LOW-COST DEVICE FOR THE EARLY PREDICTION OF VASOVAGAL SYNCOPE USING ARDUINO UNO AND MACHINE LEARNING MODEL

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***Abstract*—Vasovagal syncope (VVS) is a brief loss of consciousness brought on by an imbalance in the autonomic nervous system that frequently results in secondary damage. This paper describes a real-time embedded system for VVS prediction that uses an Isolation Forest classifier installed on an Arduino Uno and a web interface, along with ECG-derived heart rate variability (HRV) parameters. The system's accuracy in identifying pre-syncopal patterns is 95.68%. According to a recent study by Lee et al. (2024), machine learning models utilising HRV alone could predict syncope with 72% accuracy about three minutes before to onset. In order to achieve similar predictive capability without relying on external computing equipment, the current work expands on these findings by constructing a standalone embedded system. For continuous ambulatory monitoring, the suggested system provides an affordable solution.**

***Index Terms*—Vasovagal syncope, Isolation Forest, heart rate variability, Arduino UNO, embedded machine learning.**

I. Introduction

Vasovagal syncope (VVS) is a brief loss of consciousness brought on by transient global cerebral hypoperfusion as a result of an aberrant autonomic nervous system reflex reaction. This reaction lowers cardiac output and systemic vascular resistance by causing peripheral vasodilation and bradycardia at the same time. A brief loss of consciousness happens when cerebral perfusion drops below a crucial threshold. Even though recovery usually happens on its own, unexpected episodes of fainting can result in serious secondary injuries like fractures, head trauma, and cerebral haemorrhage. According to epidemiological research, over one-third of people will have at least one syncopal episode in their lives, with VVS making up almost half of all cases.

Autonomic dysregulation, which is typified by elevated parasympathetic activity and withdrawal of sympathetic tone, is the basic mechanism underlying VVS. A trustworthy non-invasive measure of autonomic nervous system function is heart rate variability (HRV), which measures variations in heart rhythm. HRV is especially useful for identifying the autonomic imbalance that precedes syncopal episodes because it represents the ongoing interaction between sympathetic and parasympathetic modulation of heart activity. While frequency-domain parameters like low-frequency (LF) power, high-frequency (HF) power, and LF/HF ratio provide insights on sympathovagal balance, time-domain parameters like SDNN (standard deviation of NN intervals) and RMSSD (root mean square of successive differences) capture overall and short-term variability.

Recent developments in machine learning have shown that using HRV parameters to predict VVS episodes is feasible. According to Lee et al. (2024), machine learning models that just used HRV parameters were able to predict syncope with 72% accuracy about three minutes prior to onset, providing a crucial window for preventive action. Nevertheless, the majority of current methods have been restricted to computing-dependent implementations or offline analysis. In order to translate research-grade predictive capability into a useful tool for clinical and home use, the current work expands on these findings by creating a comprehensive system that combines real-time ECG acquisition using an Arduino Uno with AD8232 sensor, HRV processing, and machine learning inference through an intuitive web interface.

II. METHODOLOGY

The suggested system for the early prediction of vasovagal syncope is created through a comprehensive approach that integrates training machine learning models with hardware implementation and web-based analysis. The methodology involves acquiring and preprocessing datasets, extracting features, developing models in Python with Visual Studio Code, and deploying them via a Streamlit web application that processes data from an ECG acquisition system based on Arduino Uno. The architecture of the system is structured to facilitate real-time ECG acquisition, signal processing, and detection of anomalies using the Isolation Forest classifier, with results presented through an easy-to-use web interface.

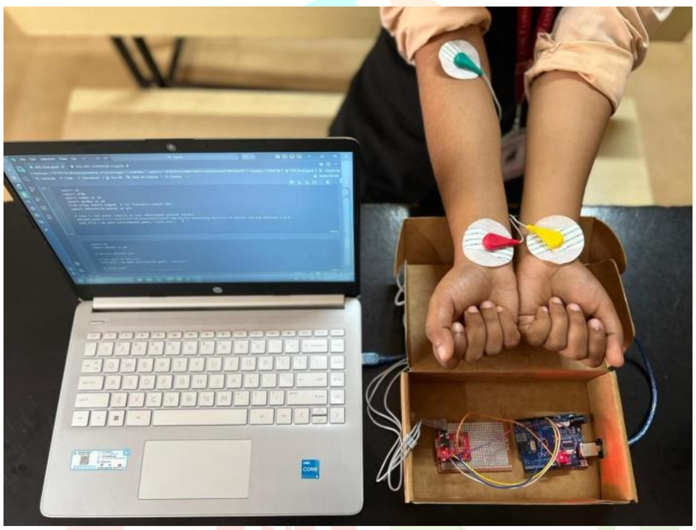

Fig. 1. Hardware Setup

A. Data Acquisition and Processing

The research relies on the PhysioNet SHAREE (Smart Health for Assessing Risk of Events via ECG) database which is publicly available and is a collection of physiological signals maintained by the MIT Laboratory of the Computational Physiology. This data set includes long term ambulatory ECG records of human subjects in controlled clinical conditions to evaluate cardiovascular risk studies. This database contains about 139 three-lead Holter recordings of 24 hours in length sampled at 250 Hz and 12-bit resolution. Clinical metadata and annotations are also available, as well as documented syncopal events that are used as ground truth labels of VVS episodes. There were three syncopal events in the dataset that were specifically diagnosed as being of vasovaginal cause by the related clinical information. The data is stored as the WaveForm DataBase (WFDB) format, which guarantees the compatibility with the existing biomedical signal processing software. A patient record is made up of several files, a .dat file which stores raw digitized samples of the ECG waveforms, a .hea header file which stores metadata such as the sampling frequency, signal gain, configuration of the lead, and the duration of recording, and .atr annotation files with R-peak locations and event markers which have been manually verified by a professional. Access and preprocessing of data were done in the WFDB Python library (wfdb) which has functions to read PhysioNet-formatted signals and annotations, which are native in Python. The library allows one to extract ECG signals directly, annotate it, and combine it with NumPy data structures to analyze it further. The standard practice leads to reproducibility and following the practice that is set in terms of biomedical signal processing.

B. HRV Processing and Feature Extraction

The extraction of HRV features was done with the custom Python programs with reference to the guidelines set by the Task Force of the European Society of Cardiology. Time-domain and frequency-domain parameters were calculated in order to reflect opposing measures of autonomic regulation. Time-domain measures were Mean RR (average time between normal beats), SDNN (standard deviation of NN intervals) which is the general HRV and RMSSD (root mean square of successive differences) which is a short-term variability that is mediated by the parasympathetic system. These time fails are computationally inexpensive and can give clinically explainable assessments of the cardiac autonomic activity.

The analysis in frequency domain also demanded more advanced processing since the RR interval series were unevenly sampled. RR intervals were initially interpolated and resampled at 4 Hz, to produce a time series with evenly spaced time intervals, which would be analyzed with spectral analysis. Welch method was used to estimate power spectral density with the Hann window and the overlap of the window is 50 percent. One sample per segment was selected to balance frequency and statistical reliability as the number of samples per segment was 256 or the length of the interpolated series, whichever was small. The Low-frequency (LF) power was calculated as the power spectral density in the range of 0.04-0.15 Hz, which is a combination of sympathetic and parasympathetic modulation. The frequency tool (high-frequency, HF) power was lifted within a range of 0.15 - 0.4 Hz, as the reference of a pure parasympathetic activity. This was further converted to LF/HF ratio that was used as a measure of sympathovagal balance. All these attributes give an overall physiological description of the activity of the autonomic nervous system and dynamic changes that occur before syncopal events.

C. Machine Learning Model and Training

Isolation Forest algorithm was chosen as the anomaly detection model to use in this application because it has a basic ability to detect abnormal physiological patterns and its nature is inherently compatible with the skewed nature of the data. Isolation Forest is an unsupervised learner in contrast to supervised methods that use balanced datasets (labeled and unlabeled), which focus on isolating irregularities as opposed to modelling normal behaviour. This property renders it especially useful in the identification of the relatively uncommon pre-syncopal states in continuous physiological records, where the number of syncopal events is by far much lower than the number of normal sinus rhythm recording.

The integrated development environment used was Visual Studio Code and Python 3.9 was used to develop the models. SHAREE dataset was used to give the pattern of the baseline norms that were extracted in non-syncopal segments, where the anomalous pre-syncopal patterns were detected. The algorithm builds an ensemble of isolation trees recursively by performing a random sampling of both features and split values that are selected, and continuous cutting up the feature space to the point that individual samples are isolated. This is based on the premise that anomalous cases are few and are distinct in the feature characteristics they have and thus fewer splits are needed in order to isolate them and as a result shorter path lengths are obtained through the trees. The mathematic expression of the anomaly score of a given sample is:

$$s(x, n) = 2 - c(n)E(h(x))$$

and E (h (x)) is the mean path length of all trees in the ensemble, and c (n) is a normalization term, taking into consideration dataset size. A score of 1 shows that there is a high probability of anomaly whereas a score of 0 shows normal patterns. The contamination parameter can be changed to shift the decision boundary to an estimated proportion of data anomalies.

The systematic experimentation on the training data was used to optimize the hyperparameters. Estimators were to be 100, which is enough to make the model very stable, but still computationally efficient enough. The empirical setting of the contamination factor was 0.02 that relied on the anticipated prevalence of aberrant data points in the physiological data and the real prevalence of syncopal cases within the dataset. The trained model was tested with the entire dataset consisting of 136 non-syncopal and 3 syncopal subject recordings with an overall accuracy of 95.68 percent in the pre-syncopal conditions detection. The confusion matrix indicated that the number of 133 true negatives, 3 false positives, and 3 false negatives showed strong discrimination ability. Precision and recall of the non-syncopal classification report indicated a value equal to 0.98, and 0.98 respectively, which demonstrates that the model could classify correctly the physiological normal conditions and at the same time sensitive to the abnormal conditions. The model has been thereafter coded with the joblib library and incorporated into the web application to make inferences in real-time.

D. Arduino Uno Integration and Web-Based Analysis

The trained Isolation Forest model was deployed within a Python-based web application rather than on the micro-controller itself, adopting a client-server architecture that leverages the computational capabilities of a host computer while maintaining a simple, low-cost data acquisition front-end. This design decision was made to ensure that the complex signal processing and machine learning computations could be performed efficiently without the constraints of embedded hardware, while still providing a practical and portable data acquisition solution.

ECG signals are acquired in real-time using an AD8232 analog front-end module connected to disposable surface electrodes in a standard three-lead configuration. The AD8232 is a dedicated integrated circuit designed for ECG signal conditioning, performing instrumentation amplification, right-leg drive noise rejection, and preliminary filtering. It outputs a conditioned analog signal within the 0-5V range compatible with the Arduino Uno's analog input pins. This analog signal is sampled by the Arduino Uno's 10-bit analog-to-digital con-

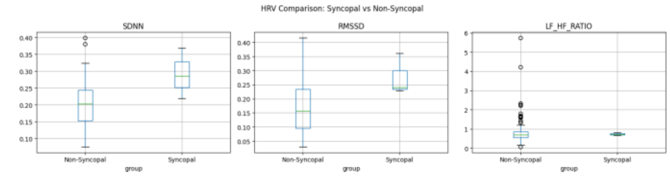

Fig. 2. HRV Comparison:syncopal vs non-syncopal

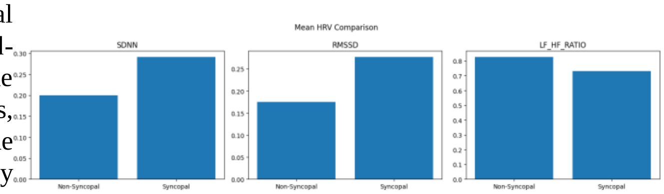

Fig. 3. Mean HRV Comparison

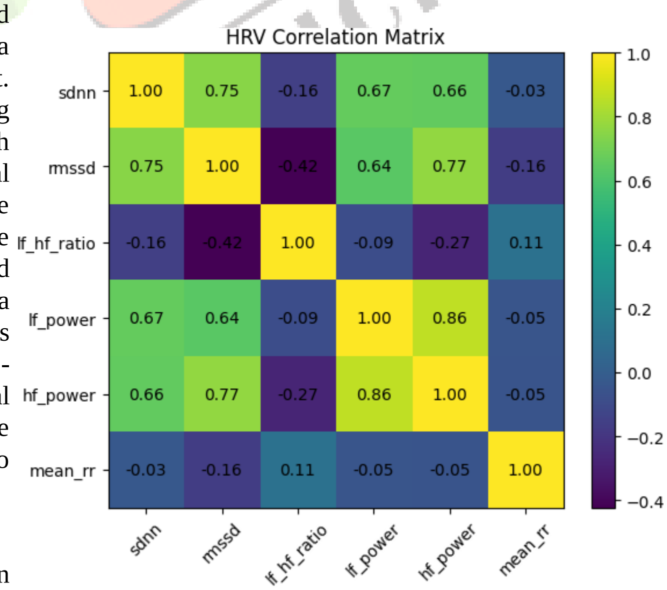

Fig. 4. HRV Correlation Matrix

verter (ADC) at 128 Hz, matching the standardized sampling rate used in the SHAREE dataset and providing sufficient temporal resolution for accurate HRV analysis while balancing data fidelity and serial transmission bandwidth.

The Arduino Uno firmware was developed in the Arduino Integrated Development Environment (IDE) using embedded C++. The firmware continuously reads the ECG signal from analog pin A0 at the specified sampling rate, converts the raw ADC values (0-1023) to signed 16-bit integers, and transmits them over USB serial communication as raw binary data. Unlike a fully embedded approach, the Arduino Uno implements no onboard signal processing, feature extraction, or machine learning inference, serving exclusively as a data acquisition front-end to minimize hardware complexity and power consumption. This design allows the Arduino to operate for extended periods on battery power while streaming data to the host computer for analysis.

A Python script (`ecg_file_extract.py`) was developed to interface with the Arduino Uno, capture the streaming ECG data, and save it in the standard WFDB format. The script includes automatic COM port detection to simplify the user experience, scanning for connected Arduino devices by matching common USB-to-serial converter identifiers. Once connected, it records ECG samples for a user-specified duration, typically 60 seconds, and saves the data using the `wfdb.wrsamp` function. The recorded signal undergoes digital bandpass filtering (0.5-40 Hz) using a second-order Butterworth filter implemented with `scipy.signal` to further enhance signal quality. R-peak detection is performed using `scipy.signal.find_peaks` with parameters optimized for ECG morphology, including a minimum distance constraint of 0.6 times the sampling rate ($0.6 \times f_s$) and an adaptive threshold based on the mean signal amplitude plus 0.6 times the standard deviation ($1.5 \times \bar{x}$, where $\bar{x}$ represents the mean signal amplitude). Detected R-peak locations are saved as WFDB annotation files (.qrs), enabling subsequent HRV analysis using the same tools and algorithms applied during model training.

A Streamlit-based web application (`app.py`) serves as the primary user interface and analysis engine, with all computational functions encapsulated in a separate `hrv_engine.py` module. The application features a clean, intuitive interface designed for ease of use by healthcare professionals and patients alike. Users can upload their recorded WFDB files (.dat, .hea, and optional .qrs) through a simple file upload interface. Upon receiving the files, the application temporarily stores them and uses the `wfdb` library to read the ECG signal and sampling frequency.

If QRS annotation files are provided, the application uses these expert-validated peak locations for RR interval computation. Otherwise, it performs automatic R-peak detection using the same `find_peaks` algorithm with empirically determined parameters. The detected R-peak locations are used to compute RR intervals, which undergo the same physiological filtering applied during training (0.3-2.0 seconds). HRV features including SDNN, RMSSD, LF power, HF power, and LF/HF ratio are extracted using the `compute_hrv` function from `hrv_engine.py`, which implements the identical algorithms used during model development.

The pre-trained Isolation Forest model is loaded within the web application and applied to the extracted three-dimensional feature vector (SDNN, RMSSD, LF/HF ratio). The model returns both a binary classification (normal or anomalous) and a continuous anomaly score. Results are displayed in real-time through an interactive dashboard featuring color-coded result panels (green for normal with checkmark icon, red for anomaly with warning icon), key HRV metrics displayed as interactive metric cards with appropriate units (milliseconds for time-domain measures, ratio for LF/HF), and a horizontal bar chart showing the anomaly score relative to the decision boundary at zero.

The application also provides comprehensive visualization tools to aid clinical interpretation. The ECG trace is displayed with overlaid R-peaks, allowing visual verification of detection accuracy. An RR tachogram shows beat-to-beat interval variations with a horizontal line indicating the mean RR interval. A power spectral density plot highlights the LF and HF bands with shaded regions, providing insight into the frequency distribution of heart rate variability. An expandable clinical interpretation guide offers reference ranges for HRV parameters and their physiological significance, helping users understand the results in the context of syncope risk assessment. All visualizations use a dark theme optimized for prolonged viewing, with clear labeling and consistent color schemes.

E. Real-Time Data Acquisition and Validation

An integrated data analysis and acquisition pipeline was built to test the full functionality of the system. Raw ECG samples are sent to the host computer with the Streamlit web application at 128 Hz by the Arduino Uno via USB serial. The application logs the streaming data over a specified time to the user, automatically creates files compatible with WFDB, and fully analyzes HRV and detects anomalies in near real-time.

The recorded signal undergoes peak finding with the `scipy.signal.find_peaks` function with the necessary parameters optimized to ECG morphology which includes the minimum distance between the two parameters as well as the amplitude threshold compared with the mean signal amplitude (1.5 x mean amplitude). R-peak locations detected may be written as wfdb annotation files (.qrs) with the wfdb.Annotation and wfdb.wrann functions in a format similar to the annotation format of the original SHAREE dataset. This validation method allows a direct comparison of the data got in real-time and the characteristics of the training dataset.

Both normal sinus rhythm records and anomalous patterns were used to test the entire system to ensure that the system could detect. Model generalization was tested of test recordings that were tested against the MIT-BIH Arrhythmia Database (records 100 and 207). Record 100 (normal sinus rhythm) was correctly called normal, and record 207 (with ventricular abnormalities) was correctly called anomalous, which proves the capability of the model to differentiate between normal and abnormal cardiac patterns with the already proven accuracy of 95.68%.

This is a two part architecture which provides a realistic trade off between simplicity in hardware and computational power. The Arduino Uno is a low-cost, low-power data acquisition front-end, and the web application contains complex signal processing, machine learning inference, and is conveniently packaged with user-friendly interface. This design effectively portrays research-quality machine learning system to an implementable device with the ability to perform continuous ambulatory monitoring and real-time physiological measurements to predict vasovagal syncope early.

III. Result and Discussions

The developed system that proposes early prediction of vasovagal syncope was built and tested both offline by evaluating the model with the help of an Arduino Uno data acquisition front-end and web-based analysis interface. The findings prove that the Isolation Forest algorithm is effective to identify pre-syncopal patterns with HRV parameters obtained through ECG signals.

The Isolation Forest model was trained using HRV features derived using the SHAREE dataset, which consists of 136 non- syncopal and 3 syncopal subject recordings. This model had a total accuracy of 95.68 percent in the classification of syncopal and non-syncopal patterns. The confusion matrix showed that there were 133 true negatives, 3 false positives and 3 false negatives which showed strong discrimination. The classification report indicated a precision of 0.98 and recall of 0.98 on the non-syncopal class, which indicated that the model is capable of classifying normal physiological conditions correctly. Such accuracy is relatively high compared to earlier studies by Lee et al. (2024), who achieved an accuracy of 72% with the help of XGBoost in VVS prediction. This can be explained by the fact that Isolation Forest is not supervised, and it is specifically better adapted to detecting anomalies when dealing with unbalanced data when syncopal events are not very frequent but are rather an exception to normal physiological conditions.

Comparison of the statistical results between syncopal and non-syncopal groups showed the presence of significant differences in important parameters of HRV. The mean SDNN (0.291 vs. 0.199, $p = 0.029$) and mean RMSSD (0.277 vs. 0.175, $p = 0.064$) were greater in the syncopal group than in the non-syncopal group. The LF/HF ratio was also a little less in the syncopal group (0.732 vs. 0.826), but this was not a statistically significant difference ($p = 0.737$). According to Cohen, the d effect size analysis revealed that SDNN ($d = 1.52$) and RMSSD ($d = 1.04$) have large effects, meaning that there are significant differences between the groups. These differences in HRV are consistent with the known facts about the involvement of the autonomic nervous system in VVS. The high SDNN and RMSSD in syncopal subjects indicate that there is more parasympathetic activity before syncopal occurrences, which is in line with the typical vagal surge reported in the literature. The significant values of these parameters show that they are strong physiological indices of pre-syncopal state.

Correlation analysis has shown that SDNN and RMSSD ($r = 0.75$), RMSSD and HF power ($r = 0.77$) and LF power and HF power ($r = 0.86$) have strong positive relationships. There were moderate negative relationships between the LF/HF ratio and RMSSD ($r = -0.42$) and HF power ($r = -0.27$), which indicate that the higher the parasympathetic activity is, the smaller is the sympathovagal balance. These high correlations confirm the physiological interpretability of the features extracted and the negative relationship between LF/HF ratio and parasympathetic markers further substantiates the interpretation of LF/HF as a sympathovagal balance measure.

The client-server model was also able to show stable performance with ECG data being sent by the Arduino Uno at 128 Hz through USB serial and the data being received by the Streamlit web app and results displayed within a few seconds. The AD8232 analog front-end acquisition of real-time ECGs showed good signal quality that can be used to detect the R-peak and extract HRV features. The web app was able to compute SDNN, RMSSD and LF/HF ratio on streaming ECG data and anomaly detection with the pre-trained Isolation Forest model. The dashboard is intuitive with the provision of color-coded results, interactive metric cards that give useful visions of key HRV parameters, the ECG trace visualizations with overlaid R-peaks, RR tachogram displaying beat-to-beat interval variations, power spectral density plot with highlighted LF and HF bands, and visualization of the anomaly score against the decision boundary. A clinical interpretation guide is also incorporated in the interface to guide users on the meaning of the HRV measures and how they are related to the risk of syncope.

System functionality was tested through validation testing with recordings of MIT-BIH Arrhythmia Database. Record 100 (normal sinus rhythm) had been appropriately labeled as normal, and record 207 (with ventricular abnormalities) was appropriately labeled as anomalous, which shows that the model can also generalize outside the training data. This validation method proves that the system has the ability to differentiate normal and abnormal cardiac patterns in real life situation.

A number of limitations must be mentioned. To begin with, SHAREE dataset has only three verified instances of vasovagal syncope which restricts the variety of abnormal patterns which can be used to train the model. Secondly, the real-time validation was based on benchmark databases as opposed to prospective clinical data of VVS patients. Third, the existing implementation uses a single-lead ECG system, which can be vulnerable to motion artifact during ambulatory recording, and needs to be connected to a host computer to analyse, which can add constraints to mobility during continuous recording. Nevertheless, the system has these weaknesses, but it still reveals a good prospect of real-time prediction of VVS and offers a basis of future clinical practice.

IV. Conclusion and Future Work

In this paper, a low-cost and portable system was developed and validated in predicting vasovagal syncope early, using ECG-based heart rate variability parameters and machine learning. The system combines real time ECG recording with Arduino Uno and AD8232 analog front-end, transmission to a host computer via serial and a web application based on Streamlit to process signals and detect anomalies using an Isolation Forest classifier. The model had a 95.68% accuracy on PhysioNet SHAREE. Statistic analysis showed high SDNN ($p = 0.029$) and RMSSD ($p = 0.064$) in syncopal, which proves the parasympathetic activation of VVS pathogenesis. Using correlation analysis confirmed the physiological interpretability of extracted features in which there were strong positive correlations between parasympathetic features. Recordings of the MIT-BIH Arrhythmia Database were used to validate that the correct classification of normal and anomalous cardiac patterns was done. The entire system allows continuous ambulatory observation with the least human intervention, which bridges the gap between clinical research and practical medical technology in the prevention of secondary injuries due to syncopal episodes.

Future research will be on multimodal sensor combination of prediction accuracy with a complete hemodynamic evaluation. A blood pressure sensor would allow measuring directly the hypotensive episodes that constitute VVS, which would be a second physiological stream that would potentially be complementary to HRV analysis. A photoplethysmography (PPG) sensor would be added to provide continuous oxygen saturation (SpO_2) and peripheral perfusion measurements to provide information about tissue oxygenation in pre-syncopal states. The sensor fusion methods could be used to combine these multimodal inputs in order to develop a more powerful and precise prediction model.

The future clinical validation of VVS patients undergoing tilt-table testing is critical in order to establish the real-life performance of the system and give chances to improve the performance by expert annotations. This type of study would additionally allow gathering of more diverse datasets of greater size that are inclusive of more syncopal events overcoming the existing constraint of small positive sample size. The application of the transfer learning methods may allow personalising the model to each individual patient, considering the inter-subject differences in the baseline HRV features and syncopal patterns. The web interface should be more mobile friendly since this would enhance portability and allow one to perform analysis using a smartphone without necessarily using a laptop computer. Remote patient monitoring, secure data storage and telemedicine consultations would be possible through cloud connectivity, further extending the utility of the system in the management of chronic diseases. Such developments will make the existing prototype a complete wearable health monitoring system that can be used in more applications than just vasovagal syncope to identify other autonomic disorders, as well as cardiac arrhythmias.

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