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Article

Application of biosensing technology in the rapid identification of pathogenic microorganisms

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Abstract: Background: Biosensing technology has developed as a capable tool for the rapid and perfect recognition of pathogenic microorganisms, determining real-time recognition capabilities that are crucial for early disease diagnosis and management. **Purpose:** This research investigates the integration of biosensors with Machine Learning (ML) techniques for the efficient detection of pathogens. **Approaches:** Data collection involved using various biosensors, including electrochemical, optical, and mass-based sensors, to capture the microbial signature of different pathogens. The collected data was pre-processed using adaptive filtering (AF) to remove noise and ensure signal clarity. *Z*-score normalization is utilized to standardize the dataset. Feature extraction was performed using the discrete wavelet transform (DWT) technique to reduce the dimensionality of the data while retaining crucial information. **Results:** This research proposes an Enhanced Snow Ablation Optimized Adaptive Support Vector Machine (ESAO-ASVM) model designed to enhance the accuracy and effectiveness of classifying complex biological data, such as microbial signatures. The proposed ESAO-ASVM model demonstrated optimal performance with an execution time of 0.58 s, memory usage of 42%, Root mean squared error (RMSE) of 0.01, Mean squared error (MSE) of 0.019, accuracy loss of 0.06, Structural similarity index measure (SSIM) of 80.4, accuracy of 98.5%, precision of 95%, recall of 94%, and an *F*1-score of 96%. This approach suggests a robust solution for rapidly identifying pathogenic microorganisms, making it an effective clinical diagnostic tool for food safety, and environmental monitoring. **Conclusion:** The incorporation of Biosensing technology with ML methods contains potential significant improvement in pathogen recognition, enabling faster and more consistent health involvements.

Keywords: pathogenic microorganisms; biosensor; machine learning (ML); discrete wavelet transform (DWT); enhanced snow ablation optimized adaptive support vector machine (ESAO-ASVM)

1. Introduction

Biosensing is an emerging analytical discipline that uses transducing technologies to detect biological markers. These transduction pathways convert biological fluctuations into readable and measurable visual, thermal, electrical, or electrochemical signals [1]. Numerous biological targets, including cells, bacteria, viruses, and bio macromolecules like nucleic acids, peptides, proteins, and enzymes, as well as tiny biomolecules like uric acid, h_2o_2, and glucose, can be detected via biosensing [2]. Very extensive possibilities for clinical trials of the biological indicators and the treatment of various illnesses with highly selective and sensitive biosensors equipped with responded promptly [3].

1.1. Biosensing technology in rapid identification

Biosensing technology has transformed several industries, including food safety, environmental monitoring, and healthcare. This technique offers major benefits in the quick detection of substances like viruses, poisons, or even disease indicators by using sensors that detect biological markers in real time [4]. Information technology, biochemistry, nanotechnology, and microelectronics make biosensors very sensitive; and provide quick and accurate information required for responding rapidly to any situation [5]. Biosensors enhance disease control, environmental monitoring, and public health management by identifying indicators quickly, improving efficiency, and promoting early diagnosis, environmental protection, and food safety [6]. These components interact with target analytes, generating measurable signals that can be processed, emphasized, and displayed on a device for monitoring, identification, and decision-making purposes [7]. **Table 1** provides an in-depth analysis of biosensors' applications, including disease diagnosis, environmental protection, food safety, biodefense, agricultural monitoring, and personalized medicine.

Table 1. Key applications of biosensing technology.

Application Area	Description	Types of Biosensors Used	Target Analytes	Key Benefits
Healthcare and Disease Diagnosis	Detect biochemical reactions of biomolecules linked to diseases like cancer, cardiovascular diseases, and infections.	Electrochemical, Optical, Enzymatic, DNA sensors	Tumor markers, glucose, cholesterol, pathogens, DNA	Rapid identification, timely interventions, personalized treatment, portable diagnostics
Environmental Monitoring	Detect pollutants, toxic chemicals, or pathogens in water, soil, and air.	Optical, Electrochemical, Mass-sensitive sensors	Heavy metals, pesticides, VOCs, microorganisms	Prevention of disasters, protection of health, safe water and air quality
Food Safety and Quality Control	Identify toxicological bacteria or pathogens in food.	Optical, Electrochemical, Immunosensors	Salmonella, E. coli, allergens, chemical residues	Ensures safety, reduces contamination risks, monitors shelf life
Biodefense and Security	Detect bioterrorism agents or biological threats in various environments.	Immunosensors, Electrochemical sensors	Anthrax, botulinum toxin, ricin, smallpox virus	Fast detection of biothreats, enhances safety, national security
Agriculture and Livestock Monitoring	Detect diseases in crops and livestock.	Enzymatic, Optical, Electrochemical	Plant pathogens, viruses, bacteria, hormones	Early disease detection, improves yield and health, cost-effective
Personalized Medicine	Evaluate health parameters and aid in precise medical treatment.	Wearable sensors, Electrochemical, Optical	Glucose, blood pressure, lactate, hormone levels	Continuous monitoring, real-time data, personalized health insights

1.2. Technological advancements and challenges

Advancements in materials science, microelectronics, and nanotechnology have enabled the development of more precise, affordable, and smaller biosensors for identifying environmental pollutants or biomarkers [8]. Micro-fabrication advancements enable real-time diagnostic devices for environmental monitoring and healthcare, transforming wearable biosensors into continuous monitoring, and enabling personalized medical procedures [9]. Despite advancements in sensor calibration, manufacturing costs, regulatory barriers, and scalability, widespread acceptance of biosensors remains hindered by scalability, regulatory barriers, and strong validation procedures [10]. Biosensing technology is positioned to improve

some sectors, including food safety, environmental protection, and illness detection, as long as research into these issues continues.

Research purpose: The research investigates the efficient use of Biosensing techniques in the detection of pathogens.

1.3. Research contribution

- The research explores the integration of biosensors with ML techniques for efficient pathogen detection;
- Data collection includes various biosensors, including electrochemical, optical, and mass-based sensors, which were used to capture microbial signatures of pathogens;
- The noise is removed using an AF, and *z*-score normalization was applied to standardize the dataset for data preprocessing;
- Feature extraction using DWT is employed to reduce data dimensionality while retaining essential information;
- The ESAO-ASVM model was developed to improve the correctness and effectiveness of classifying complex biological data;
- The ESAO-ASVM model compared metrics like execution time, accuracy, precision, memory usage, RMSE, MSE, accuracy loss, SSIM, recall, and *F*1-score.

Research organization: Section 2 contains the research's review of the literature, and section 3 explains the methodology of this research. The results of the research are illustrated in section 4. Section 5 demonstrates the discussion, and the research's conclusion is presented in section 6.

2. Literature survey

Table 2 denotes a comprehensive overview of the literature on Biosensing technology in rapid identification, outlining data, research objectives, proposed method, and limitations of each research. Refer to the Appendix for relevant abbreviations (Table A1. Abbreviations and corresponding full forms).

Table 2. Collection of various articles related to biosensing technology.

Ref	Objective	Data	Proposed Method	Limitations
[11]	To use nanosensor arrays with aggregation-induced emissive nanosilicons for pathogen identification in food.	Tested on eight pathogens, including *C. sakazakii* and *L. monocytogenes* in milk at specific concentrations.	ANN for rapid and accurate pathogen identification.	Requires specific pathogen concentrations; validation is limited to milk samples.
[12]	To develop a DL-enhanced digital microfluidic platform for multiplex detection of viable foodborne pathogens.	Tested on four bacterial species with detection limits of 63 CFU/mL.	TLENTNet for bacterial typing and quantification.	Detection time: 7 h; detection limit: 63 CFU/mL; requires a specialized microfluidic chip.
[13]	To improve biosensor performance by ensuring DL classification model predictions align with domain knowledge for rapid and accurate biosensing.	Validation using the dynamic response of cantilever biosensors to quantify microRNA across the nanomolar to femtomolar concentration range.	TGRNN with cost function supervision for improved classification performance and consistency with experimental observations.	Requires data augmentation, cost function supervision, and model tuning, adding complexity to real-world applications.

Table 2. (*Continued*).

Ref	Objective	Data	Proposed Method	Limitations
[14]	To investigate the efficiency of wearable technology for audio meditation and real-time stress detection in lowering levels of stress during academic engagement.	Physiological data was collected during the MIST.	Bayesian optimization for hyperparameter tuning, and GB algorithm for stress classification.	Limited to academic stress context; depends on feature selection and ML model performance for accuracy.
[15]	To develop a novel T-shaped square SRR-based biosensor for early and accurate detection of brain tumors using ML.	Investigated variations in materials as resonators for optimal response characteristics.	ML for parameter improvement and in-depth analysis, using the T-shaped SRR-based biosensor for real-time, label-free monitoring of brain tumor cells.	Accuracy depends on material selection and wavelength range; limited specificity for multi-sclerosis and brain tissues.
[16]	Research aimed to predict detection times for rotating microfluidic biosensors designed for detecting CRPs using input variables.	The data included input variables such as ω, XS, θ, and RD for predicting the response time of a lab-on-a-CD device.	The proposed method is a hybrid model, PSO-ANN, which combines ANN with PSO.	Evaluated using MAE, RMSE, VAF, and R^2 metrics.
[17]	The research involved designing and evaluating a THz metasurface biosensor for malaria detection using plasmonic materials and AI for early and accurate diagnosis.	The data includes sensor performance metrics such as sensitivity, detection accuracy, and figure of merit, optimized through electromagnetic simulations.	The proposed method integrates a multi-layer structure of graphene, gold, and silver for SPR effects with the XGBoost ML algorithm for performance prediction.	Achieved up to 100% R^2, but real-world limitations include variability in parasite concentrations and environmental conditions.
[18]	The research introduced an approach integrating SPR biosensing with ML to enhance fuel adulteration detection and improve fuel quality control.	The data includes sensor performance metrics such as sensitivity, figure of merit, and predictions achieved through electromagnetic simulations.	The proposed method combines SPR biosensing with the CatBoostGB algorithm.	Achieved 100% R^2, but challenges in real-world applications with complex fuel mixtures and environmental conditions.
[19]	The research represented DL-based architecture for designing an IAM to enhance trace detection of THz molecular fingerprints, specifically for α-lactose sensing.	The meta grating's sensing structure and resonance frequency were enhanced 9.3 times using THz fingerprint spectra.	It utilized a bidirectional neural network DL architecture for THz fingerprint sensing, utilizing angle multiplexing to stimulate guided-mode resonances.	Enhanced THz fingerprint detection but faces challenges in scaling design and optimizing fabrication for broader analyte applications.
[20]	Research presented a metasurface-based biosensor integrating graphene, gold, and silver for enhanced hemoglobin detection.	The data included performance metrics such as peak sensitivity, quality factor, sensor resolution, and an R^2 of 1.0 for predictive accuracy.	Research integrated a metasurface design with graphene, gold, and silver, optimized using the GB Algorithm for behavior prediction.	Achieved perfect predictive accuracy, but challenges remain in scaling and biomolecule detection for broader applications.
[21]	Research developed a portable, DL-assisted smartphone-based ECL sensing platform for cost-effective and selective lactate detection.	The data included ECL images used to train DL models, with performance metrics such as linear range and limit of detection.	The proposed method uses DL models trained on ECL images, integrated with a smartphone, and low-cost components for portable lactate sensing.	Demonstrated good performance in controlled environments, but field-testing and accuracy across diverse conditions remain challenging.
[22]	Research determined the design, simulation, and performance analysis of a terahertz-based biosensor for hemoglobin detection, utilizing graphene, gold, and silver metasurfaces.	The data included performance metrics such as sensitivity, figure of merit, and detection range.	The proposed method employs a terahertz-based sensor with ML optimization using a DTR, achieving an optimal R^2 score of 100%.	High sensitivity and optimized performance, but scaling and application challenges for diverse biological analyses in real-world scenarios.
[23]	Research demonstrated the novel terahertz-based biosensing platform for SARS-CoV-2 detection, utilizing a hybrid architecture of TiO_2, black phosphorus, and graphene-based metasurfaces.	The data included sensitivity, figure of merit, minimum detection threshold, and coefficient of determination.	The proposed method integrates ML using the K-NN regression algorithm with computational electromagnetics for predicting absorption coefficients and sensor optimization.	High sensitivity, but challenges in adapting platform for large-scale, real-world applications and diverse analytes.

Table 2. (*Continued*).

Ref	Objective	Data	Proposed Method	Limitations
[24]	Research provides a terahertz-based biosensor that is calibrated for the 0.1–0.6 THz bandwidth and uses SPR principles for direct dopamine identification.	The data included sensitivity, figure of merit, detection limit, and KNN regression over test cases with R^2 values of up to 1.0.	The biosensor integrates SPR with KNN regression to predict absorption values based on structural parameters for enhanced sensitivity and detection limits.	Integration into clinical settings can face scalability, cost, and sample adaptation challenges.
[25]	It develops a cost-effective OFET-based biosensor for detecting lactate and troponin using a carrier transport electronic model and ML optimization.	Key data includes sensitivity for lactate and troponin and polyaniline's lower power consumption with a threshold voltage of −170 mV.	RF model is employed to optimize the OFET biosensor, incorporating polyaniline and pentacene as active layers for improved sensitivity and lower power usage.	Scalability of the OFET biosensor for clinical use and potential variability in performance across biological samples.

Research gap

Biosensing technology has made progress in identifying pathogenic microorganisms, but gaps remain in sensitivity, specificity, scalability, operational stability, and real-time data analysis. Addressing these challenges can improve pathogen identification effectiveness, accessibility, and disease control tactics.

3. Methodology

This research investigates the well-organized utilization of biosensors and ML techniques in the detection of pathogens. This research uses biosensors to recognize pathogens from blood, saliva, and urine samples. These sensors are correlated to ML algorithms to analyze data, classify patterns, and predict infection spread. A real-time detection model is qualified using a dataset of various diseases, using preprocessing methods to ensure data features. Feature extraction is utilized to capitalize the approach capability to correctly categorize pathogens. The research's overview is demonstrated in **Figure 1**.

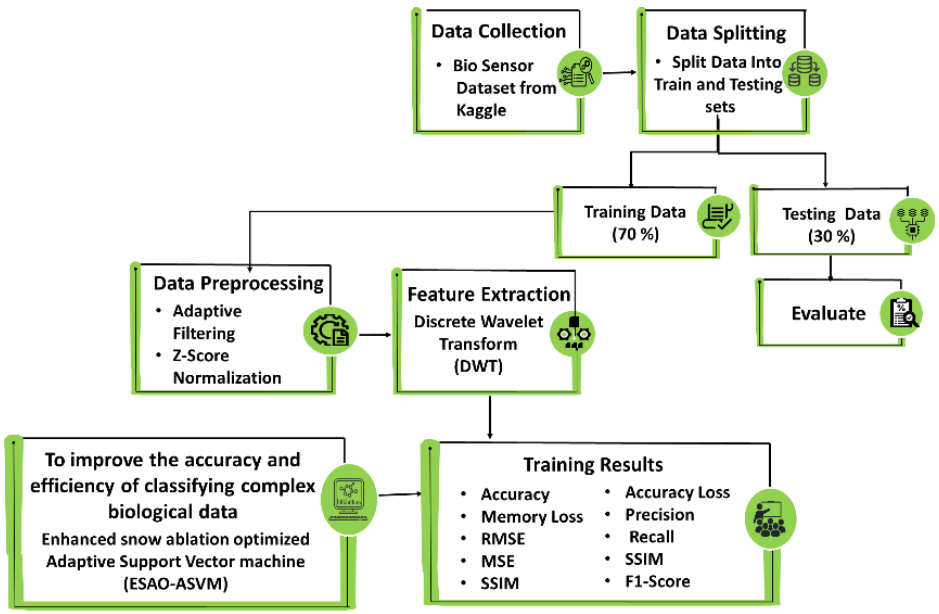

Figure 1. Research outline.

3.1. Data collection

Research gathers the Biosensing Technology for Pathogen Detection [26] dataset from Kaggle. The system uses biosensor information to improve pathogen safeguard suitability in clinical diagnostics, food safety, and ecological monitoring, focusing on harmful microorganism determination using biosensing technologies. Pathogenic microorganisms, which include a wide range of bacteria, viruses such as influenza and HIV, and fungi such as Candida and Aspergillus, are significant contributors to human diseases and impose substantial public health risks. Detecting these pathogens early and correctly is important in preventing the outbreak and ensuring public health safety. Biosensing technologies are promising as allow for rapid, sensitive, and non-invasive detection methods, which are of utmost importance for monitoring the presence of pathogens in, food, clinical, and environmental surroundings.

3.2. Data Preparation

This research highlights the significance of data preprocessing in biosensor data quality and reliability, using AF and *Z*-score normalization to eliminate noise and enhance detection accuracy.

3.2.1. Adaptive filtering (AF)

By removing unnecessary signals from harmful microbes, noise reduction in biosensor data improves signal intelligibility. Methods such as signal denoising, smoothing, and filtering safeguard relevant data for precise analysis, principally in real-time biosensor monitors where data consistency is important. AF is a dynamic method for removing noise in biosensor data, adjusting filter parameters based on input and output differences, and removing artifacts like motion and power line interference while discarding useless ones. This is best illustrated by the utilization of Equation (1).

$$z[m] = \sum_{j=0}^{N-1} x_j\,[m].\,w[m-j] \tag{1}$$

Modify the rule

$$x_j[m+1] = x_j[m] + \mu.\,f[m].\,w[m-j]$$

The filtered signal is represented by $z[m]$, with adaptive filter coefficients $x_j[m]$, and step size $\mu[m]$, where $f[m]$ is the desired signal. The system dynamically adjusts filter parameters in real-time to eliminate noise, such as motion artifacts and power line interference, ensuring cleaner signals for accurate analysis.

3.2.2. *Z*-score normalization

After collecting the dataset, pre-processing is done by normalizing and fixing errors, which constitute certain ways that preprocessing assists in clearing up the data. *Z*-score normalization is a procedure that transforms biosensor data by focusing on a zero mean and scaling it based on SD. The method improves pathogenic microorganism uncovering by eliminating biases due to sensor sensitivities or

environmental conditions and normalizes the calculated SD and mean for each signal feature. The signal quality alteration is provided as in Equation (2).

$$Z = \frac{(y - mean(Y))}{std(Y)} \tag{2}$$

The technique minimizes the impact of outliers on data by scheming the mean and SD of the attributes. The regularity of biosensor data reduces biases and enhances the accuracy of pathogenic microorganism recognition by achieving zero mean and unit variance.

3.3. Feature extraction using discrete wavelet transform (DWT)

DWT is a technique used to extract features from biosensor data, particularly for detecting pathogenic microorganisms. It decomposes time-series data into frequency components, identifying rapid and slow trends. DWT enhances biosensor sensitivity by capturing transient microbial activity and subtle fluctuations, reducing data dimensionality, and detecting finer details. DWT pre-processing, the DWT technique converts remote sensing noises into frequencies with several resolutions, boosting feature extraction, preserving spatial information, and lowering noise to improve analysis. A wavelet is a function $\psi\hat{}$that satisfies the following admissibility condition in Equation (3).

$$D_\psi = \int_{-\infty}^{+\infty} \frac{\left|\hat{\psi}(\xi)\right|^2}{|\xi|}\, c\xi < +\infty \tag{3}$$

$$w(s) = \sum_{l=-\infty}^{\infty} d(l)\, \phi(s-l) + \sum_{i=0}^{\infty} \sum_{l=-\infty}^{\infty} c(i,l)\, 2^{\frac{j}{2}} \psi\left(2^i s - l\right) \tag{4}$$

In Equation (4) D_ψ Must be determinate safeguarding the function, $\phi(s-l)$ is the function of scale, and $c(i,l)$ includes the high-energy element of the image, using the WS $\psi\left(2^i s - l\right).w(s)$ is represented individually, with all signal analogous, a quantity of shifted and opened wavelet functions ψ (s) and removed scale meanings $\phi(s)$ can be used to decay limited influence.

$$d(l) = \int_{-\infty}^{+\infty} w(s)\, \phi(s-l) cs \tag{5}$$

Equation (5) is a DWT version where $d(l)$ represents scale coefficients and $c(i,l)$ represents wavelet coefficients. Equation (6) computes the wavelet and scale coefficients using scalar products.

$$c(i,l) = 2^{\frac{j}{2}} \int_{-\infty}^{+\infty} w(s)\, \psi\left(2^i s - l\right) cs \tag{6}$$

By connecting high-pass and low-pass filters to wavelet and scale functions, the DWT may be built efficiently, utilizing filters with perfect reconstruction properties. The research investigates the efficient use of biosensors and ML techniques in the detection of pathogens.

3.4. Enhanced snow ablation optimized adaptive support vector machine (ESAO-ASVM)

This research introduces an ESAO-ASVM model, aimed at improving the classification accuracy and efficiency of intricate biological datasets. The ESAO-ASVM model uses snow ablation processes for optimal performance by energetically adjusting SVM parameters. The advance utilizes adaptive learning mechanisms to handle biological data unpredictability, ensure robust classification, and demonstrate potential for advancing computational biology and bioinformatics application.

3.4.1. Adaptive support vector machine (ASVM)

ASVM is an advanced ML method designed to adaptively adjust its hyperparameters for optimal classification presentation in dynamic or complex data environments. In biosensing technology, ASVM excels in identifying microbial signatures by efficiently handling nonlinear associations and multidimensional data. It uses adaptive learning to refine decision boundaries for better separation of pathogenic microorganisms from benign ones. The ASVM classifier is an ML algorithm for swift pathogen detection, enhancing pattern recognition and analysis, and can categorize high-dimensional attacks, The vector input signal (x) is present in the input layer. In the hidden layer (y), it is considered between the vector of the input signal (x) and the assistance vector (s). The linear outputs O of the buried layer neurons are added together by the output neuron. The detection of DDoS attacks utilizes the ASVM algorithm's advantages, switching information for training characteristic values, determining effective hyperplanes for categorization, and validating the research model with test data shown in Equation (7). **Figure 2** depicts how the input signal vector (x) passes through the hidden layer, where interactions with support vectors (s) occur, and how the output neuron computes the final classification.

$$O = \sum W_i k(x_i s_i) \tag{7}$$

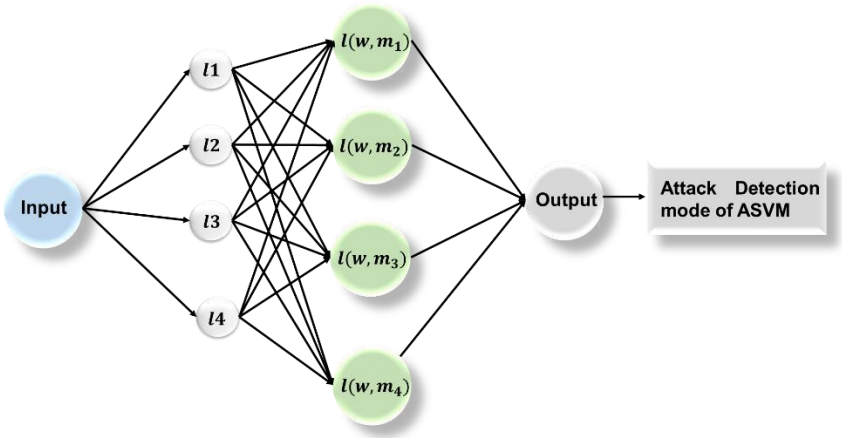

Figure 2. Framework for ASVM architecture.

The ASVM, based on the decision function or hyperplane, addresses unbalanced binary categorization issues as described in Equation (8),

$$z(y) = u^D y + p = 0 \tag{8}$$

With bias denotes $p\epsilon K$ and weighted vector $u\epsilon K^M$. The following represents the constrained issue of an ASVM having a maximum margin hyperplane Equation (9):

$$\underset{u,p,\beta_-,\beta_+}{min} \frac{1}{2}\|u\|^2 + b_-\beta_- + b_+\beta_+ s.t. Y_-u + b_-p \le b_- - \beta_- Y_+u + b_+p \le v_+ - \beta_+\beta_- \ge 0 \tag{9}$$

where the maximal margins of two parallel hyperplanes are represented by the regularization term$\frac{1}{2}\|u\|^2$, and the penalty parameters for controlling the weights between components for the positive and negative classes are b_+ and b_-, respectively. Slack variables for the negative classes and the positive class are $\beta -$and $\beta +$. The training matrix for the negative classes and positive class are denoted by Y_- and Y_+, and the vectors used for the negative classes and the positive class are, respectively, b_- and b_+.

3.4.2. Enhanced snow ablation optimized (ESAO)

ESAO is an optimization algorithm inspired by the natural process of snow ablation, where environmental factors influence the melting and reshaping of snow. In biosensing, ESAO fine-tunes model parameters by simulating this adaptive reshaping to navigate complex search spaces effectively. It is applied to enhance the precision of microbial detection by optimizing the hyperparameters. ESAO balances exploration and exploitation for efficient pathogen identification systems, while snowfall reduces unwanted elements in remedy areas through environmental factors.

i. Initial stage

In ESAO, the iterative procedure starts from a randomly formed swarming. Usually, the complete swarming can be seen as a matrix containing M rows, and Dim columns where M represents the swarm dimensions and Dim is the number of measurements present in the approached areas as shown in Equation (10).

$$Y = K + \theta \times (V - K) = \begin{bmatrix} Y_{1,1} & Y_{1,2} & \dots & Y_{1,C\,im-1} & Y_{1,Dim} \\ Y_{2,1} & Y_{2,2} & \dots & Y_{1,C\,im-1} & Y_{2,Dim} \\ \vdots & \vdots & \vdots & \vdots & \vdots \\ Y_{M-1,1} & Y_{M-1,2} & \cdots & Y_{M-1,C\,im-1} & Y_{M-1,C\,im} \\ Y_{M,1} & Y_{M,2} & \cdots & Y_{M,C\,im-1} & Y_{M,Dim} \end{bmatrix}_{M\times Dim} \tag{10}$$

K Along with V indicates, accordingly, the bottom and higher boundaries of the resulting area. In [0, 1], a number produced at random is denoted through θ.

ii. Exploration stage

ESAO's exploratory strategy involves modeling the unpredictable travel of agents during snow melt or water transformation, using the Brownian motion method. The approach studies events like animal behavior and particle movement using a distribution of normality, mean, and variability to determine the increment size for average Brownian movement (Equation 11).

$$e_{BM}(w; 0,1) = \frac{1}{\sqrt{2\pi}} \times exp(-\frac{w^2}{2}) \tag{11}$$

The procedure for calculating locations during the exploration phase works as follows in Equation (12),

$$Y_j(s+1) = Elite(s) + BM_j(s) \otimes (\theta_1 \times \left(H(s) - Y_j(s)\right) + (1-\theta_1) \times \left(\bar{Y}(s) - Y_j(s)\right) \quad (12)$$

Symbols of $\otimes$ determined entry-level multiplying $\theta_1$represents a figure chosen at randomness by [0, 1] $Y_j(s)$ detects j^{th} entity beyond the s^{th} iterations, as well as $BM_j(s)$. Furthermore, $\bar{Y}(s)$ determines the location of the whole swarm's center, $Elite\ (s)$ represents a single of the numerous experts within the swarms who were selected at erratic, as well as $H(s)$ represents the most suitable answer available at the moment as shown in the Equations (13) and (14),

$$\bar{Y}(s) = \frac{1}{M}\sum_{j=1}^{M} Y_j\ (s) \quad (13)$$

$$\text{Elite(s)} \in [\text{H(s)}, Y_{second}(s), Y_{third}(s),\ Y_d(s)] \quad (14)$$

where $Y_{third}(s)$ along with $Y_{second}(s)$ represent correspondingly. The center of gravity location is chosen for individuals with the highest health scores within the second and third best in the current population, as shown in Equation (15),

$$Y_d(s) = \frac{1}{M_1}\sum_{j=1}^{M_1} Y_j(s) \quad (15)$$

where $Y_d(s)$ represents j^{th} finest boss as well and M_1 one is a set of administrators or half the swarm's total population. $Elite\ (s)$are chosen randomly from a collection of the top three center locations, most effective solutions, second-best job performer, and third-best job throughout the process.

iii. Exploitation stage

The exploiting aspects of ESAO are introduced in the following paragraphs. Instead of expanding with an extremely dispersed characteristic in the remedy region consider using excellent solutions around the present optimal approach when the precipitation evaporates and turns into solid water. A number of the commonly prevalent models for melting snow involve the degree-day method, which shows the procedure for melting as shown in Equation (16),

$$N = CCE \times (S - S_1) \quad (16)$$

wherein CCE differs with the value from 0.35 to 0.6, denotes the degree-days factories. Equation (17) illustrates the iterative values of CCE as follows,

$$CCE = 0.35 + 0.25 \times \frac{f^{\frac{s}{s_{max}}} - 1}{f - 1} \quad (17)$$

where $s_{\max}$ represents the terminated regulations, a melt space for ESAO is as shown in Equation (18),

$$N = \left(0.35 + 0.25 \times \frac{f^{\frac{s}{s_{max}}} - 1}{f - 1}\right) \times S(s), S(s) = f^{\frac{-s}{s_{max}}} \quad (18)$$

Throughout the ESAO exploitation phase, Equation (19) is displayed in the following manner for changing the location.

$$Y_j(s+1) = N \times H(s) + BM_j(s) \otimes (\theta_2 \times \left(H(s) - Y_j(s)\right) + (1 - \theta_2) \times \left(\bar{Y}_j(s) - Y_j(s)\right) \quad (19)$$

The randomized integers θ_2 and N indicate snow melting ratings, making communication easier and allowing people to take advantage of potential places during this time.

iv. Dual population mechanism

Metaheuristic computations compromise between snow accumulation and heat generation, using dual-population techniques to maintain combined investigation and utilization in complex human-like behavior. Research refers to each of these subgroups as $O_b \; and \; O_a$ correspondingly, and the whole populations as O additionally O, O_b as well as O_a dimensions $M,\ M_b, and\ M_a$ correspondingly. O_b Seems trustworthy to the investigation when O_a indicates trustworthiness with exploitations. A dimension O_b through the steady decline in O_a as shown in the Equation (20),

$$Y_j(s+1) = \begin{cases} \text{Elite(s)} + BM_j(s) \otimes (\theta_1 \times \left(H(s) - Y_j(s)\right) \\ +(1 - \theta_1) \times (\bar{Y}(s) - Y_j(s)) \\ N \times H(s) + BM_j(s) \otimes ((\theta_2 \times \left(H(s) - Y_j(s)\right) \\ -(1 - \theta_2) \times (\bar{Y}(s) - Y_j(s)) \end{cases} \quad (20)$$

As mentioned, the community as a whole is a position matrix in Equation (20). $index_b \; and \; index_a$ Add the individuals' numbers to the lines in $O_b \; and \; O_a$. The ESAO algorithm enhances optimization efficiency by utilizing snow ablation techniques, enhancing convergence speed and global search capabilities, and ASVMs are highly effective in complex biosensing tasks. By combining ESAO-ASVM, the method provides a hybrid solution that optimizes parameter selection while maintaining adaptive flexibility, resulting in highly accurate and rapid identification of pathogenic microorganisms in biosensing technology. Algorithm 1 represents the ESAO-ASVM.

Algorithm 1 Enhanced snow ablation optimized adaptive support vector machine (ESAO-ASVM)

```
Initialize parameters for ESAO and Adaptive SVM
Input: Training dataset {(xi, yi)}, SVM parameters (C, kernel type, tolerance),
      ESAO parameters (Population size M, MaxIter, exploration θ1, exploitation θ2)

Adaptive SVM Initialization
Initialize SVM weights (w) and bias (b)
Define the decision function: f(x) = sign (w.T * x + b)

Snow Ablation Optimization
Initialize swarm particles with random positions and velocities
For iter = 1 to MaxIter:
   For each particle i in swarm:
      Evaluate fitness function based on SVM classification error
      Update personal best and global best positions
      Update positions using exploration factor θ1 and refine with exploitation factor θ2
   End For
End For
ESAO-ASVM
For each data point (xi, yi):
   Solve SVM quadratic optimization problem: Minimize ||w||^2 subject to yi(w.T * xi + b) ≥ 1
   If misclassification rate > threshold:
      Adjust SVM parameters (C, kernel) based on ESAO-optimized values
   End If
End For
Return: Optimized Adaptive SVM model (w, b) with ESAO-tuned parameters
```

4. Performance analysis

To achieve an efficient detection of pathogens, this research focuses on the biosensors fused with ML algorithms. The ESAO-ASVM model evaluated metrics such as execution time, memory usage, RMSE, MSE, accuracy loss, SSIM, accuracy, precision, recall, and *F*1-score.

4.1. Experimental setup

This research uses an HP laptop with a 2.10 GHz Intel Core i7-8250U and i7-13700 CPU, 16GB RAM, Windows 10 Pro, and Python 3.12 to implement biosensing technology for rapid identification of pathogenic microorganisms (**Table 3**).

Table 3. Experimental setup.

Processor	**Intel(R) Core (TM) i5-8250U**
Laptop Brand	HP
CPU	Intel Core i7-13700
CPU Speed	2.10 GHz
RAM	16 GB
Operating System	Windows 10 Pro
Python Version	3.12
L3 Cache	6 MB

Table 4 presents performance metrics for biosensing technology, assessing accuracy, efficiency, and resource utilization, comparing the proposed approach with existing methodologies, and supporting real-world biosensing technology. **Table 5** summarizes the findings of performance metrics.

Table 4. Performance metrics and equations.

Equation number	Metrics	Equations
21	RMSE	$\text{RMSE} = \sqrt{n1\sum_{i=1}^{n}(Ai - Fi)2}$
22	Accuracy Loss	$Accuracy\ Loss = 1 - \frac{TP + TN}{Total\ Pixels}$
23	Accuracy	$Accuracy = \frac{TP + TN}{TP + TN + FP + FN}$
24	Precision	$\text{Precision} = \frac{TP}{TP + FP}$
25	Recall	$\text{Recall} = \frac{TP}{TP + FN}$
26	*F*1-score	$F1 - score = 2 \times \frac{Precision \times Recall}{Precision + Recall}$
27	Memory Usage	$Memory\ Usage = Total\ Memory\ Allocated - Memory\ Freed$
28	Execution Time	$Execution\ Time = End\ Time - Start\ Time$
29	MSE	$\text{MSE} = \sqrt{n1\sum_{i=1}^{n}(yi - \hat{y}i)2}$
30	SSIM	$SSIM(w, \widehat{w}) = \frac{(2\mu_y\mu_{\bar{y}} + D_1)(2_{\sigma w\widehat{w}} + D_2)}{(\mu_y^2 + \mu_{\hat{y}}^2 + D_1)(\sigma_w^2 + \sigma_{\widehat{w}}^2 + D_2)}$

Table 5. Outcomes of performance analysis.

Metrics	Values
Execution time	0.58 s
Memory Usage	42%
RMSE	0.01
MSE	0.019
Accuracy loss	0.06
SSIM	80.4
Accuracy	98.5
Precision	95
Recall	94
*F*1-score	96

4.2. Mean squared error (MSE)

MSE quantifies the mean squared discrepancy between expected and actual values. In biosensing, MSE helps to evaluate the accuracy of predictions made by models that estimate the concentration or presence of pathogens (Equation 29). A

lower MSE indicates that the model has better precision in detecting pathogens accurately (**Figure 3a**). The MSE value of the ESAO-ASVM model is 0.019, showing minimal squared prediction error.

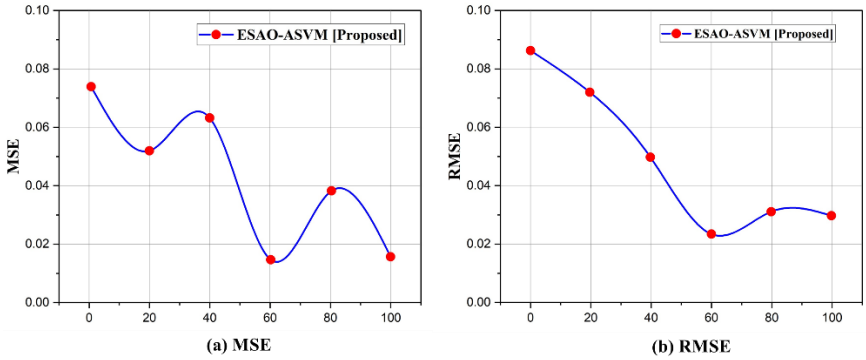

Figure 3. Graphical outcomes of **(a)** MSE and **(b)** RMSE.

4.3. Root mean squared error (RMSE)

RMSE is a metric employed to measure the change and observed principles in biosensing technology (Equation 21). It quantifies the error magnitude, where a lower RMSE indicates better model accuracy in detecting pathogenic microorganisms. This metric is especially relevant when comparing continuous data values such as sensor readings for pathogen detection. The model achieves an RMSE value of 0.01, indicating a low prediction error. **Figure 3** despite an extensive investigation of how the RMSE value of 0.001 indicates the model's high precision in pathogen detection.

4.4. Accuracy loss

Accuracy loss refers to the difference between the theoretical accuracy of the framework and its actual performance in a biosensing system (Equation 22). The model experiences an accuracy loss of only 0.06 during execution. In rapid pathogenic microorganism detection, accuracy loss helps to evaluate the reliability of the sensor in providing correct identifications, with a focus on minimizing the discrepancy between expected and observed outcomes. **Figure 4** illustrates in detail the evolution of accuracy loss in the model performance over iterations in the process of pathogen detection.

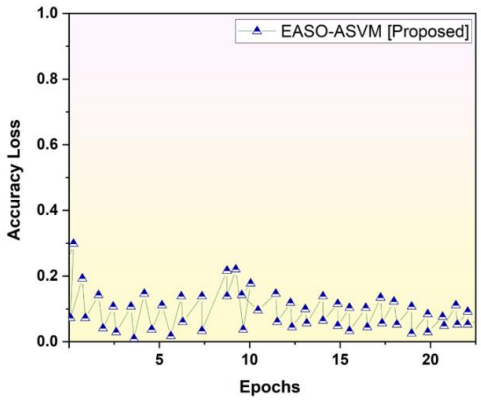

Figure 4. Graphical outcomes of accuracy loss.

4.5. Accuracy

Accuracy is a crucial factor in biosensing systems, as it measures the proportion of correctly identified pathogenic microorganisms in a system, ensuring rapid and reliable real-time diagnostics of pathogens (Equation 23). **Figure 5** depicts that the ESAO-ASVM model reaches a cross-validation accuracy of 98.5%, which means that it correctly identifies 98.5% of all the instances present in the dataset. That is, high accuracy ensures that for real-time pathogen diagnostics, the system is not to frequently misidentify pathogens.

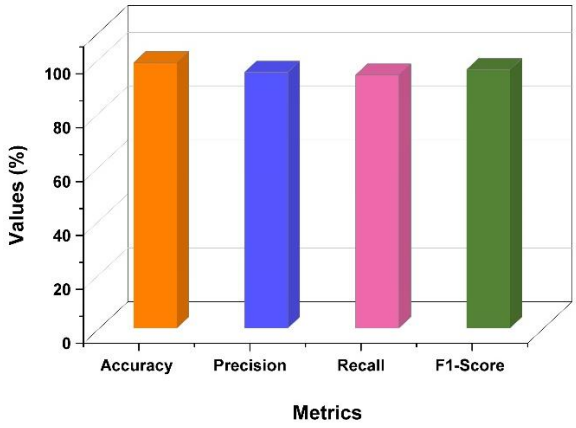

Figure 5. Graphical outcomes of performance analysis.

4.6. Precision

Precision measures a biosensor's ability to accurately identify pathogenic microorganisms, reducing false positives and minimizing the risk of misidentification during detection, as shown in (Equation 24). **Figure 5** shows 95% precision, meaning that the model correctly predicted the positive pathogen predictions. This high precision reduces the false positives and limits the possibility of a false report of the existence of a pathogen when none is actually there, which can be important for avoiding unnecessary treatments or interventions.

4.7. Recall

Recall, also known as sensitivity, measures the ability of the biosensing technology to correctly identify all true pathogenic microorganisms (Equation 25). The system's high recall value indicates its effectiveness in the detecting most pathogens, even in complex environments or at lower concentrations. The ESAO-ASVM model recognizes all of the real pathogens in the dataset, as seen by the 94% recall shown in **Figure 5**. The high recall in the model ensures detection of the majority of pathogens, including those that are available in low numbers or in complex conditions, thereby minimizing the possibilities of false negatives.

4.8. *F*1-score

The *F*1-score is a statistic that combines accuracy and recall to provide an accurate evaluation of a biosensor's performance, especially crucial in the rapid identification of pathogenic microorganisms, where both missed and incorrect

detections must be minimized (Equation 26). **Figure 5** displays a 96% *F*1-score indicating a balance between recall and accuracy. Therefore, it confirms that the model is well performing in minimizing false positives as well as avoiding missed detections.

4.9. Memory usage

Memory usage refers to the amount of computer memory required to process the data from biosensing devices in real-time (Equation 27). Efficient memory usage is crucial for pathogen detection in biosensing systems to handle large sensor data volumes without performance degradation, especially in portable or embedded systems. **Figure 6** demonstrates that ESAO-ASVM utilizes 42% of the available memory when executed. The usage is thus balanced and allows for the processing without degradation in system performance.

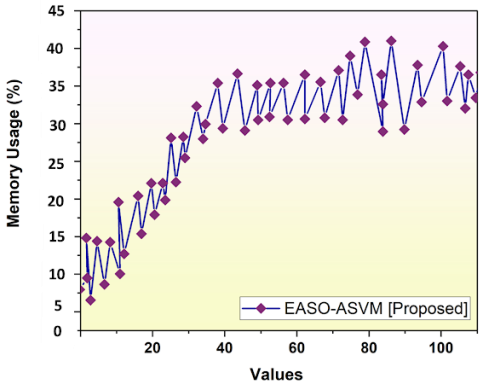

Figure 6. Graphical outcomes of memory usage.

4.10. Execution time

Execution time measures how quickly the biosensing system processes data to deliver results. For rapid identification of pathogenic microorganisms, minimizing execution time is crucial for ensuring that diagnostic results are delivered on time, allowing for quick decision-making and action in clinical or field settings (Equation 28). The ESAO-ASVM model has an execution time of 0.58 seconds, as depicted in **Figure 7**. It can effectively process large amounts of data to provide real-time results.

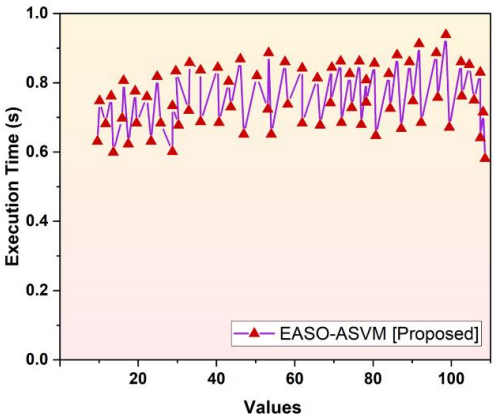

Figure 7. Graphical outcomes of execution time.

4.11. Structural similarity index measure (SSIM)

SSIM is a statistic that evaluates the similarity of two images or signals. It evaluates structural information, luminance, and contrast. In biosensing for pathogen detection, SSIM helps to compare the similarity between original and predicted images of microorganisms (Equation 30). As illustrated in **Figure 8**, the SSIM value of 80.4 clearly indicates that there is a strong correlation between the predicted and actual pathogen images, thereby demonstrating the efficacy of the model for pathogen identification.

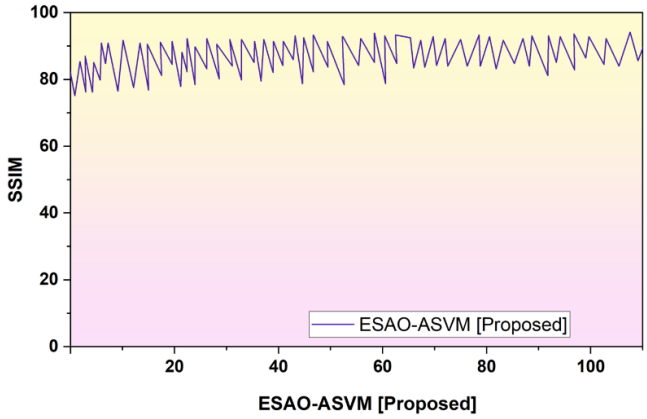

Figure 8. Graphical outcomes of SSIM.

5. Discussion

The limitations with previous research of biosensing systems integrated with ML integration from the numerous challenges are as follows, the generalizability in realistic settings was significantly limited because it relies heavily on specific experimental conditions, including concentration of pathogen and control over the environment. Furthermore, the complexity incurs significant amounts of data pre-processing and augmentation together with parameter tuning before model use. Moreover, detection performances were not stable for different analyses because sensor sensitivities differ in response to a sample type or conditions. Some more problems associated with long detection time, high expense, and the necessity of expensive devices also affect its widespread acceptance and practical implementation in real applications. All these combined factors together affect the scaling-up and in-situ applications of biosensing systems for wide-scale applications. The proposed ESAO-ASVM model presents several advantages compared to the previously developed models: higher accuracy (98.5%), precision (95%), and recall, (94%), which ensure for accurate pathogen detection in real-time scenarios. It integrates ESAO for enhanced optimization and ASVM for accurate classification resulting in faster execution times of (0.58s) and lower memory usage of (42%), thereby making it more efficient for processing large-scale data. Compared to other models, suggested ESAO-ASVM reduces false positives and increases sensitivity, and balances precision and recall, thereby making it appropriate for use in clinical diagnostics, food safety, and environmental monitoring. This is because the proposed model has a higher capacity for handling complex biological data effectively.

6. Conclusion

Biosensing technology has revolutionized the identification of pathogenic microorganisms, offering speed, accuracy, and sensitivity. The integration of nanotechnology, microfluidics, and genetic-based sensors further enhances recognition capabilities. Biosensing technology is crucial for timely diagnostics, patient intervention, food safety, and environmental monitoring. Challenges include standardization, validation, and the development of robust sensors. Despite these challenges, biosensors are expected to continue evolving as a cornerstone of microbial detection in various sectors. The ESAO-ASVM achieved the best outcomes with Execution Time (0.58 s), Memory Usage (42%), RMSE (0.01), MSE (0.019), Accuracy Loss (0.06), SSIM (80.4), Accuracy (98.5%), Precision (95%), Recall (94%), and *F*1-Score (96%).

Drawbacks and future scope: Despite its capable probability, biosensing equipment faces challenges such as limited sensitivity for low-concentration pathogens and the need for better integration with existing diagnostic systems; however, future advancement in nanomaterial, multiplexed sensing, and Artificial Intelligence (AI) incorporation hold the promise of overcome these restrictions and attractive its applicability in dissimilar fields.

Ethical approval: Not applicable.

Conflict of interest: The author declares no conflict of interest.

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26. Dataset from Kaggle: https://www.kaggle.com/datasets/ziya07/biosensing-technology-for-pathogen-detection/data

Appendix

Table A1. Abbreviations and corresponding full forms.

Abbreviation	Full Form
WT	Wavelet Transform
ESAO-ASVM	Enhanced Snow Ablation Optimized Adaptive Support Vector Machine
VOCs	Volatile Organic Compounds
E. coli	Escherichia coli
DNA	Deoxyribonucleic Acid
VOCs	Volatile Compounds
ANN	Artificial Neural Network
CFU/mL	Colony Forming Units per milliliter
TLENTNet	Time-Lapse images driven EfficientNet-Transformer Network
TGRNN	Theory-guided Recurrent Neural Network
GB	Gradient Boosting
SRR	Split-Ring Resonator
PSO-ANN	Particle Swarm Optimization - Artificial Neural Network
MAE	Mean Absolute Error
RMSE	Root Mean Square Error
VAF	Variance Accounted For
R^2	Coefficient of Determination
XGBoost	Extreme Gradient Boosting
CatBoost	Categorical Boosting
DL	Deep Learning
IAM	Inverted All-Dielectric Metagrating
SPR	Surface Plasmon Resonance
K-NN	K-Nearest Neighbors
OFET	Organic Field-Effect Transistor
SVR	Support Vector Regression
AI	Artificial Intelligence
ML	Machine Learning
AF	Adaptive Filtering
SD	standard deviation
DWT	discrete Wavelet Transform
ESAO	Enhanced Snow ablation optimization
ASVM	Adaptive Support vector machine
QP	Quadratic Programming
DDoS	Distributed Denial-of-Service
XS	biosensor position
ω	rotational velocity
θ	angular alignment
RF	random forest
RD	radial displacement

Table A1. (*Continued*).

Abbreviation	Full Form
CRP	Complex reactive proteins
THz	TunablSe terahertz
ECL	Electrochemiluminescence
DTR	Decision tree regressor
TiO_2	Titanium dioxide
KNN	K-nearest neighbors
MIST	Montreal Imaging Stress Task