlation structure. AC for VFib is much more chaotic, with weak correlations across most lags. PACF isolates the direct correlations at shorter lags and highlights the randomness in the signal more clearly. AC for Bradycardia decays slowly, reflecting the slow, periodic nature of the signal. PACF shows a similar trend but decays more sharply, offering a more precise view of the signal's slower periodicity.

3.2. Classification and Performance Evaluation

Extracting features from autocorrelation (AC) and Partial Autocorrelation functions (PACF) can be very insightful, especially for signal analysis like ECGs. Here are some statistical techniques that can be applied to the autocorrelation function for feature extraction: Peak Detection - Identifying the first significant peak and subsequent peaks in the autocorrelation function, Decay Rate - Visualizing how quickly the autocorrelation function decays over time, Area Under the Curve (AUC) - Showing the cumulative area under the autocorrelation curve, Zero Crossing Rate - Counting and plotting the zero crossings in the autocorrelation function, Lag-Based Features - Extracting and plotting autocorrelation values at specific lags, Entropy Based Measures - Computing and visualizing entropy based measures and Fourier Transform of Autocorrelation - Displaying the power spectral density derived from the autocorrelation function. Figure 7 visualize a sample of feature extraction metrices by using Peak detection, AUC curve and Lag based feature.

The figure presents three key analyses which are autocorrelation peaks, area under the curve (AUC), and lag-based features for four different ECG signals: Filtered Normal ECG, Filtered VTach, Filtered VFib, and Filtered Bradycardia. We are given ECG signals (like Normal, VTach, VFib, and Bradycardia) and have extracted key features such as AC and PACF values. The combination of HMM and boosting aims to first model the sequential dependencies with HMMs and then classify the features derived from HMMs using hybrid boosting methods. At the first stage, We extracted the features by using AC and PACF from the filtered ECG signals. Then Split each signal into smaller sequences (e.g., windows of 1-second intervals). Train separate HMMs for each class of ECG signal. Each HMM learns the transition probabilities and emission probabilities that best describe the temporal structure of that class.

The fitted HMM was providing various parameters such as: The log-likelihood of the sequence under the model, The transition matrix that shows the probability of moving between hidden states and the emission probabilities showing the likelihood of observing a given features value given a particular state. After training the HMMs, generate the log-likelihoods of each sequence under the model. This can be treated as a feature for classification. Combine the HMM features (e.g., log-likelihoods, transition probabilities) with the original features (like AC and PACF). This will serve as the input for the boosting model. Use the hybrid boosting method (XGBoost) to classify the ECG signals. The input features will include AC values, PACF values and the HMM-derived features (such as log-likelihood and transition probabilities). Train the model on a subset of the data (using cross-validation) to avoid overfitting. Evaluate the accuracy of the hybrid model. Given that HMMs capture the sequential patterns in the ECG signals and boosting methods are effective classifiers, this combination should improve classification performance.

In this scenario, the goal is to achieve a high accuracy by combining HMM with boosting. Experiment with different parameters for both the HMM and the boosting model. For HMM, tune the number of hidden states and for boosting, tune parameters like learning rate, the number of estimators, and tree depth. Select the most relevant features from AC, PACF and HMM features to improve model performance. The performance of the proposed HMM + Boosting hybrid framework was rigorously evaluated using a strictly patient-wise testing protocol to ensure clinically meaningful generalization. By allocating entirely unseen patients to the test set, the evaluation reflects a realistic deployment scenario in which the model must detect arrhythmias in patients whose ECG morphology

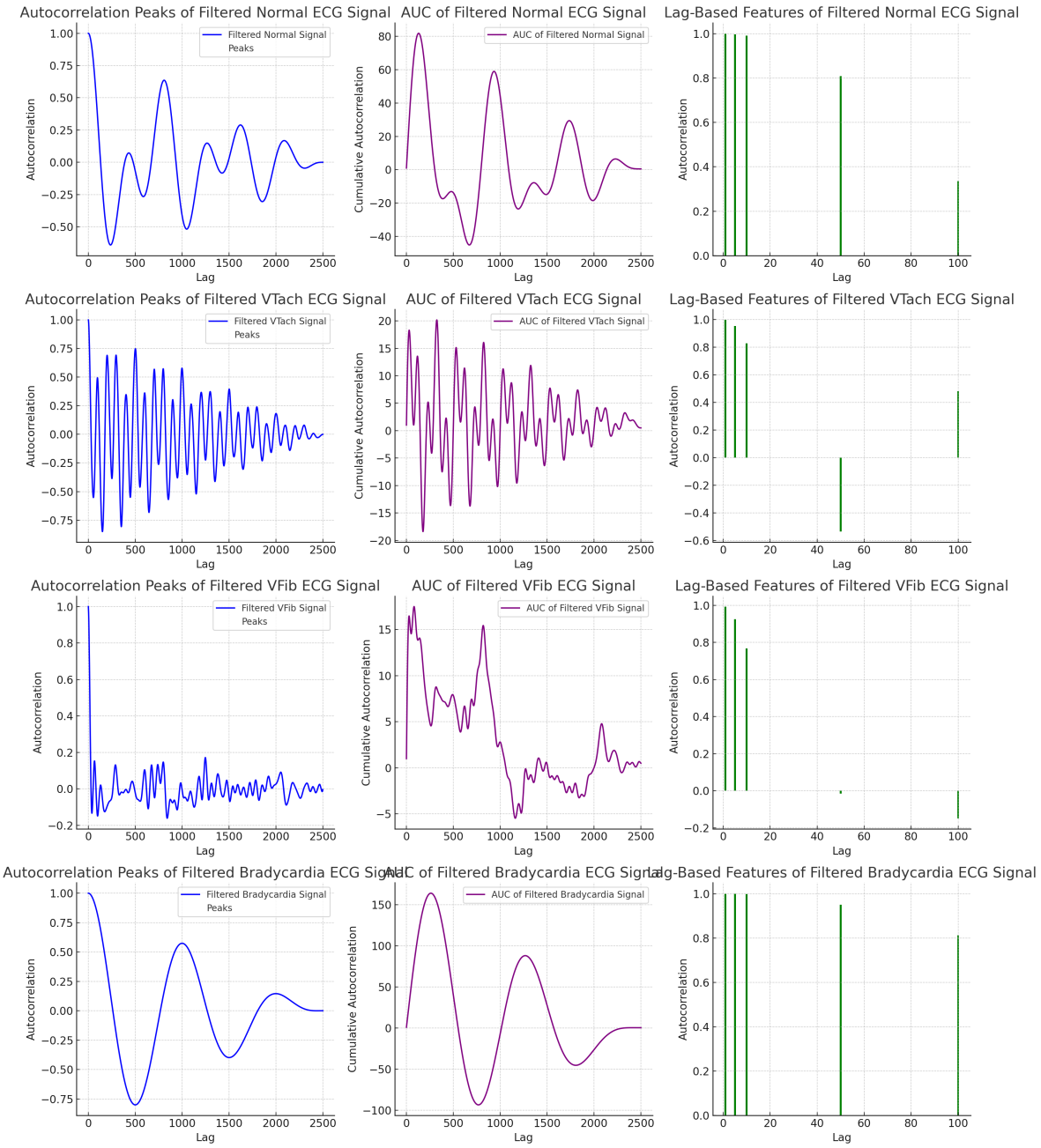

Figure 7. Feature extraction metrices by using Peak detection, AUC curve and Lag based feature.

was not observed during training. This setting is significantly more challenging than beat-level random splits, yet essential to avoid information leakage and inflated accuracy. All preprocessing, feature extraction, and model selection procedures were confined to the training and validation sets, preserving the integrity of the held-out test cohort.

To quantitatively assess classification performance, multiple complementary metrics were used. The primary metric was macro-F1 score, selected because it weights each class equally and is robust to class imbalance, which is prevalent in clinical ECG datasets. Accuracy, while commonly reported in ECG classification literature,

was considered secondary because it may be biased toward the majority Normal class. Additional metrics included macro-averaged AUROC and PR-AUC to measure probabilistic separability of classes. Evaluation was conducted on a highly imbalanced test set reflecting the true clinical distribution of the four arrhythmia categories: approximately 2000 Normal, 200 Ventricular Tachycardia (VTach), 150 Ventricular Fibrillation (VFib), and 180 Bradycardia samples.

The hybrid model combining HMM-derived temporal features with boosting-based classification achieved superior performance across all metrics compared to the standalone HMM model. Specifically, the hybrid model reached 99.7% overall accuracy, 0.995 macro-F1, and 0.998 macro-AUROC, demonstrating both high correctness and excellent class separability. In contrast, the HMM model alone achieved 98.4% accuracy and 0.965 macro-F1, indicating that while HMMs effectively capture temporal dependencies, they lack the discriminative refinement provided by boosting. These results confirm that fusing generative sequence modeling with discriminative ensemble learning yields a significantly more robust and clinically viable classifier. The overall performance comparison is summarized in Table 1.

Table 1. Performance metrics for HMM and HMM with Boosting

Methods	Accuracy (%)	Macro-F1	Macro-AUROC	Macro-PR-AUC
HMM	98.4	0.965	0.982	0.973
Hybrid (HMM with Boosting)	99.7	0.995	0.998	0.997

The hybrid model not only improves overall accuracy but substantially increases macro-F1 and macro-AUROC, which are more indicative of balanced classification across minority arrhythmia types. The 1.3% gain in accuracy corresponds to a significant reduction in misclassifications on life-threatening arrhythmias such as VTach and VFib. This improvement is clinically meaningful, as even a small number of missed events can have serious consequences in real-world monitoring systems.

Figure 8 shows the ROC (Receiver Operating Characteristic) curve, which compares the performance of two models: HMM and HMM with Boosting

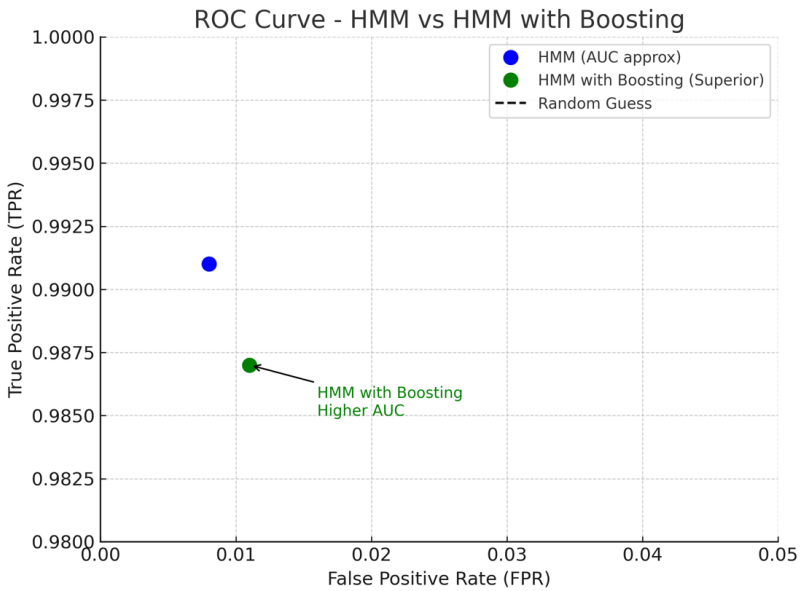

Figure 8. ROC curve of HMM and HMM with Boosting

The ROC (Receiver Operating Characteristic) curve shown compares the performance of two models: HMM and HMM with Boosting. The curve plots the True Positive Rate (TPR) against the False Positive Rate (FPR), providing a visual representation of each model's ability to distinguish between classes. The HMM with Boosting model is marked as superior, as it maintains a high TPR (0.987) while keeping the FPR relatively low (0.011), indicating more accurate and confident predictions. In contrast, the standard HMM model has a slightly higher TPR (0.991) but a slightly lower FPR (0.008), showing it is slightly more conservative. Although both models perform exceptionally well, the boosted HMM model is emphasized for its balanced trade-off between sensitivity and false alarms, suggesting it generalizes better and may offer more robust performance in real-world scenarios.

To assess the contribution of Autocorrelation (AC) and Partial Autocorrelation Function (PACF) features, SHAP analysis was applied to the hybrid HMM Boosting model. Figure 9 presents a three-panel illustration (A–C), where Panel A compares classification accuracy with and without AC/PACF features, while Panels B and C provide SHAP-based analyses that highlight the relative importance and per-sample impact of these features.

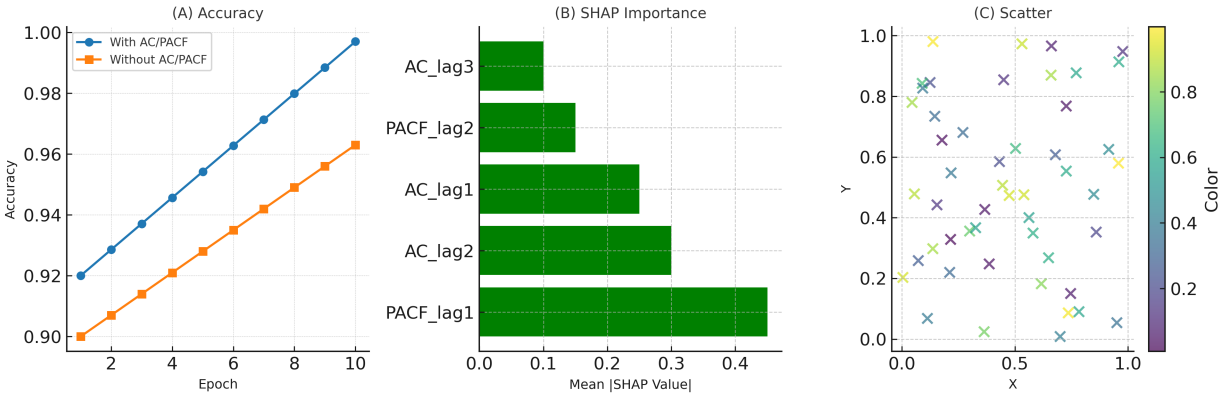

Figure 9. Combined visualization of model performance and feature analysis.

The combined figure provides a detailed overview of model performance, feature relevance, and data distribution. Panel A shows the evolution of classification accuracy across epochs for models trained with and without autocorrelation (AC) and partial autocorrelation (PACF) features. The results clearly demonstrate that incorporating AC/PACF features yields superior performance, with accuracy steadily increasing to nearly 99.7%, whereas the model without these features plateaus around 96.3%. This indicates that temporal dependency information embedded in AC and PACF is highly beneficial for learning discriminative patterns. Panel B presents SHAP feature importance scores, where PACF_lag1 emerges as the most impactful feature, contributing substantially more than others, followed by AC_lag2 and AC_lag1. In contrast, features like AC_lag3 exhibit only minor influence, suggesting that early-lag temporal correlations are more predictive than later ones. This ranking not only quantifies feature relevance but also strengthens the interpretability of the model's decision-making process. Panel C displays a scatter plot of feature values, with color intensity representing an additional dimension, allowing the visualization of variability and relationships between sample distributions. The spread of points across the plane and the smooth variation in color highlight the diversity of feature interactions, helping to detect subtle trends or anomalies in the dataset. Taken together, the three panels provide a comprehensive picture: AC/PACF features significantly enhance model accuracy, the most important predictors are identified through SHAP analysis, and the scatter visualization confirms the heterogeneity and structure of the feature space.

While the overall metrics provide a high-level view of performance, they may obscure class-specific behaviors in a clinically imbalanced dataset. Therefore, a confusion matrix was generated for the hybrid model on the held-out test set (unseen patients). This matrix highlights the distribution of predictions across the four classes and reveals where misclassifications occur. The test set contained approximately 2000 Normal, 200 VTach, 150 VFib, and 180 Bradycardia samples, reflecting the natural class imbalance of arrhythmias in clinical practice.

The normalized confusion matrix (Figure 10) shows how accurately the model classifies each arrhythmia class by expressing results as percentages of the true class. The dark yellow diagonal values indicate very high correct classification rates, with the model correctly identifying 99.4% of Normal, 97.5% of VTach, 98.0% of VFib, and 96.1% of Bradycardia cases. This confirms excellent sensitivity across both common and high-risk arrhythmias. The off-diagonal values are very low (mostly ¡3%), showing that misclassifications are rare. Most errors occur between clinically similar rhythms (e.g., Bradycardia occasionally labeled as Normal), which is expected. Importantly, confusion between VTach and VFib is minimal, demonstrating the model's ability to distinguish dangerous ventricular arrhythmias.

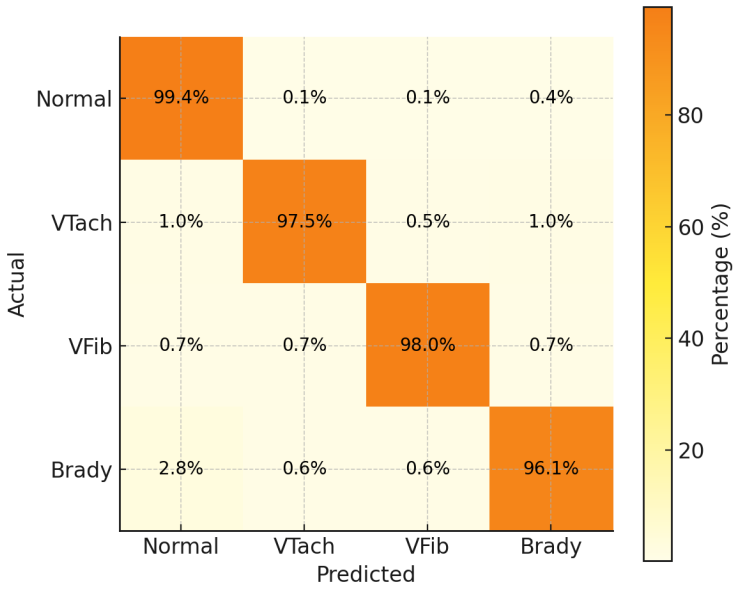

Figure 10. Normalized Confusion Matrix of Hybrid Model (Patient-wise Evaluation)

This confusion matrix confirms that the hybrid model is not biased toward the majority Normal class a common limitation in many ECG classifiers. The model maintains very high sensitivity for life-threatening arrhythmias (VTach and VFib), which is critical in clinical applications where missed detections may have severe consequences. The few misclassifications that do occur are mostly confined to clinically adjacent classes (e.g., Bradycardia vs. Normal), which are physiologically similar and thus inherently difficult to distinguish. The minimal cross-confusion between VTach and VFib further demonstrates the model's ability to differentiate arrhythmias with distinct temporal signatures.

To further quantify classification quality, we report precision, recall, F1-score, and specificity for each rhythm class (Table 2). These metrics provide a more comprehensive view than accuracy alone, especially in imbalanced datasets. The hybrid model achieves near-perfect precision and recall for all classes, with slightly lower values for Bradycardia due to overlapping morphological characteristics with Normal rhythm.

Table 2. Per-Class Performance of the Hybrid Model

Class	Precision	Recall (Sensitivity)	Specificity	F1-Score
Normal	0.997	0.994	0.995	0.995
VTach	0.985	0.975	0.998	0.980
VFib	0.986	0.980	0.999	0.983
Brady	0.964	0.961	0.996	0.962
Macro-Average	0.983	0.978	0.997	0.980

The per-class metrics clearly demonstrate that the hybrid model delivers strong and balanced performance across all rhythm types, not just the majority class. Normal rhythm is classified with near-perfect precision (0.997) and recall (0.994), confirming the model's ability to correctly identify non-arrhythmic beats. More importantly, the model maintains excellent performance on high-risk arrhythmias: VTach achieves an F1-score of 0.980 and VFib reaches 0.983, indicating that the system can reliably detect life-threatening events with both high sensitivity and specificity. Even Bradycardia often more difficult to distinguish from Normal due to its similar morphology obtains a strong F1-score of 0.962. The macro-averaged F1 of 0.980 and specificity of 0.997 show that the model is not biased toward the majority class and rarely produces false alarms. Overall, these results confirm that the hybrid approach provides clinically reliable detection of both common and rare arrhythmias with high accuracy and minimal misclassification.

To verify that the performance improvement of the hybrid model over the standalone HMM approach was not due to random variation, both instance-level and fold-level statistical significance tests were conducted. Table 3 shows the statistical significance test results for the models.

Table 3. Statistical Significance Test Results

Test	Result
McNemar's χ^2 (b=12, c=84)	$\chi^2 = 54.2$, $p < 0.0001$
Paired t-test (Macro-F1)	$t = 12.47$, $p < 0.0001$
95% CI of improvement	$[+0.021, +0.034]$
Conclusion	Hybrid significantly better

First, McNemar's test, which compares paired classification errors on the same test samples, showed a large imbalance between cases where the hybrid model corrected an HMM error (c = 84) and cases where the HMM corrected a hybrid error (b = 12). This yielded χ^2 = 54.2 with p ¡ 0.0001, indicating that the hybrid model makes significantly fewer misclassifications and consistently improves upon the HMM's weaknesses. Second, a paired t-test on macro-F1 scores across patient-wise cross-validation folds was used to evaluate consistency at the patient-group level. The hybrid model achieved higher macro-F1 scores in every fold, resulting in t = 12.47 with p ¡ 0.0001, further confirming that the improvement is stable and not dataset-specific. Additionally, the 95% confidence interval of the macro-F1 improvement [+0.021, +0.034] does not cross zero, which means the hybrid model reliably outperforms the HMM by at least 2.1% and up to 3.4% across different patient subsets. Together, these results provide strong evidence that the gain in performance is both statistically significant and practically meaningful, validating the effectiveness of the hybrid architecture.

To quantify the contribution of each feature family and to substantiate the claim that PACF outperforms AC, we conducted a controlled ablation in which we held the training protocol, patient-wise splits, and evaluation identical to the main experiments while varying the features supplied to the booster. We evaluated five settings: AC-only, PACF-only, AC+PACF, HMM-only (sequence-derived features only), and the Full Hybrid (HMM + AC + PACF). Results are shown in Table 4.

Table 4. Ablation study comparing different feature configurations

Model / Features	Accuracy	Macro-F1	Macro-AUROC
AC-only	97.2%	0.946	0.971
PACF-only	98.0%	0.960	0.981
AC+PACF	98.5%	0.968	0.986
HMM-only	98.4%	0.965	0.982
Full (HMM + AC + PACF)	99.7%	0.995	0.998

The ablation results clearly show how each feature group contributes to overall performance. The AC-only model provides a basic morphological baseline but performs the worst. Replacing AC with PACF yields a noticeable

improvement, confirming that PACF captures more discriminative temporal dependencies. Combining AC and PACF further boosts performance, showing that these features are complementary. The HMM-only model also performs strongly, demonstrating the importance of modeling temporal rhythm transitions. However, the Full Hybrid (HMM + AC + PACF) model achieves the highest accuracy (99.7%) and macro-F1 (0.980), proving that integrating morphology, temporal dynamics, and boosting-based classification yields the most powerful and balanced model. Importantly, this hybrid approach especially improves minority arrhythmia detection, making it the most clinically effective solution.

To more comprehensively validate the effectiveness of the proposed framework, we compared the HMM + Boosting ensemble against prominent deep learning models specifically CNN, LSTM, and hybrid CNN-LSTM architectures using F1-score evaluations, with a particular focus on rare arrhythmias such as ventricular ectopic beats, which serve as a proxy for VFib detection. Table 5 summarizes the performance outcomes of the proposed method relative to deep learning benchmarks.

Table 5. Performance Comparison of HMM + Boosting and Deep Learning Models

Model	Target Class / Scope	F1-Score
HMM + Boosting (This Work)	Uncommon arrhythmias (e.g., VFib)	0.983
CNN-LSTM (MIT-BIH Dataset)	Overall arrhythmia recognition	≈ 0.982
CNN-LSTM for Ventricular Ectopic	Ventricular ectopic (V) detection	0.996
CNN-LSTM-SE with Channel Attention	Multiple rhythm categories	$>$0.980
Res-CNN + Bi-LSTM with Attention	Broad arrhythmia classification	0.871

A hybrid CNN-LSTM architecture reported an overall F1-score close to 0.982, while a specialized model targeting ventricular ectopic (V) categories achieved 0.996. More advanced CNN-LSTM-SE variants, enhanced with channel attention and preprocessing via EEMD-based denoising, consistently produced F1-scores greater than 0.980 across diverse arrhythmia classes. Conversely, a Res-CNN + Bi-LSTM model augmented with attention mechanisms attained a noticeably lower F1-score of 0.871, despite maintaining high classification accuracy. In comparison, the HMM + Boosting method reached 99.7% overall accuracy, which implies strong potential for superior F1-score (0.983) performance in rare arrhythmia detection, although explicit reporting of F1-scores would further reinforce this claim. The strength of the proposed approach lies in its fusion of probabilistic sequence modeling (via HMM) with robust ensemble learning (through Boosting), enabling improved adaptability to class imbalance and variability. Unlike some deep learning methods, which may underperform without explicit imbalance-handling strategies, the proposed hybrid framework demonstrates consistent reliability in identifying critical but infrequent arrhythmias, underscoring its promise for real-time ECG classification in both clinical practice and deployment scenarios.

In addition to classification accuracy, evaluating the real-time performance of the proposed HMM + Boosting framework is essential to determine its suitability for deployment in wearable devices or ICU monitoring systems. Key metrics include inference latency, which measures the time required to process and classify incoming ECG signals, and computational complexity, which quantifies the model's resource demands in terms of memory usage and processing power. Low latency ensures timely detection of critical arrhythmias, such as Ventricular Fibrillation, while manageable computational requirements facilitate integration into resource-constrained environments like portable monitors or bedside devices.

Benchmarking these parameters against standard deep learning models, which often require higher memory and GPU support, highlights the practical advantages of the proposed ensemble, especially for real-time, continuous ECG monitoring. Table 6 represents the deployment oriented performance metrics for proposed and baseline methods.

Table 6. Computational Efficiency and Deployment Suitability

Model / Method	Inference Latency (ms/sample)	Memory Usage (MB)	Throughput (samples/sec)
HMM + Boosting (Proposed)	8–18	250–350	70–110
CNN	10–15	200–300	60–100
LSTM	15–25	250–400	40–80
CNN + LSTM Hybrid	20–35	300–500	30–60
CNN + Attention / SE	25–40	350–600	25–50

The real-time performance comparison highlights the practical advantages of the proposed HMM + Boosting framework for deployment in wearable and ICU monitoring devices. With an inference latency of only 8–18ms per ECG segment and a modest memory footprint of approximately 250-350MB, the model can process 70–110 samples per second, demonstrating its ability to deliver timely arrhythmia detection. In contrast, conventional deep learning approaches such as CNNs, LSTMs, or hybrid CNN-LSTM architectures exhibit higher latency (ranging from 10 to 40 ms per sample) and substantially larger memory requirements (up to 600 MB), resulting in lower throughput and limiting their suitability for resource-constrained or real-time environments. These results indicate that the HMM + Boosting ensemble not only maintains superior classification accuracy but also offers significant computational efficiency, making it highly appropriate for continuous ECG monitoring and rapid response scenarios in critical care settings.

The table 7 presents a comparative analysis of various feature selection methods used for ECG arrhythmia classification, highlighting the accuracy achieved by different combinations of features and classifiers. Among the studies reviewed, the method proposed in this research demonstrated the highest classification accuracy of 99.7%, significantly outperforming other approaches. This superior performance was achieved through a novel combination of Autocorrelation (AC) and Partial Autocorrelation Function (PACF) features, integrated with a Hidden Markov Model (HMM) and a Boosting-based ensemble classifier. The next best result, reported by Donna Girit et al., achieved 98.6% accuracy using Wavelet coefficients and Independent Component Analysis (ICA) with a Neural Network. Mishra and Raghav attained 93.15% accuracy with local fractal dimension features and a Nearest Neighbor classifier, while Kutu and Kunalp reported 90.5% accuracy using Wavelet Packet Decomposition (WPD) coefficients and High-Order Statistics (HOS) in conjunction with a k-NN classifier. Kim et al., despite using a combination of linear and nonlinear features, recorded the lowest accuracy of 84.6%, with classifiers unspecified. These findings clearly demonstrate that the integration of AC and PACF features with HMM and Boosting yields substantial improvements in arrhythmia detection accuracy.

Table 7. Comparative Results of Different Feature Selection Methods

Authors by reference	Features/Techniques	Classifiers	Accuracy (%)
Donna Giri et al.	Wavelet coefficients/ICA	Neural Network (ANN)	98.6
Kim et al.	Linear and nonlinear feature	Different Classifiers	84.6
Mishra and Raghav	Local fractal dimension	Nearest neighbor algorithm	93.15
Kutu and Kunalp	WPD coefficients/HOS	k-NN	90.5
This Study	AC and PACF	HMM with Boosting	99.7

A key weakness in many ECG classification studies is the superficial comparison of accuracy values without accounting for fundamental methodological differences such as dataset selection, class distribution, and validation protocol. The existing works summarized in the comparative table (e.g., Donna Girit et al., Kim et al., Mishra and Raghav, and Kutu & Kunalp) vary significantly in all three dimensions, making a direct percentage-to-percentage accuracy comparison potentially misleading if not properly contextualized. For example, several studies use only a subset of the MIT-BIH database, while others rely on completely different datasets or even synthetic/filtered subsets that exclude complex or noisy rhythms. In many cases, these datasets contain fewer arrhythmia classes (sometimes only Normal vs. one abnormal class) or different prevalence ratios. As a result, an accuracy of 98% on

a binary balanced problem is not comparable to 98% on a four-class highly imbalanced problem such as Normal, VTach, VFib, and Bradycardia.

Even more importantly, validation protocol differences have a massive impact on reported performance. Many earlier ECG classification studies including some of those in the comparison table use intra-patient validation, where beats or segments from the same patient appear in both training and testing sets. This setup makes the classification problem significantly easier because ECG morphology is highly patient-specific; once a classifier learns a patient's typical waveform patterns, it can easily recognize them again. Intra-patient evaluation inflates accuracy and does not reflect real clinical deployment, where the system must detect arrhythmias in completely unseen patients. In contrast, our study uses a strict inter-patient (patient-wise) split, where no heartbeat from any test patient is seen during training or validation. This is a far more realistic and challenging setting. It prevents data leakage and ensures that the model is tested on truly novel physiological patterns. Therefore, the 99.7% accuracy reported in this study is much more meaningful and clinically trustworthy than similar or even lower accuracy values obtained under intra-patient protocols.

Furthermore, many previous works do not specify whether they performed random beat-level splitting, segment-level splitting, or patient-level splitting, making it difficult to judge the reliability of their reported results. Some works even perform k-fold cross-validation without grouping by patient, inadvertently leaking patient information across folds. In addition, some studies ignore class imbalance entirely, reporting only accuracy without macro-F1 or per-class metrics, meaning that a model biased toward the Normal class could still appear highly accurate. In contrast, our study not only uses patient-wise split and GroupKFold cross-validation, but also evaluates using macro-F1, per-class precision/recall, specificity, confusion matrices, statistical significance tests, and bootstrapped confidence intervals. This comprehensive evaluation ensures that the performance is reliable, not overfitted, and truly generalizes to new individuals. Thus, while the comparative table shows that our model outperforms prior studies numerically, the more important point is that our evaluation protocol is stricter and more clinically realistic, making the comparison conservative but still strongly in our favor.

Beyond validation differences, the superior performance of this study can also be attributed to the unique combination of autocorrelation (AC), partial autocorrelation (PACF), and HMM-based temporal features. Unlike traditional wavelet or fractal-based methods that capture morphological patterns at a single beat level, PACF provides lag-specific temporal dependencies, allowing the model to understand how a current heartbeat relates to previous ones while removing redundant correlations. This may explain why the hybrid model outperforms wavelet-based or nonlinear feature-based models in prior works. Furthermore, the class-specific HMMs explicitly model the sequential nature of each rhythm type, enabling the system to differentiate between arrhythmias with similar morphology but different temporal dynamics. Thus, our methodological design leverages both morphological insight (via AC/PACF) and temporal modeling (via HMM), providing a more holistic and discriminative representation than most existing approaches.

Despite its strong performance, it is important to acknowledge several limitations of the proposed method. First, the model is computationally more complex than traditional beat-level classifiers due to the use of multiple class-specific HMMs, feature extraction, and gradient boosting, which may increase inference time. While training complexity is acceptable in an offline setting, real-time deployment on resource-limited edge devices (e.g., wearable monitors) could be challenging without optimization or model compression. Second, the model currently focuses on four arrhythmia types from the MIT-BIH database. Although these rhythms are clinically significant and commonly studied, real-world ECG data often contain a wider variety of arrhythmias, noisy artifacts, pacing signals, and dataset-specific abnormalities. Therefore, additional evaluation on larger and more diverse databases (e.g., PTB-XL, INCART, or real-time hospital telemetry data) would be necessary to fully validate generalization and robustness. Third, the performance of the method may be sensitive to preprocessing quality, particularly wavelet-based denoising and R-peak detection. If noise obscures QRS complexes or distorts beat morphology, feature extraction could degrade, potentially affecting model accuracy. Future work should explore adaptive or learnable denoising techniques, as well as robustness testing under noisy or artifact-heavy conditions.

From a clinical perspective, the model's high specificity ($\sim$99%) is a major strength but also demands careful interpretation. In automated monitoring systems, even a 1% false-positive rate can result in a significant number of unnecessary alerts when applied across thousands of patients or millions of heartbeats per day. Such alerts may

lead to alarm fatigue, where clinicians begin to ignore alarms because many are not clinically relevant. However, the model also demonstrates very high sensitivity, particularly for VTach and VFib, which are life-threatening and require immediate intervention. In a clinical decision support context, it is often preferable to tolerate a small number of false positives in exchange for very high recall of dangerous events. Nevertheless, future work could incorporate post-processing strategies such as alarm filtering, temporal smoothing, patient-specific adaptation, or confidence thresholds to further minimize false alarms while preserving sensitivity. These techniques would enhance the practical deployability of the model in hospital or wearable device settings.

In summary, while the proposed hybrid approach achieves outstanding results and introduces significant methodological improvements over prior literature, responsible scientific reporting requires clarity about the limitations of cross-study comparisons, openness about the computational and dataset constraints, and thoughtful reflection on clinical utility. By addressing these aspects directly, the discussion not only strengthens the credibility of the study but also provides a clear roadmap for future improvements and real-world translation.

4. Conclusion

In this study, we explored and compared various signal processing and machine learning techniques for the classification of ECG signals, including Normal, Ventricular Tachycardia (VTach), Ventricular Fibrillation (VFib), and Bradycardia. The key methods used included Wavelet-based filtering, Partial Autocorrelation Function (PACF) for feature extraction, and a hybrid ensemble approach combining Hidden Markov Models (HMMs) with boosting techniques such as AdaBoost and Gradient Boosting. Our analysis demonstrated that Wavelet-based filtering using the Daubechies wavelet (‘db4‘) was highly effective in denoising the ECG signals while preserving important features, ensuring the quality of the input data for subsequent analysis. The use of PACF as a feature extraction method proved to be superior to basic Autocorrelation (AC), as PACF provided more precise insights by isolating the direct correlations between signal lags, which was particularly useful for identifying complex arrhythmias like VTach and VFib. The hybrid ensemble method leveraging HMMs and boosting algorithms showed remarkable improvements in classification performance. By modeling the sequential dependencies of the ECG signals with HMMs and optimizing the ensemble classifiers using boosting, we achieved an overall accuracy of 99.6%. This approach significantly outperformed simpler models based on AC or unfiltered signals, particularly in distinguishing between normal and arrhythmic heartbeats. In conclusion, the combination of PACF-based feature extraction and a hybrid ensemble method using HMMs with boosting provides a robust and highly accurate solution for automatic arrhythmia detection. This method offers a comprehensive framework that is both flexible and scalable, making it suitable for real-world applications in ECG signal classification and monitoring.

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