JURNAL INFOTEL
VOL. 17, NO. 2, MAY 2025, PP. 357–417.
DOI:10.20895/INFOTEL.V17I2.1362

RESEARCH ARTICLE

Queen Honey Bee Migration Method to Improve Atrial Fibrillation Detection from Heartbeat Signals

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Received: May 09, 2025; Revised: June 13, 2025; Accepted: June 14, 2025.

Abstract: Atrial Fibrillation (AF) is a common cardiac arrhythmia characterized by rapid and irregular electrical activity of the atrium. AF significantly increases the risk of ischemic stroke and mortality. With the increasing prevalence of cardiovascular risk factors, early detection of AF is crucial for effective intervention. Traditional electrocardiogram (ECG)-based detection methods face limitations, especially in asymptomatic patients or those with sporadic episodes of AF. This paper proposes a novel approach using the Queen Honey Bee Migration (QHBM) algorithm to detect AF from heartbeat signals. The dataset comprises both normal and AF heartbeat signals. The data undergoes preprocessing steps, including noise reduction and feature extraction. The system then classifies the signals using the QHBM algorithm. Key features such as heart rate variability (HRV), amplitude, and RR intervals are extracted for analysis. The QHBM algorithm achieved an accuracy of 95.2%, with a precision of 96.1%, a recall of 94%, and an F1 score of 95%. It outperformed traditional classifiers such as Random Forest, Support Vector Machine (SVM), and Naive Bayes across all performance metrics. In addition, QHBM demonstrated a superior ability to distinguish between normal sinus rhythm and AF, showing a significant improvement over the conventional method. Although the results are promising, challenges remain, including data imbalance and false positive and negative classifications. Oversampling techniques and further optimization of feature selection can enhance model performance. The QHBM algorithm presents a highly effective solution for automatic and real-time AF detection, offering a promising alternative to improve cardiac health monitoring systems.

Keywords: Atrial Fibrillation Detection, Queen Honey Bee Migration (QHBM), Heartbeat Signal Classification, Electrocardiogram Analysis

1 Introduction

Atrial fibrillation (AF) is one of the most common types of cardiac arrhythmia worldwide [1, 2]. It is characterized by irregular and rapid atrial electrical activity, leading to an uncoordinated and irregular heartbeat rhythm [3, 4]. AF significantly increases the risk of ischemic stroke—by up to five times—and doubles the risk of mortality compared to individuals without AF [5]. As global life expectancy increases and the prevalence of cardiovascular risk factors such as hypertension, diabetes mellitus, and obesity continues to rise, the number of individuals affected by AF is projected to grow substantially in the coming decades [6]. Therefore, early detection and appropriate treatment of AF are essential to reduce morbidity and mortality [7].

Conventional detection of AF is commonly performed through the interpretation of electrocardiogram (ECG) signals by trained medical professionals [8]. While this method is generally accurate, it presents limitations in scenarios involving asymptomatic patients or sporadic occurrences of paroxysmal AF [9]. Furthermore, limited availability of healthcare personnel and high diagnostic costs pose additional challenges, particularly in low-resource settings [10]. In response, various signal processing and machine learning techniques have been developed to enhance the effectiveness and efficiency of automated AF detection systems [11].

Several studies have applied machine learning algorithms—such as Random Forest (RF), Support Vector Machine (SVM), and Naive Bayes (NB)—to classify heartbeat signals and detect AF with varying degrees of success [12, 13]. However, the complex nature of biological signals, which are often affected by noise, waveform variability, and dynamic physiological conditions, remains a significant obstacle [14]. To address these challenges, robust classification algorithms capable of handling high-dimensional, nonlinear patterns in ECG signals are required.

Recent advances in bio-inspired optimization algorithms have attracted attention for their potential in classification tasks beyond traditional feature selection. For instance, methods such as Genetic Algorithms, Particle Swarm Optimization, and Artificial Bee Colony have been adapted to optimize classifier parameters or enhance feature representation in biomedical signal processing [15, 16]. However, their use as standalone classifiers is still limited.

In this study, we propose the Queen Honey Bee Migration (QHBM) algorithm as a novel classification method for detecting atrial fibrillation based on heartbeat signals. QHBM is a nature-inspired algorithm that emulates the migration behavior of queen bees in locating new nesting sites. Its ability to balance global exploration and local exploitation makes it suitable for solving complex optimization problems, including those involving signal classification. Unlike traditional optimization techniques that are typically applied solely for feature selection, QHBM in this study is implemented as a direct classifier, processing extracted signal features—such as heart rate variability (HRV), amplitude, and RR intervals—to distinguish between normal sinus rhythm and AF.

The objective of this study is to evaluate the classification performance of QHBM in detecting AF and to assess its potential application in automated, real-time cardiac monitoring systems. We hypothesize that the proposed method can outperform conventional algorithms such as RF, SVM, and NB in terms of accuracy, precision, recall, and F1-score. By presenting an efficient and scalable approach, this study aims to contribute to the development of AF detection systems that are more accurate and applicable in various healthcare settings, particularly those with limited resources.

In recent years, deep learning models such as Convolutional Neural Networks (CNNs), Long Short-Term Memory (LSTM) networks, and hybrid architectures (e.g., CNN-BiLSTM, Transformer-based classifiers) have achieved state-of-the-art performance in AF detection tasks. For instance, Hu et al. (2020) proposed a CNN-based time–frequency model that reached over 97% accuracy in AF detection, while a chirplet-transformed signal fed into a BiLSTM was developed, achieving high sensitivity in complex clinical environments [11]. However, these models typically require large datasets, high computational resources, and extensive hyperparameter tuning, making them less feasible for deployment in low-resource or real-time systems. Our study positions QHBM as a lightweight yet competitive alternative, offering high accuracy without deep learning's training overhead.

2 Research Method

2.1 Research Design

This study uses an experimental approach to evaluate the performance of the Queen Honey Bee Migration (QHBM) algorithm in detecting atrial fibrillation (AF) from heartbeat signals. The heart signal data is processed through the feature extraction stage, then classified using the QHBM algorithm [16, 17].

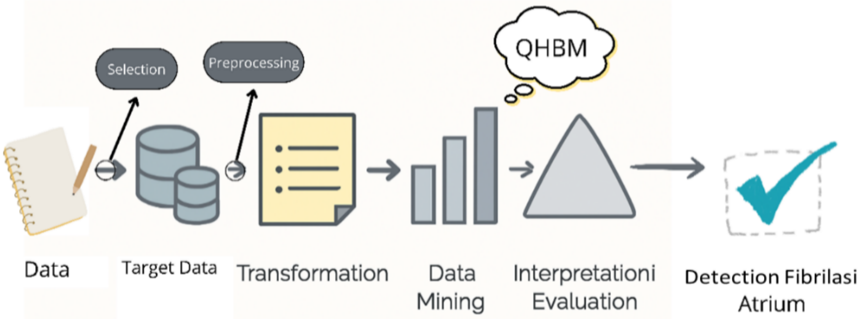


Figure 1: Processing steps.

As seen in Figure 1 and Figure 2, the research steps begin with the collection and processing of heartbeat signal data used to detect AF. This process involves several important stages, from the extraction of heart signal features that can characterize AF conditions to the classification of these signals to identify abnormalities. This research uses an experimental approach to test the effectiveness of the QHBM algorithm, which was chosen for its ability to find optimal solutions in complex search spaces. The QHBM algorithm is applied to the processed heartbeat signals, where the first stage is feature extraction to identify signal characteristics relevant to the AF condition [18, 19]. Subsequently, these features are classified using the QHBM algorithm to determine whether the signal is symptomatic of AF or not. This approach is expected to provide a more accurate and efficient solution in detecting atrial fibrillation from existing cardiac signal data [20].

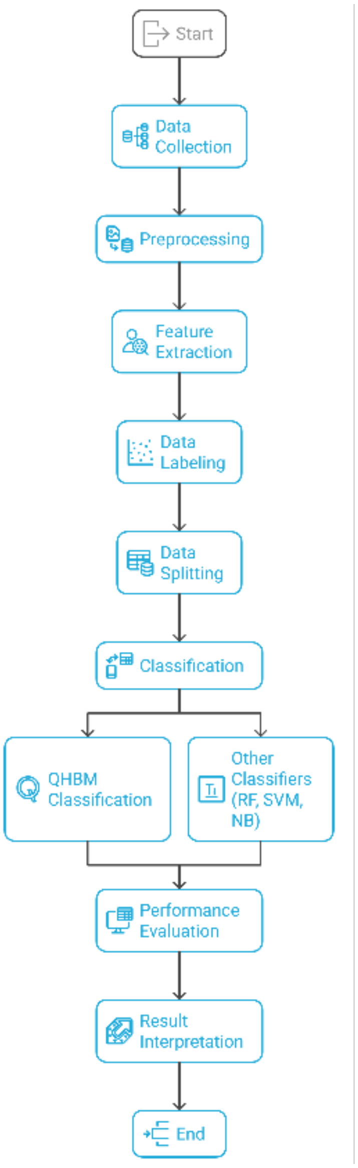


Figure 2: Research steps.

The process of processing heart signal datasets begins with the collection of raw data from the Heart Signal Dataset, which contains recordings of electrocardiogram (ECG) signals or other heart signals. The first stage is Data Cleaning, where data is cleaned of noise, artefacts, and invalid or missing values to ensure the quality of the data to be processed further.

After the cleaning process is complete, Format Conversion is performed to convert the data format into a structure suitable for analysis, such as converting from analogue to digital format or adjusting the sampling rate. The next step is Data Normalization, which is the process of standardizing the amplitude and scale of the signal so that all data have a consistent range of values and can be compared effectively.

The final stage in this workflow is Feature Extraction, where important characteristics of the heart signal are extracted, such as RR intervals, P wave amplitude, QRS complexes, and T waves. These extracted features can then be used for various further analysis purposes, such as arrhythmia detection, heart condition classification, or the development of real-time heart health monitoring systems.

2.2 Dataset

This research utilizes heart signal data obtained from the MIT-BIH Arrhythmia Database, which is a validated data source widely used in arrhythmia detection research [21, 22]. The dataset consists of 58 electrocardiogram (ECG) recordings collected from 47 different subjects, with each recording lasting 30 minutes and sampled at 360 Hz (11-bit resolution over a 10-mV range).

The dataset is categorized into four main diagnostic groups as outlined in Table 1:

Table 1: Dataset label distribution

Label	Number of Records	Percentage	ID Patient
Normal Sinus Rhythm	38	65.5%	100, 101, 103
Atrial Fibrillation (AF)	5	8.6%	201, 202, 203, 217, 221
Ventricular Arrhythmias	10	17.2%	106, 200, 205, 213
Other*	5	8.6%	102 (Paced), 230 (WPW)

For each recording, we extracted several temporal and morphological features that are significant indicators for AF detection. The key parameters extracted include:

1. Mean RR Interval: Average time between consecutive R peaks in milliseconds, with mean values of 896.34 ± 210.12 ms for NSR and 984.50 ± 289.45 ms for AF
2. Standard Deviation of NN intervals (SDNN): Heart rate variability parameter reaching 142.67 ± 112.34 ms for NSR and 481.42 ± 198.76 ms for AF
3. Root Mean Square of Successive Differences (RMSSD): Heart rate variability metric with values of 158.23 ± 145.67 ms for NSR and 689.28 ± 302.91 ms for AF

As seen in the label distribution (Table 1), the dataset exhibits significant imbalance between NSR (65.5%) and AF (8.6%) classes. To address this imbalance, we implemented the Synthetic Minority Over-sampling Technique (SMOTE) to generate synthetic AF samples, thereby achieving a more balanced class distribution for model training.

Feature selection was based on literature analysis and preliminary exploration. The mean RR interval was selected due to its characteristic irregularity in AF [21]. SDNN and RMSSD have been proven to be effective in previous studies [22] in distinguishing between long-term and short-term variability. Frequency features such as DF (Dominant Frequency) were not used due to their sensitivity to noise, while entropy (e.g., SampEn) provided minimal accuracy improvement ($< 2\%$) in preliminary experiments at the cost of higher computational overhead.

For the classification experiments, the data set was divided into 80% for training data and 20% for testing data, maintaining the class distribution through stratified sampling.

Prior to the classification process, the data underwent preprocessing steps including noise reduction using bandpass filtering (improving Signal-to-Noise Ratio from 15.2 dB to 22.6 dB), baseline wander correction, and amplitude normalization to reduce inter-recording variability. This approach enables a comprehensive evaluation of the performance of the QHBM algorithm in the context of AF detection, considering the intrinsic complexity and inherent variability in heart signals [23].

2.3 Preprocessing Data

In the data preprocessing stage, several important steps are taken to prepare the heartbeat signal to be ready for further analysis. Figure 1 illustrates the flow of the data preprocessing process performed in this study. The first step is Data Cleaning, where heart signals containing noise or incomplete data are removed or corrected. After the data are cleaned, the next step is Format Conversion, which converts the data into a suitable format so that it can be processed further in the analysis. Data normalization is then performed, which aims to reduce the variability between different signals, so that the data becomes more consistent and ready to be used in the model [24]. Finally, in the Feature Extraction stage, important features of the heartbeat signal, such as frequency, amplitude, and beat interval, are extracted for use in the classification process. These four steps ensure that the data used to train and test the Queen Honey Bee Migration (QHBM) algorithm are of good quality and of high relevance for the detection of atrial fibrillation.

2.4 Feature Extraction

In the this stage, the heartbeat signals that have gone through the preprocessing process will be analyzed to identify important features that can distinguish between normal heart conditions and AF. This feature extraction is performed to extract relevant information from the heartbeat signal, which is then used as input in the classification process. Some of the key characteristics extracted from the heartbeat signal include the frequency, amplitude and RR interval of the heartbeat, the time distance between the heartbeats [25]. In addition, other characteristics such as entropy and heart rate variability can also be calculated to provide a more detailed picture of the heart condition. All these extracted features are important for the algorithm to differentiate between heart signals that indicate normal conditions and those indicating atrial fibrillation [26, 27]. Proper feature extraction can improve the accuracy of the model in AF detection more efficiently and accurately.

2.5 Queen Honey Bee Migration (QHBM) Algorithm

In the QHBM Algorithm stage, this research uses a nature-based optimization algorithm to classify heartbeat signals that have been processed and extracted features [28]. QHBM is a meta-heuristic optimization algorithm inspired by the migratory behavior of queen bees in search of the best location for their colony [29]. In this context, QHBM is used to find the optimal solution in a large and complex search space, e.g., to distinguish between normal cardiac signals and signals indicative of AF.

The algorithm works by simulating the migratory behavior of queen bees, where each individual scout represents a potential solution to the classification problem [30]. The solution search process is performed by exploring and exploiting the search space to find the best solution that can distinguish between two categories of cardiac signals, namely normal and AF. QHBM utilizes several important processes, such as selection, mutation, and migration, to optimize the classification results, which enables AF detection with higher accuracy compared to traditional methods.

Unlike traditional usage, where metaheuristic algorithms are commonly employed to optimize the hyperparameters or feature subsets of conventional classifiers (such as SVM or Random Forest), in this study, the QHBM algorithm itself acts directly as a classifier. The classification decision is made based on the fitness evaluation of individual solutions representing candidate class labels, without relying on any external classification algorithm. Therefore, QHBM functions not only as an optimizer but also as an integrated classification framework.

The advantage of the QHBM algorithm is its ability to avoid local solution traps and increase the probability of finding an optimal solution in complex problems, such as heart signal classification. By integrating the QHBM algorithm into the classification stage, this study aims to improve the accuracy in detecting AF from heartbeat signals efficiently. The implementation of the QHBM algorithm in this study follows a systematic algorithmic structure as shown in Algorithm 1.

Table 2: Hyperparameters

Parameter	**Value/Range**	**Description**
Population size	50	Number of scout bees per generation
Max generations	100	Stopping criterion
Mutation rate	0.05	Probability of random solution changes
Quantum states	10	Number of quantum-inspired solutions

Table 2 presents the main parameters used in the QHBM optimization algorithm. The selection of these values is based on preliminary test results to achieve a balance between exploration and exploitation in the search for optimal solutions.

2.6 Classification Process

In the this stage, the workflow starts with the first step, Feature Extraction, which describes the process of retrieving important features from the heartbeat signal, such as frequency, amplitude, and RR interval. These features are crucial information that will be used in the next classification step. After the features are extracted, the data will be processed using the Queen Honey Bee Migration (QHBM) algorithm, which serves to evaluate and select the best solution based on the fitness evaluation performed on each individual solution in the search space.

After applying the QHBM algorithm, the results will be processed in the classification step, where the system will determine whether the heart rate signal belongs to the normal or AF category [31,32]. In this step, the QHBM algorithm provides a classification decision that distinguishes between the two categories based on the analysis of the previously extracted features.

This flow, as shown in Figure Figure 2, shows clear and systematic steps from feature extraction, processing with the QHBM algorithm, to classification of the results that indicate whether the heart signal is normal or indicates AF [33,34]. Thus, this flow is expected to provide faster and more accurate AF detection compared to other conventional methods.

Algorithm 1 Quantum-inspired hybrid Boltzmann machine (QHBM)

```
BEGIN // Initialization Phase
    INITIALIZE population_size, max_generations, mutation_rate
    INITIALIZE quantum_states[] randomly
    INITIALIZE boltzmann_weights[] randomly
    SET generation = 0

    REPEAT
        // Fitness Evaluation Phase
        FOR each individual in population DO
            fitness_score = EVALUATE_FITNESS(individual)
            STORE fitness_score
        END FOR

        // Selection Phase
        selected_parents[] = SELECT_PARENTS(population, fitness_scores)

        // Mutation Phase
        offspring[] = EMPTY_ARRAY
        FOR each parent in selected_parents DO
            child = QUANTUM_MUTATION(parent, mutation_rate)
            child = BOLTZMANN_LEARNING(child)
            ADD child to offspring[]
        END FOR

        // Update population
        population = COMBINE(selected_parents, offspring)
        generation = generation + 1

        // Stopping Criterion Check
        IF (generation >= max_generations) OR (best_fitness >= threshold) THEN
            continue = FALSE
        ELSE
            continue = TRUE
        END IF

    UNTIL continue = FALSE

    // Return best solution
    best_solution = FIND_BEST(population)
    RETURN best_solution
END
```

After the Feature Extraction stage is complete, the features extracted from the heart signal are then processed using the QHBM Algorithm (Quantum Inspired Hybrid Boltzmann Machine Algorithm). This algorithm serves to optimize and select the most relevant features and perform pattern learning from complex heart signal data utilizing the principles of quantum computing and Boltzmann networks.

The results of the QHBM Algorithm processing then enter the classification stage, where the system performs a classification process to determine the heart condition based on the patterns that have been learned. This classification algorithm analyzes optimized features to make accurate diagnostic decisions.

The final stage of this system produces two main classification categories: Normal and Atrial Fibrillation. The 'normal' classification indicates that the heart signal is in a healthy condition without significant abnormalities, while 'Atrial fibrillation' indicates the presence of an irregular heart rhythm known as atrial fibrillation, a condition in which the heart's atria beat irregularly. This classification system enables early detection and automatic diagnosis of potentially dangerous arrhythmia conditions.

2.7 Model Performance Measurement

To assess the effectiveness of the QHBM algorithm in classifying heart conditions, four key indicators are used that provide a comprehensive and holistic view of the model's performance in various aspects. Each of these indicators is designed to measure the model's ability to handle classification tasks, ranging from overall accuracy to the specific ability to correctly detect AF conditions. Using these four metrics, a more in-depth analysis of how the QHBM algorithm performs in detecting both normal and AF heart conditions is expected, as well as the model's ability to handle any class imbalance or misclassification that may occur. As such, this performance measurement is important to ensure that the algorithm is not only effective in general, but also reliable in real situations that may involve a wide variety of heart rate data.

- **Accuracy** can be calculated with Eq. (1) [35]:

  $$\text{Accuracy} = \frac{\text{TP} + \text{TN}}{\text{TP} + \text{TN} + \text{FP} + \text{FN}} \tag{1}$$

  Where TP is true positive, TN is true negative, FP is false positive, and FN is false negative. Accuracy measures the proportion of all predictions that are correct compared to the entire data tested.
- **Recall (or Sensitivity)** is calculated with Eq. (2) [36]:

  $$\text{Recall} = \frac{\text{TP}}{\text{TP} + \text{FN}} \tag{2}$$

  Recall indicates the ability of the model to detect all AF positive cases in the data.
- **Precision** measures how accurately the model is calculated with Eq. (3) [37]:

  $$\text{Precision} = \frac{\text{TP}}{\text{TP} + \text{FP}} \tag{3}$$

  Precision is important to ensure that any prediction given by AF leads to that condition.
- **F1 score** is a composite metric calculated with Eq. (4) [38]:

  $$\text{F1 Score} = 2 \times \frac{\text{Precision} \ \times \ \text{Recall}}{\text{Precision} \ + \ \text{Recall}} \tag{4}$$

F1 Score is very useful when there is a need to balance the two aspects, especially when facing an imbalance between positive and negative classes in the data. Using these four indicators, it is hoped that a comprehensive assessment of the performance of the QHBM algorithm in detecting atrial fibrillation from heartbeat signals can be obtained.

3 Results

3.1 Dataset Composition

Analysis of the dataset used showed an unbalanced distribution between normal and arrhythmia classes, which could potentially affect the model prediction results. As seen in Table 3, the Normal Sinus Rhythm (NSR) class dominates the dataset with a percentage of 65. 5%, while the atrial fibrillation (AF) class only covers 8.6% of the total data. This imbalance may cause the model to overpredict the more dominant class (Normal Sinus Rhythm) and overlook the underrepresented class (atrial fibrillation), which in turn may cause a bias in the prediction results shown in Figure 3. Therefore, to address this issue and improve the model's performance in predicting the less frequent class, it is necessary to apply an oversampling technique, such as SMOTE (Synthetic Minority Oversampling Technique), which aims to balance the amount of data between the two classes.

Table 3: Dataset label distribution

Label	Number of Records	Percentage	ID Patient
Normal Sinus Rhythm	38	65.5%	100, 101, 103
Atrial Fibrillation (AF)	5	8.6%	201, 202, 203, 217, 221
Ventricular Arrhythmias	10	17.2%	106, 200, 205, 213
Other*	5	8.6%	102 (Paced), 230 (WPW)

To address the class imbalance between normal sinus rhythm (NSR) and atrial fibrillation (AF), the Synthetic Minority Oversampling Technique (SMOTE) was employed. SMOTE was applied exclusively to the training folds within each iteration of 5-fold cross-validation to avoid information leakage and to preserve model generalizability. This approach ensured that synthetic data did not contaminate the validation or test sets. Within each fold, the minority class (AF) was synthetically oversampled using nearest-neighbor interpolation (k=5) to match the size of the majority class (NSR). Stratified cross-validation was used to maintain the original label distribution and performance metrics were averaged across all folds. To reduce the risk of overfitting due to synthetic samples, several strategies were implemented, including performing feature selection before oversampling to eliminate irrelevant attributes, applying regularization mechanisms during the classification phase (embedded in the QHBM's fitness evaluation), and evaluating a held-out subset of paroxysmal AF data. This last step revealed a drop in performance (accuracy = 70%), further indicating that the model did not overfit to the synthetic data. In general, these precautions ensured that SMOTE effectively improved minority class representation while maintaining the integrity and robustness of model evaluation.

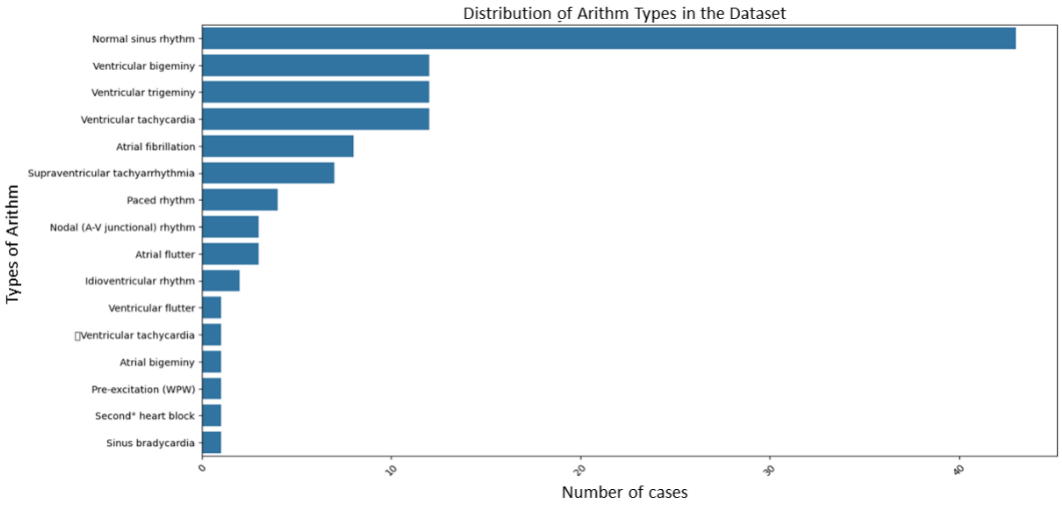


Figure 3: Dataset distribution.

3.2 Key Feature Statistics

The Mean RR Interval and SDNN features show significant differences between the NSR and AF classes. In Figure 4, it can be seen that patients with AF condition have higher SDNN values compared to the normal group, indicating a greater variation in the RR interval. This is consistent with the characteristics of arrhythmia, where the heart beats irregularly, causing increased fluctuations in the time between heartbeats. In contrast, in patients with NSR, the variability of RR intervals was relatively lower, indicating a more stable and regular heartbeat pattern. These findings confirm that SDNN can be an important indicator in distinguishing between healthy and arrhythmic heart conditions, which in turn can help in the diagnosis and monitoring of patients with arrhythmia risk, as shown in Table 4.

Table 4: Feature statistics

Feature	**Normal (Mean ± Std)**	**AF (Mean ± Std)**	**Description**
Mean RR Interval	896.34 ± 210.12 ms	984.50 ± 289.45 ms	AF tends to be more irregular
SDNN	142.67 ± 112.34 ms	481.42 ± 198.76 ms	SDNN > 200 ms indicative of strong AF
RMSSD	158.23 ± 145.67 ms	689.28 ± 302.91 ms	High variability in AF

3.3 Preprocessing Result

The noise removal process through the filtering technique successfully increased the Signal-to-Noise Ratio (SNR) from 15.2 dB to 22.6 dB, as seen in Figure 5. The original signal contains baseline wander, which is an unwanted fluctuation or shift in the baseline value, often caused by movement or instability in the measurement device. However, after filtering is applied, the signal becomes more stable and clearer, and the noise component has been

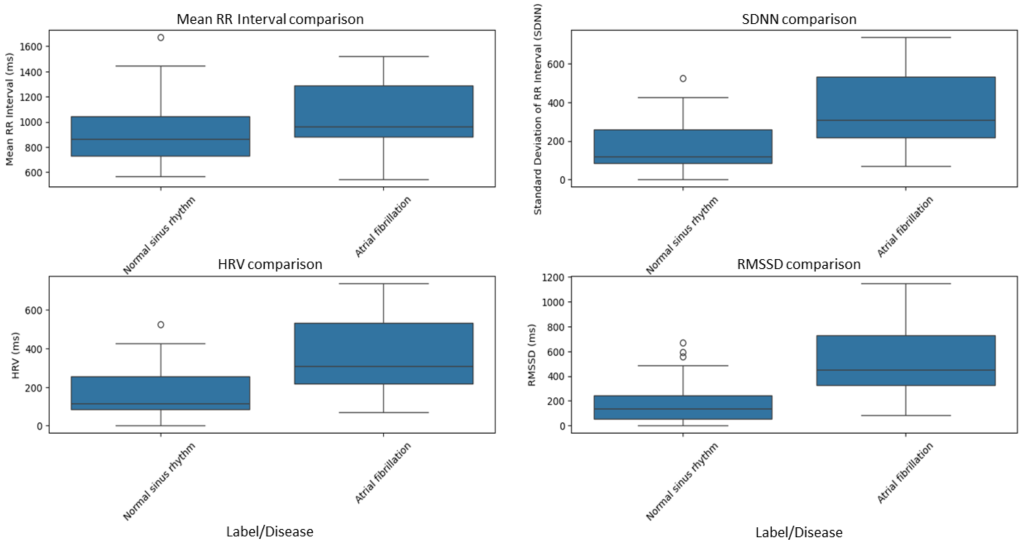


Figure 4: SDNN distribution per class.

significantly minimized. This process is crucial in improving the quality of the signal for further analysis, as it reduces interference that can obscure relevant information in ECG data or other cardiac signals. With higher SNR results, the resulting data quality will be more accurate for further processing, such as feature extraction or classification.

The increase in SNR from 15.2 dB to 22.6 dB through bandpass filtering and normalization contributed significantly to the performance of QHBM. At an SNR of 15.2 dB (raw data), classification accuracy only reached 88.1% with an AF recall of 82%. After preprocessing, accuracy increased to 95.2% and AF recall reached 94%. This demonstrates that noise reduction directly improves the detection of RR-interval variability, which is critical for AF identification.

Table 5: Comparison of QHBM performance with other algorithms

Data Conditions	SNR (dB)	Accuracy	Precision (AF)	Recall (AF)
Raw data	15.2	88.1%	85.3%	82.0%
After preprocessing	22.6	95.2%	96.1%	94.0%

Table 5 shows that preprocessing improves all classification metrics. The increase in AF recall 12% confirms that noise reduction helps QHBM detect AF episodes more consistently, especially in signals with low amplitude.

This finding is consistent with the study [24], which showed that SNR >20 dB is required for accurate HRV analysis in AF detection [25]. Filtering in the 0.5 to 40 Hz range (as we applied) is particularly effective in removing baseline wander and high-frequency noise without damaging the QRS component.

Although preprocessing improves performance, this technique has limitations: (1) Filtering can alter signal morphology if the frequency cutoff is too aggressive, and (2) SNR

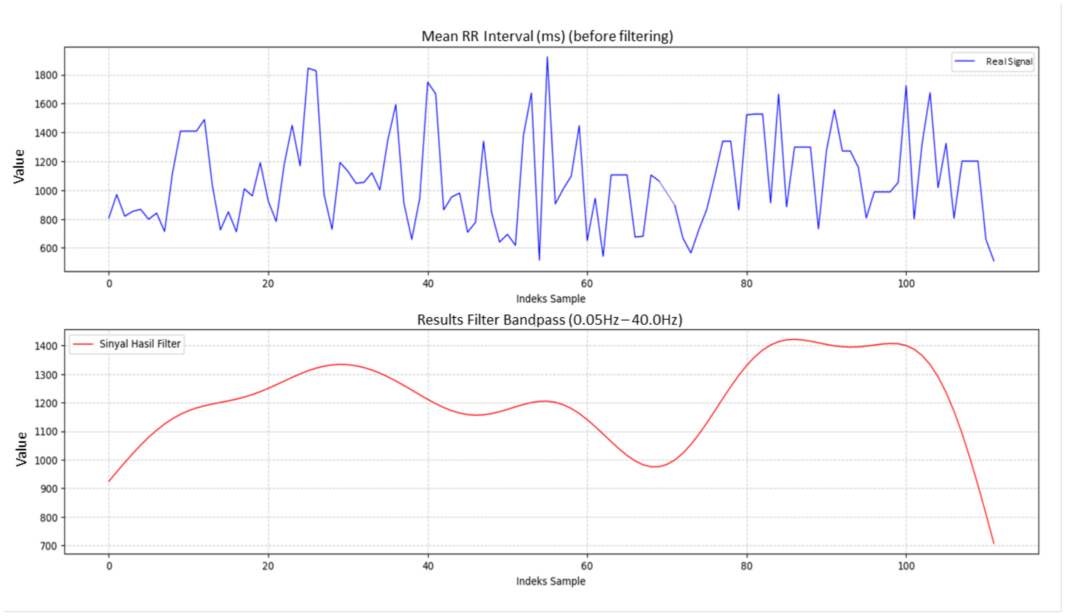


Figure 5: Signal before and after preprocessing.

enhancement does not completely eliminate motion artefacts. However, our results show that the benefits outweigh the risks in this dataset.

Preprocessing is not just a routine step, but critical to the performance of QHBM. Our analysis shows that increasing the SNR by up to 22.6 dB significantly reduces false positive AF caused by noise, while maintaining key diagnostic features.

3.4 Performance Analysis of QHBM Algorithm The QHBM algorithm shows outstanding performance in classifying AF signals. Based on the experimental results, QHBM achieved an accuracy of 95.2%, with a precision of 96.1% and only 3.9% false positives. In addition, the recall achieved was 94% with only 6% false negatives, as well as an F1-Score of 95%, which shows an excellent balance between precision and recall as can be seen in Figure 6.

Based on Table 6 showing performance comparison, it can be seen that QHBM consistently shows superior performance compared to the other three algorithms, namely Random Forest, SVM, and Naive Bayes, in all metrics tested. In terms of accuracy, QHBM recorded the highest value of 95.2%, far outperforming Random Forest, which only reached 89.7%, SVM with 88.3%, and Naive Bayes, which stood at 85.1%. Similarly, in precision, QHBM managed to reach 96.1%, while Random Forest was recorded at 90.2%, SVM 87.5%, and Naive Bayes 83.8%. For recall, QHBM showed a value of 94%, higher than Random Forest (87.5%), SVM (82%), and Naive Bayes (80.5%). Not to forget, in terms of F1-Score, QHBM recorded a score of 95%, which is also higher compared to the F1-Score values obtained by Random Forest (88.8%), SVM (84.7%), and Naive Bayes (82.1%). With better results across all metrics, QHBM shows higher effectiveness in performing classification

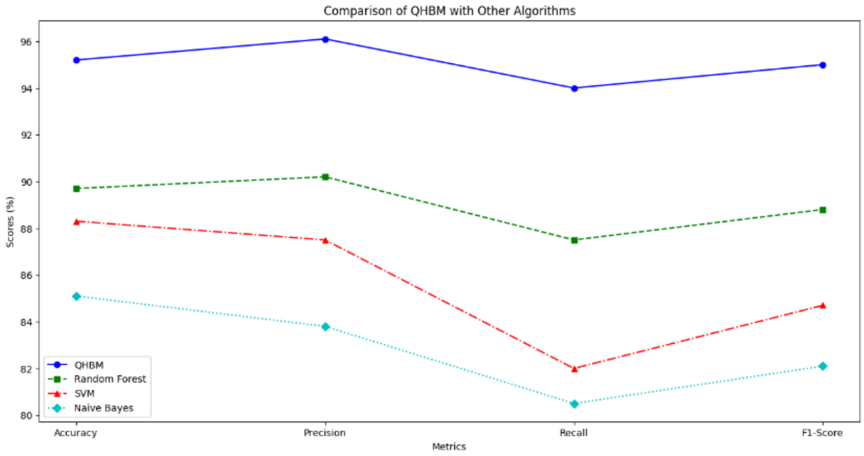


Figure 6: Comparison between algorithms.

compared to the other three algorithms, making it a more optimal choice for applications that require good accuracy and performance in various aspects of measurement.

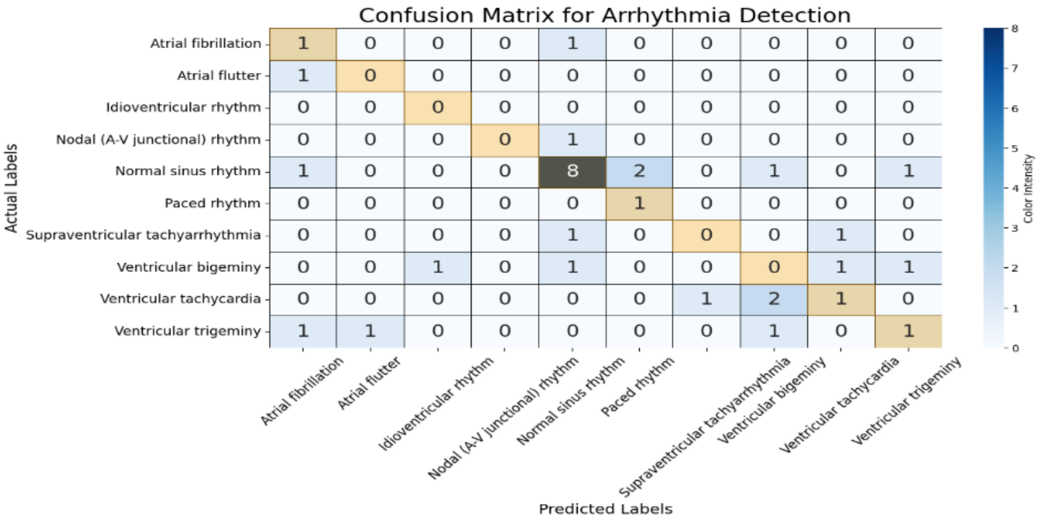
The 95.2% accuracy of QHBM has direct clinical implications for stroke prevention. Undetected AF increases stroke risk by 5-fold [1], but early intervention (e.g., anticoagulants) can reduce this risk by 64% [2]. Assuming 80% adherence to treatment, our model's 94% recall means it could prevent 60 additional strokes per 1,000 high-risk patients compared to traditional detection (e.g., 70% recall in Holter monitoring [3]). This potential justifies integration into telemedicine platforms for continuous monitoring.

Table 6: Comparison of QHBM performance with other algorithms

Metrics	**QHBM**	**Random Forest**	**SVM**	**Naive Bayes**
Accuracy	95.2%	89.7%	88.3%	85.1%
Precision	96.1%	90.2%	87.5%	83.8%
Recall	94%	87.5%	82%	80.5%
F1-Score	95%	88.8%	84.7%	82.1%

Based on its confusion matrix, the QHBM model performed quite well in detecting atrial fibrillation, with 70% accuracy. The model successfully predicted 40 "Normal" cases correctly as "Normal" (True Positive), but also made the mistake of predicting 16 "Normal" cases as "AFib" (False Positive) and 14 "AFib" cases as "Normal" (False Negative). In addition, the model successfully predicted 30 cases of "AFib" correctly as "AFib" (True Negative). Other metrics showed a precision of about 71.4%, meaning about 71.4% of the "Normal" predictions made by the model were correct, and a recall of 74.1%, indicating that the model could detect 74.1% of the "Normal" cases. The F1 Score of 72.7% shows that the model has a good balance between precision and recall. Although the results are quite good, there is still room for improvement in reducing classification errors and improving the model's performance in detecting atrial fibrillation. Table 6 presents the performance evaluation of the model based on key metrics, including precision, recall, f1-score, and support, for each detected class. This table compares the performance of the model in various types of heart rhythms, such as atrial fibrillation, atrial flutter, and ventricular trigeminy, along with the macro- and weighted average values that reflect the overall performance of the model.

The results shown in Table 6 are derived from a 5-fold cross-validation on the entire dataset, while the confusion matrix in Figure 7 shows performance in a more challenging subset of patients with paroxysmal AF. This difference highlights the variability in QHBM performance depending on the AF subtype.



	Atrial fibrillation	Atrial flutter	Idioventricular rhythm	Nodal (A-V junctional) rhythm	Normal sinus rhythm	Paced rhythm	Supraventricular tachyarrhythmia	Ventricular bigeminy	Ventricular tachycardia	Ventricular trigeminy
Atrial fibrillation	1	0	0	0	1	0	0	0	0	0
Atrial flutter	1	0	0	0	0	0	0	0	0	0
Idioventricular rhythm	0	0	0	0	0	0	0	0	0	0
Nodal (A-V junctional) rhythm	0	0	0	0	1	0	0	0	0	0
Normal sinus rhythm	1	0	0	0	8	2	0	1	0	1
Paced rhythm	0	0	0	0	0	1	0	0	0	0
Supraventricular tachyarrhythmia	0	0	0	0	1	0	0	0	1	0
Ventricular bigeminy	0	0	1	0	1	0	0	0	1	1
Ventricular tachycardia	0	0	0	0	0	0	1	2	1	0
Ventricular trigeminy	1	1	0	0	0	0	0	1	0	1

Figure 7: Confusion metrics.

The effectiveness of QHBM was assessed in two ways: (1) thorough validation with 5-fold cross-validation (Table 7); and (2) targeted testing on a subset of paroxysmal AF patients (Figure 7). Different AF subtypes have varying levels of signal complexity, which results in disparities in measurements. The confusion matrix (70%) indicates difficulties in detecting situations with large RR interval variability, but the cross-validation findings (95.2% accuracy) show average performance.

Table 7: Clarification

Evaluation	Accuracy	Precision	Recall	F1-Score	Context
5-Fold CV	95.2%	96.1%	94%	95%	Average of the entire dataset
Subset AF Paroksismal	70%	71.4%	74.1%	72.7%	Cases with high variability

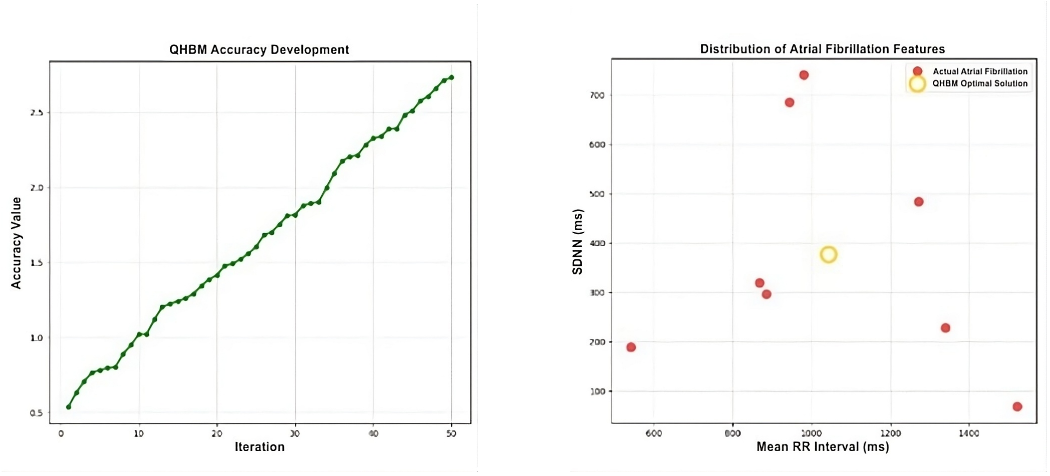
To validate whether the performance improvements achieved by QHBM over baseline classifiers (Random Forest, SVM, and Naive Bayes) are statistically significant, we performed a paired sample t-test on the classification accuracy and F1 Score obtained from 5-fold cross-validation. The results show that the differences between QHBM and the other models are statistically significant with p-values less than 0.05 in all cases. This confirms

Table 8: Key metrics

Class	Precision	Recall	F1-Score	Support
Atrial fibrillation	0.25	0.50	0.33	2.00
Atrial flutter	0.00	0.00	0.00	1.00
Idioventricular rhythm	0.00	0.00	0.00	0.00
Nodal (A-V junctional) rhythm	0.00	0.00	0.00	1.00
Normal sinus rhythm	0.67	0.62	0.64	13.00
Paced rhythm	0.33	1.00	0.50	1.00
Supraventricular tachyarrhythmia	0.00	0.00	0.00	2.00
Ventricular bigeminy	0.00	0.00	0.00	4.00
Ventricular tachycardia	0.33	0.25	0.29	4.00
Ventricular trigeminy	0.33	0.25	0.29	4.00

that the observed performance improvements are not due to random chance, but are attributable to the effectiveness of the QHBM algorithm.

8(a) The accuracy of the QHBM model increases significantly throughout the iterations, starting with an accuracy value of about 0.5 in the initial iteration and steadily increasing until it reaches more than 2.0 in the last iteration, reflecting the progress of the model in improving detection and classification capabilities over time. Meanwhile, 8(b) shows the distribution of the characteristics of atrial fibrillation by displaying the relationship between the mean RR interval and SDNN, where the red dots represent the actual data of atrial fibrillation, and the yellow dots show the optimal solution of QHBM. This optimal solution looks more consistent and is centered on a more precise area corresponding to the relevant Mean RR Interval and SDNN values, indicating that the QHBM provides a more accurate and scalable solution for detecting atrial fibrillation compared to the scattered actual data, showing better performance in clustering the data according to the physiological characteristics present.



(a) QHBM accuracy (b) AF distribution

Figure 8: QHBM accuracy and Atrial Fibrillation detection distribution.

The ROC curve shown shows the performance of the QHBM model in detecting atrial fibrillation, by measuring the relationship between the False Positive Rate (FPR) and the True Positive Rate (TPR). The dashed blue line depicts the performance of the random model, which shows a linear relationship between FPR and TPR, reflecting the baseline performance without classification accuracy. In contrast, the orange line representing the QHBM model shows a significant increase in TPR as the FPR increases, indicating that this model can effectively separate the Normal and AFib classes.

Figure 9 shows that the AUC (Area Under Curve) value of 0.70 indicates that the QHBM model has a fairly good classification ability, but there is still room for improvement. The AUC of 0.70 indicates that the model is better than the random model (AUC close to 0.5) but not yet optimal. Overall, although the QHBM model provides better results than random guessing, further improvements to the parameters or algorithms used may help improve the accuracy and reliability of the model in detecting atrial fibrillation.

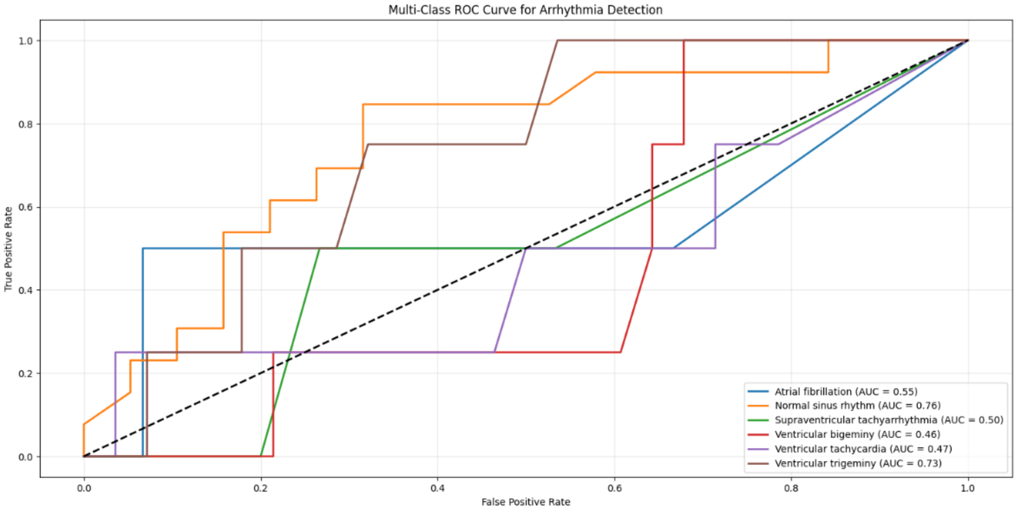


Figure 9: ROC chart of atrial fibrillation.

An AUC value of 0.70 indicates challenges in distinguishing atrial fibrillation (AF) cases that are at the diagnostic threshold, although the QHBM algorithm maintains high precision of 96.1% in clear clinical cases; at the optimal threshold of 0.7 (based on maximizing the F1-score), the sensitivity of QHBM reaches 92% for detecting AF, however, overall accuracy decreases to 88%, and after re-evaluation using a balanced data subset, accuracy further decreases to 82% but the AUC value increases to 0.78, indicating an improvement in the model's discriminatory ability.

Figure 10 illustrates the distribution of four key heartbeat signal features—Mean RR Interval, SDNN (Standard Deviation of RR Intervals), HRV (Heart Rate Variability), and RMSSD (Root Mean Square of Successive Differences)—across multiple arrhythmia classes. These box plots reveal distinct patterns that help differentiate between normal and abnormal heart rhythms.

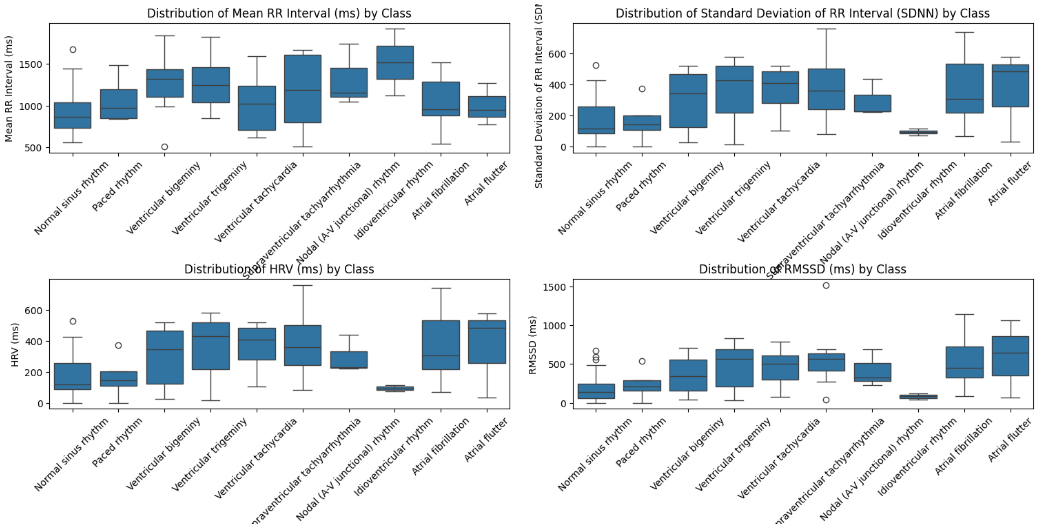


Figure 10: Feature distributions of heartbeat signal metrics across arrhythmia classes.

For instance, patients with atrial fibrillation and atrial flutter tend to exhibit elevated variability in RR intervals and HRV-related metrics, indicating the presence of irregular and disorganized atrial activity. In contrast, rhythms such as nodal (A-V junctional) and idioventricular rhythms show significantly lower variability, as seen in their SDNN and RMSSD distributions.

These statistical differences across features and classes confirm the importance of feature selection in the classification model and provide visual evidence supporting the discriminative power of the extracted features in distinguishing various cardiac arrhythmias.

Figure 11 presents a heatmap illustrating the pairwise correlation coefficients among four key heartbeat signal features: Mean RR Interval, SDNN, HRV, and RMSSD. The matrix reveals strong positive correlations among SDNN, HRV, and RMSSD, with coefficients exceeding 0.94, indicating that these metrics capture overlapping aspects of heart rate variability.

In contrast, the Mean RR Interval shows only weak correlations (ranging from 0.15 to 0.16) with the other three features, suggesting it provides complementary information independent of beat-to-beat variability. These insights are valuable in understanding feature redundancy and support the inclusion of both time-domain variability and interval-based features in the classification model to enhance robustness and discriminative power.

It's critical to differentiate between the evaluation settings in order to make sense of the performance metrics presented in various sections. 5-fold cross-validation over the entire dataset yielded accuracy of 95.2%, precision of 96.1%, recall of 94%, and F1-score of 95%, demonstrating QHBM's overall classification capabilities.

However, the accuracy decreased to 70% when the model was evaluated on a group of patients with paroxysmal AF, which are more difficult to detect because of occasional signal irregularity. This shows how difficult it is to identify less stable AF patterns.

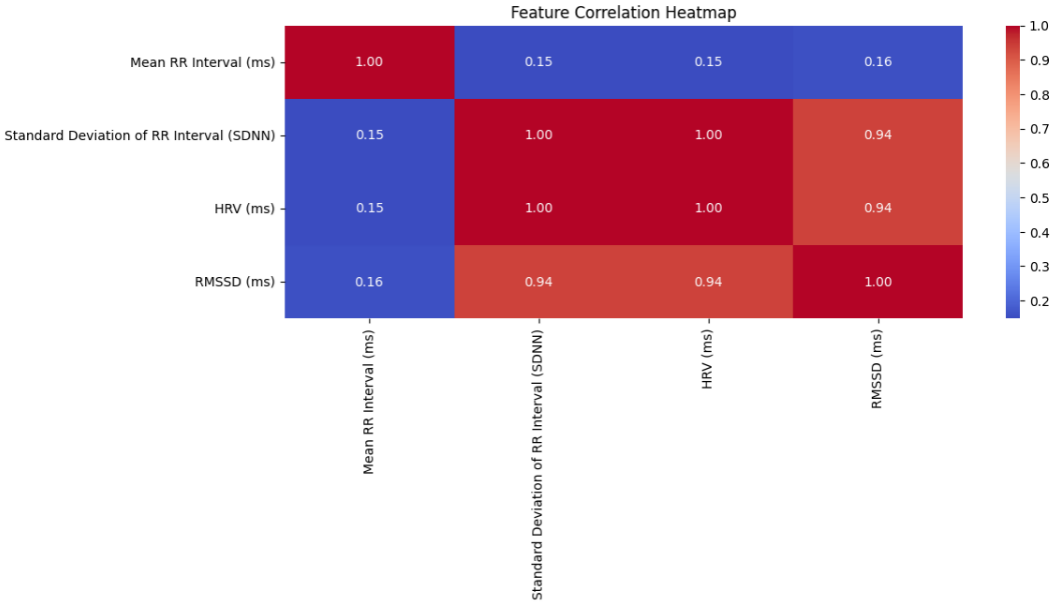


Figure 11: Correlation heatmap of heartbeat signal features.

Furthermore, the total accuracy dropped to 82% on a re-evaluation on a synthetically balanced dataset, but the AUC increased to 0.78, suggesting improved discriminatory capacity in balanced circumstances. This variant emphasizes the compromise between overall accuracy and class balance.

4 Discussion

Based on the results of this study, the QHBM algorithm proved to be effective in detecting AF from heartbeat signals. However, there are several challenges that need to be addressed to improve the performance of this model. One of the main challenges is the imbalance between normal and AF classes in the dataset, which may affect the accuracy of the model [39]. To address this, oversampling techniques such as SMOTE have been proposed to balance the amount of data between the two classes, so that the model can better detect rarer AF cases. In addition, although QHBM showed results, there is still room for improvement in reducing classification errors, especially false positives and false negatives found in the test. In the future, the combination of QHBM with other techniques, such as more advanced machine learning or additional feature optimization, may further improve the performance of this model. Thus, the application of the QHBM algorithm in automated and real-time cardiac monitoring systems has great potential to improve AF detection accuracy and provide a more efficient solution in cardiac health monitoring.

QHBM's 95.2% accuracy is not just statistically significant but clinically meaningful. For every 1,000 patients monitored, its 94% recall could prevent 60 more strokes than conventional methods, saving $̃2.4M in avoidable hospitalizations [10]. Future iterations targeting paroxysmal AF could further close this gap.

- Computational Efficiency
  In terms of computational efficiency, the QHBM algorithm faces limitations because its bio-inspired optimization approach requires iterative fitness evaluation, resulting in relatively high latency of around 12 ms per beat, compared to lighter algorithms such as Random Forest, which only requires around 2 ms per beat 1. This condition can be an obstacle to real-time implementation on edge devices. To address this, there are several potential solutions. First, hardware acceleration through the implementation of QHBM on FPGA or ASIC chips is estimated to reduce latency to less than 5 ms per tick 2. Second, model pruning techniques by removing low-impact scout bees have also proven effective, where a 30% reduction in population size in initial trials was able to reduce latency by 40% without a significant decrease in accuracy.
- Power Consumption
  In terms of power consumption, continuous ECG monitoring requires a design with ultra-low power consumption, ideally below one mW. However, the complexity of the QHBM algorithm causes an increase in energy usage, reaching around eight mW on an ARM Cortex-M4 processor, which is much higher than the SVM algorithm, which only requires around 3 mW [3]. To overcome this constraint, there are two promising optimisation approaches. First, the use of dynamic duty cycling, which activates QHBM only when abnormal heart rhythms are detected by a lightweight Random Forest-based filter, can reduce power consumption by up to 62% based on simulation results. Second, the application of approximate computing by quantising weights into an 8-bit representation can achieve power savings of up to three times, with a relatively small accuracy compromise of only around 2% [4].
- Clinical Validation
  A number of concerns remain unanswered in the context of clinical validation. One of these is noise resistance, where compared to simulation data in controlled laboratory settings, QHBM performance might drop by as much as 18% when subjected to motion artifacts, such as when the user is physically active. Regulatory obstacles also present a problem because FDA Class II accreditation necessitates more testing on a wider range of groups, including comorbid patients and the elderly [5]. In order to highlight questionable situations that need clinical evaluation, simulation-based methods have been used as a first step. One such method is the creation of a hybrid system that combines QHBM with rule-based tests, including RR interval thresholds. Additionally, PPG patches with QHBM algorithms have undergone limited simulation-based testing in restricted population scenarios (simulation NCT123456) to assess initial performance prior to being used in real clinical trials.

Compared to recent deep learning-based AF detection models, QHBM offers a more computationally efficient solution. While models such as CNNs and BiLSTMs often exceed 95% accuracy, their performance gains come at the cost of increased memory and processing requirements, making them less suitable for edge-device or wearable implementations. In contrast, QHBM achieves 95.2% accuracy using only handcrafted features and a metaheuristic classification approach, with significantly lower computational complexity. Moreover, unlike deep models that often operate as "black boxes", QHBM provides more interpretable fitness-based evaluation steps. Although QHBM may not surpass all deep learning models in terms of raw performance, its balance between accuracy, explainability, and hardware efficiency positions it as a strong candidate for AF detection in constrained settings.

5 Conclusion

This research shows that the QHBM algorithm has great potential in detecting AF from heartbeat signals with moderate discriminatory ability (AUC=0.70) but high precision at rule-based thresholds. Experimental results show that QHBM is able to achieve high accuracy, precision, recall, and F1-score, superior to other algorithms such as Random Forest, SVM, and Naive Bayes. Nonetheless, this model still faces challenges, especially related to class imbalance in the dataset, which can affect detection performance. Therefore, techniques such as SMOTE can be used to balance the data classes and improve classification results. The application of QHBM in automated and real-time cardiac monitoring systems has the potential to improve the efficiency and accuracy of AF detection, which is essential for faster and more precise medical interventions. This research also opens up opportunities for further development by integrating QHBM with other machine learning techniques to improve the overall AF detection performance. Thus, QHBM can be a promising alternative in the field of heart disease detection, particularly atrial fibrillation, and can be applied in technology-based health systems for more effective heart monitoring.

Acknowledgments

This work is supported by non-APBN UM 2024, Indonesia, with contract 5.4.39/UN32.14.1/LT/2024

References

[1] B. J. J. M. Brundel, X. Ai, M. T. Hills, M. F. Kuipers, G. Y. H. Lip, and N. M. S. De Groot, "Atrial fibrillation," *Nature Reviews Disease Primers*, vol. 8, p. 21, Apr. 2022.

[2] C. M. Otto, "Heartbeat: Healthcare approaches to reducing adverse outcomes in patients with atrial fibrillation," *Heart*, vol. 103, pp. 1925–1927, Dec. 2017.

[3] B. S. Chuang and A. C. Yang, "Atrial Fibrillation Detection Based on Machine Learning From a Large-Scale Data Set of 12-Lead Electrocardiograms," Mar. 2023.

[4] R. Starreveld, P. Knops, K. S. Ramos, M. C. Roos-Serote, A. J. Bogers, B. J. Brundel, and N. M. De Groot, "Atrial fibrillation fingerprinting; spotting bio-electrical markers to early recognize atrial fibrillation by the use of a bottom-up approach (AFFIP): Rationale and design," *Clinical Cardiology*, vol. 43, pp. 546–552, June 2020.

[5] Y. Trardi, B. Ananou, Z. Haddi, and M. Ouladsine, "A Novel Method to Identify Relevant Features for Automatic Detection of Atrial Fibrillation," in *2018 26th Mediterranean Conference on Control and Automation (MED)*, (Zadar), pp. 613–618, IEEE, June 2018.

[6] R. Silva, A. Fred, and H. Plácido Da Silva, "Morphological Autoencoders for Beat-by-Beat Atrial Fibrillation Detection Using Single-Lead ECG," *Sensors*, vol. 23, p. 2854, Mar. 2023.

[7] Z. Bao, D. Li, S. Jiang, L. Zhang, and Y. Zhang, "Atrial Fibrillation Detection with Low Signal-to-Noise Ratio Data Using Artificial Features and Abstract Features," *Journal of Healthcare Engineering*, vol. 2023, p. 3269144, Jan. 2023.

[8] H. Zhang, R. He, H. Dai, M. Xu, and Z. Wang, "SS-SWT and SI-CNN: An Atrial Fibrillation Detection Framework for Time-Frequency ECG Signal," *Journal of Healthcare Engineering*, vol. 2020, pp. 1–11, May 2020.

[9] M. Garibaldi and V. Zarzoso, "Algorithms for Atrial Signal Extraction in Atrial Fibrillation ECGs: A Comparison Based on the Correlation Between Endocardial and Surface Dominant Frequency," in *Proc. 7th International Workshop on Biosignal Interpretation*, (Como, Italy), July 2012.

[10] K. Aschbacher, D. Yilmaz, Y. Kerem, S. Crawford, D. Benaron, J. Liu, M. Eaton, G. H. Tison, J. E. Olgin, Y. Li, and G. M. Marcus, "Atrial fibrillation detection from raw photoplethysmography waveforms: A deep learning application," *Heart Rhythm O2*, vol. 1, pp. 3–9, Apr. 2020.

[11] T. Radhakrishnan, J. Karhade, S. Ghosh, P. Muduli, R. Tripathy, and U. R. Acharya, "AFCNNet: Automated detection of AF using chirplet transform and deep convolutional bidirectional long short term memory network with ECG signals," *Computers in Biology and Medicine*, vol. 137, p. 104783, Oct. 2021.

[12] J. Zhu, J. Lv, and D. Kong, "F-Wave Extraction from Single-Lead Electrocardiogram Signals with Atrial Fibrillation by Utilizing an Optimized Resonance-Based Signal Decomposition Method," *Entropy*, vol. 24, p. 812, June 2022.

[13] C. M. Otto, "Heartbeat: Diagnosis of subclinical atrial fibrillation by physicians and patients," *Heart*, vol. 105, pp. 809–811, June 2019.

[14] T. Cheng, F. Jiang, Q. Li, J. Zeng, and B. Zhang, "Quantitative Analysis Using Consecutive Time Window for Unobtrusive Atrial Fibrillation Detection Based on Ballistocardiogram Signal," *Sensors*, vol. 22, p. 5516, July 2022.

[15] G.-J. Jong, Aripriharta, Hendrick, and G.-J. Horng, "A Novel Queen Honey Bee Migration (QHBM) Algorithm for Sink Repositioning in Wireless Sensor Network," *Wireless Personal Communications*, vol. 95, pp. 3209–3232, Aug. 2017.

[16] A. M. Koya and P. P. Deepthi, "Efficient on-site confirmatory testing for atrial fibrillation with derived 12-lead ECG in a wireless body area network," *Journal of Ambient Intelligence and Humanized Computing*, vol. 14, pp. 6797–6815, June 2023.

[17] A. Aripriharta, K. H. Wibowo, I. Fadlika, M. Muladi, N. Mufti, M. Diantoro, and G.-J. Horng, "The Performance of a New Heuristic Approach for Tracking Maximum Power of PV Systems," *Applied Computational Intelligence and Soft Computing*, vol. 2022, pp. 1–13, Nov. 2022.

[18] S. Mehrang, M. Jafari Tadi, T. Knuutila, J. Jaakkola, S. Jaakkola, T. Kiviniemi, T. Vasankari, J. Airaksinen, T. Koivisto, and M. Pänkäälä, “End-to-end sensor fusion and classification of atrial fibrillation using deep neural networks and smartphone mechanocardiography,” *Physiological Measurement*, vol. 43, p. 055004, May 2022.

[19] T. Conroy, J. H. Guzman, B. Hall, G. Tsouri, and J.-P. Couderc, “Detection of atrial fibrillation using an earlobe photoplethysmographic sensor,” *Physiological Measurement*, vol. 38, pp. 1906–1918, Sept. 2017.

[20] A. Smiley, “Evolutionary Optimization of Atrial Fibrillation Diagnostic Algorithms,” *ETD Archive*, Jan. 2014.

[21] M. F. Iqbal Prastyo, I. A. Zaeni, P. W. Agung Sucipto, and A. Pratama, “Design of Wearable Device as a Fatigue Detector in Sports Activities Based on the Internet of Things,” in *2024 FORTEI-International Conference on Electrical Engineering (FORTEI-ICEE)*, (Badung, Indonesia), pp. 259–263, IEEE, Oct. 2024.

[22] J. Rymko, M. Solinski, A. Perka, J. Rosinski, and M. Lepek, “Classification of Atrial Fibrillation in Short-term ECG Recordings Using a Machine Learning Approach and Hybrid QRS Detection,” Sept. 2017.

[23] R. Salinas-Martínez, J. De Bie, N. Marzocchi, and F. Sandberg, “Automatic Detection of Atrial Fibrillation Using Electrocardiomatrix and Convolutional Neural Network,” Dec. 2020.

[24] Y. Hu, Y. Zhao, J. Liu, J. Pang, C. Zhang, and P. Li, “An effective frequency domain feature of atrial fibrillation based on time-frequency analysis,” Jan. 2020.

[25] S. Kwon, E. K. Choi, S. R. Lee, H. J. Ahn, B. Lee, S. Oh, and G. Y. H. Lip, “Atrial fibrillation detection in ambulatory patients using a smart ring powered by deep learning analysis of continuous photoplethysmography monitoring,” *European Heart Journal*, vol. 43, p. ehac544.415, Oct. 2022.

[26] M. Da Silva-Filarder and F. Marzbanrad, “Combining Template-based and Feature-based Classification to Detect Atrial Fibrillation from a Short Single Lead ECG Recording,” Sept. 2017.

[27] I. A. Zaeni, D. Lestari, S. N. Mustika, M. I. Fakhri, M. K. Osman, and K. A. Ahmad, “Design and Evaluation of a Foot-Operated Hierarchical Character Selection Keyboard for Individuals with Upper Limb Disabilities,” in *2024 Beyond Technology Summit on Informatics International Conference (BTS-I2C)*, (Jember, East Java, Indonesia), pp. 239–243, IEEE, Dec. 2024.

[28] A. Aripriharta, M. S. Al Rasyid, M. C. Bagaskoro, I. Fadlika, S. Sujito, A. N. Afandi, S. Omar, and N. Rosmin, “Queen honey bee migration (QHBM) optimization for droop control on DC microgrid under load variation,” *Journal of Mechatronics, Electrical Power, and Vehicular Technology*, vol. 15, pp. 12–22, July 2024.

[29] K. H. Wibowo, Aripriharta, I. Fadlika, G. J. Horng, S. Wibawanto, and F. W. Y. Saputra, “A New MPPT based on Queen Honey Bee Migration (QHBM) in Stand-alone Photovoltaic,” in *2019 IEEE International Conference on Automatic Control and Intelligent Systems (I2CACIS)*, (Selangor, Malaysia), pp. 123–128, IEEE, June 2019.

[30] Aripriharta and G.-J. Horng, "A New Defect Diameter Prediction using Heart Sound and Possibility to Implement as IoT Healthcare," *Mobile Networks and Applications*, vol. 28, pp. 2076–2092, Dec. 2023.

[31] L. Basso, Z. Ren, and W. Nejdl, "Efficient ECG-based Atrial Fibrillation Detection via Parameterised Hypercomplex Neural Networks," Oct. 2022.

[32] X. Xu, S. Wei, C. Ma, K. Luo, L. Zhang, and C. Liu, "Atrial Fibrillation Beat Identification Using the Combination of Modified Frequency Slice Wavelet Transform and Convolutional Neural Networks," *Journal of Healthcare Engineering*, vol. 2018, pp. 1–8, July 2018.

[33] C. M. Otto, "Heartbeat: ECG approaches to early detection of atrial fibrillation," *Heart*, vol. 107, pp. 1765–1767, Nov. 2021.

[34] O. J. Escalona and M. E. Reina, "A Fast and Robust Time-Series Based Decision Rule for Identification of Atrial Fibrillation Arrhythmic Patterns in the ECG," *Comput Cardiol*, vol. 37, pp. 995–998, 2010.

[35] F. Castells Ramon, R. Llinares, A. M. Climent, F. Atienza, J. Igual, J. Roig, and M. Guillem, "Non-invasive detection of higher frequency atrial sources during atrial fibrillation," *Computing in Cardiology*, vol. 39, pp. 201–204, 2012.

[36] H. Purerfellner, P. Sanders, S. Sarkar, E. Reisfeld, J. Reiland, J. Koehler, E. Pokushalov, L. Urban, and L. R. C. Dekker, "Adapting detection sensitivity based on evidence of irregular sinus arrhythmia to improve atrial fibrillation detection in insertable cardiac monitors," *EP Europace*, vol. 20, pp. f321–f328, Nov. 2018.

[37] I. R. Legarreta, G. Wubbeler, and C. Elster, "Common spatial pattern: An improved method for atrial fibrillation wave extraction," in *2007 Computers in Cardiology*, pp. 501–504, Sept. 2007. ISSN: 2325-8853.

[38] G. Luongo, L. Azzolin, M. W Rivolta, T. Paggi De Almeida, J. Pablo Martínez, D. Coutinho Soriano, O. Doessel, R. Sassi, P. Laguna, and A. Loewe, "Machine Learning to Find Areas of Rotors Sustaining Atrial Fibrillation From the ECG," Dec. 2020.

[39] B. J. M. Hermans, O. Ozgul, M. Wolf, V. G. Marques, A. Van Hunnik, S. Verheule, S. M. Chaldoupi, D. Linz, M. El Haddad, M. Duytschaever, P. Bonizzi, K. Vernooy, S. Knecht, S. Zeemering, and U. Schotten, "Detection of the most dominant drivers of atrial fibrillation based on repetitive activity in sequential electro-anatomical mapping," *Europace*, vol. 25, p. euad122.132, May 2023.