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Hybrid brave-hunting optimisation for heart disease detection model with SVM coupled deep CNN

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Abstract: This research proposes a novel hybrid optimisation method called brave-hunting optimisation (BHO) inspired by lion optimisation (LO) and coyote optimisation (CO). The BHO algorithm is employed to fine-tune the SVM parameters, enhancing its classification performance. Simultaneously, a deep CNN model extracts complex and informative features from medical data. The combined approach capitalises on the strengths of both optimisation techniques to create a robust and accurate model for heart disease diagnosis. The performance evaluation of our model is conducted using comprehensive metrics, which achieve an accuracy of 94.89%, an F1-score of 94.48%, a precision of 94.48%, and a recall of 94.58% for a 90 TP. In the context of a ten k-fold evaluation, achieved 94.78% accuracy, 94.36% F1-score, 94.55% precision, and 94.13% recall.

Keywords: cardiovascular disease detection; support vector machines; deep convolutional neural network; DCNN; brave-hunting optimisation; BHO; early prediction.

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1 Introduction

The heart serves as the human body’s vital core, accountable for propelling oxygen-influenced blood throughout the human body via veins. Any ailment that disrupts the heart’s normal function is collectively known as cardiovascular disease (Kumar and Rani, 2020; Rani et al., 2021). Heart disorder is a formidable malady that leads to problems like coronary artery infection and diminished function of the blood vessels (Ali et al., 2020; Khan, 2020). Cardiovascular disease often goes unnoticed by patients until it reaches an advanced stage, at which point irreversible damage has typically occurred (Reddy et al., 2021). This cardiac disease encompasses a range of conditions, including symptoms like elevated blood pressure, dysrhythmia, brain attack, and myocardial infarction (Khan and Algarni, 2020). The information provided by the World Health Organization (WHO), says that around 20.5 million people succumb to cardiovascular disease annually, accounting for roughly 31.5% of all global fatalities. Projections suggest that this number could climb to 24.2 million by the year 2030 (Reddy et al., 2021). Shockingly, one-third of these fatalities affect individuals under the age of 70 (Szczepańska et al., 2022). Key risk factors for cardiovascular disease include smoking, becoming old, an unhealthy food intake, elevated cholesterol levels, sedentary lifestyle, Elevated blood pressure, obesity, and Drinking alcoholic beverages (Pirgazi et al., 2022). The domain of medical research has been significantly intrigued by the complex dataset related to heart diseases. Numerous machine-learning techniques have been explored in pursuit of accurately predicting cardiovascular disease (Hassan et al., 2022).

Machine learning (ML) techniques offer a cost-effective and efficient means of developing a system for supporting decision-making for the early detection of cardiovascular disorders using clinical data (Pirgazi et al., 2022). Among these techniques, classification stands out as a powerful method for prediction (Tomov and Tomov, 2018). It operates under the supervision of appropriate training data, effectively identifying diseases such as cardiovascular disease (Reddy et al., 2021). The comprehensive model comprises a combination of a differential evolution (DE) approach, and a feed-forward neural network (FNN) (El-Hasnony et al., 2022). Initially, predictor attributes are carefully selected, followed by a thorough data cleaning process to address data incompleteness and inaccuracies (Rani et al., 2021). The modified DE method is then applied to select the most crucial features. Subsequently, a refined series of features is input into an optimiser to make predictions regarding cardiovascular disease (Dutta et al., 2020; Khan and Algarni, 2020). To further enhance the detection of risk factors in coronary cardiovascular disease treatment, a k-means method coupled with particle swarm optimisation has been developed (Hassan et al., 2022). The data extracted from this process are subjected to classification using multilayer perceptron algorithms. These approaches have demonstrated promising levels of accuracy in their results (Pirgazi et al., 2022). However, it is important to note that the existing studies mentioned above

have certain limitations (Sharma et al., 2020), which need to be addressed before implementing them for cardiovascular disease prediction.

One of the most pressing and formidable challenges in contemporary medicine revolves around the accurate prediction of the onset of cardiovascular disease (Reddy et al., 2021). ML-based analyses often delve into the search for complex, nonlinear associations among tens or even thousands of distinct variables (Botros et al., 2022; Khan, 2020). To harness the full potential of these methods, a substantial volume of training data is imperative. However, in cases where data is abundant, obtaining intricate labels can be a laborious, time-consuming, or costly endeavour (Ponikowski et al., 2014; El-Hasnony et al., 2022). In the preprocessing phase, the majority of researchers opted to handle missing values by either replacing them with the attribute's mean or the most frequent value, ensuring the dataset's comprehensiveness (Ma et al., 2020; Ozaltin and Yeniay, 2023; Sharma et al., 2020). The removal of instances with missing values, although expedient, adversely impacted preprocessing accuracy. Feature selection poses a formidable challenge due to the exponential growth in exploration space, directly proportional to features available in the dataset (Almalchy et al., 2020 Reddy et al., 2021). Within the context of the modified deep convolutional neural network (MDCNN) employing cuttlefish optimisation, the outcomes substantiate that the proposed architecture yields exceptional results by reducing access time overhead. Significantly, this configuration demonstrates the lengthiest key generation time when taking into account validation and transmission durations (Khan, 2020). Furthermore, there are outstanding issues, such as discretising numeric feature values, categorisation, and binning levels. These issues can be addressed through advanced metaheuristic algorithms to fine-tune predictive model parameters and the adoption of enhanced classification algorithms (El-Hasnony et al., 2022).

The contribution of the cardiovascular disease model with SVM coupled deep CNN using sequential data lies in its innovative approach to tackling cardiovascular disease prediction and diagnosis. The cardiovascular disease model that integrates SVM with a deep CNN represents a significant contribution to the field of medical diagnostics. By synergising the strengths of both techniques, it enhances diagnostic accuracy, provides early detection capabilities, and offers interpretable results, all of which are critical factors in improving patient care and healthcare decision-making.

- *SVM coupled deep convolutional neural network (DCNN)*: The hybrid model leverages the strengths of both SVM and CNN. SVMs are effective for handling structured data, while CNNs excel at extracting intricate features from unstructured data like medical data. By combining these two approaches, the model enhances identification accuracy for heart disease.
- *Brave-hunting optimisation (BHO)*: By combining LO and CO, hybrid BHO can achieve a more optimal equilibrium between exploitation and exploration. LO is known for its exploitation capabilities, while CO is more exploratory in nature. The combination helps the algorithm find high-quality solutions efficiently.

The manuscript is organised into clear and separate sections. Section 2 conducts a thorough analysis of the shortcomings present in existing cardiovascular disease detection methods. In Section 3, the mathematical underpinnings of the BHO algorithm and elucidate our devised approach for cardiovascular disease detection, which combines

SVM with DCNN are explained in detail. Section 4 puts forward the results and analysis, while Section 5 conveys the conclusion, summarising the research efforts.

2 Literature review

Pirgazi et al. (2022) devised a novel method for cardiovascular disease diagnosis, leveraging both image and numerical data resources. The methodology involves a multi-step process. First, they harnessed transfer learning with a CNN to get relevant features from the data. The results of their study underscored the critical importance of feature selection, emphasising the choice of an optimal feature subset and the overall performance of such diagnostic systems. However, the use of multiple ML models and feature selection techniques can significantly increase computational complexity. Hassan et al. (2022) employed 11 ML classifiers to enhance the predictability of cardiovascular disease by identifying crucial features. To introduce their predictive model, they utilised various combinations of features and well-established classification algorithms. The results demonstrated improved accuracy, as outlined in the performance table. One of the key challenges ahead involves effectively integrating additional datasets to enhance the reliability of our conclusions in cardiovascular disease detection. Another significant challenge is the optimisation of the ML classifier and deep learning (DL) method parameters. El-Hasnony et al. (2022) presented a manuscript with several goals. First, they aimed to express the effectiveness of active learning algorithms, which allows for the generalisation of findings and outcomes to be applied to new cases, irrespective of whether they are part of the training samples. For, which was achieved through the grid search method. Additionally, the authors addressed several outstanding issues in their research. These challenges included the discretisation of numeric feature values. Furthermore, the manuscript discussed the exploration of enhanced classification algorithms, as an alternative to the label ranking classifier, to further advance the field of cardiovascular disease diagnosis. The primary objective of Khan and Algarni's (2020) research is to pinpoint the crucial attributes in predicting cardiovascular disease through the utilisation of ML techniques. The proposed MSSO-ANFIS framework aims to enhance the search capabilities by incorporating the Levy flight algorithm. ANFIS typically relies on gradient-based learning, which can sometimes get stuck in local minima. To mitigate this, the research optimises the learning parameters using MSSO, thereby yielding improved results for ANFIS. The challenges in this field involve, there is a need to adapt and implement this research using wearable technologies and readily available market products. Rani et al. (2021) introduced a hybridised feature selection algorithm. However, it is essential to acknowledge certain limitations of this proposed system. It can determine whether a person is affected by cardiovascular disease or not but cannot assess the severity of the heart condition. The work by Khan (2020), introduces an IoT framework designed to enhance the precision of cardiovascular disease evaluation, leveraging a MDCNN. This framework incorporates a smartwatch and a heart monitor device. The MDCNN plays a pivotal role in categorising the sensor data received and distinguishing between normal and abnormal patterns. The proposed framework has not been trained and tested using fully wearable devices. Sharma et al. (2020) have introduced an algorithm, which serves as an effective feature selector in conjunction with various ML algorithms. Their research demonstrates that the relational MAPO algorithm is highly proficient in selecting optimal features from diverse relational datasets. It

exhibits exceptional accuracy when applied to a range of datasets, including those related to heart disease, MNIST, and Framingham. Furthermore, there is potential for extending MAPO's utility to create a fully functional mobile application designed for easy and independent use by individuals, minimising the need for external assistance. In the research conducted by Reddy et al. (2021), the research focused on training ten ML classifiers belonging to various categories. This method's outcome underscores the significance of selecting appropriate attributes of the classifiers, as it led to a substantial enhancement in prediction accuracy. To identify cardiac issues, Menshawi et al. (2023) created a hybrid architecture that combines DL and ML techniques. The data pipeline is fully automated, allowing the model to operate in several modes and being impartial toward the quality of the input data; nevertheless, this research does not account for processing time. Chandrasekhar and Peddakrishna (2023) utilised six ML techniques for enhancing heart prediction. Although the research utilised a small quantity of patient data, the models achieve great accuracy in these techniques when the soft voting ensemble classifier is applied. A supervised ML technique, the classification and regression tree (CART) algorithm was utilised by Ozcan and Peker (2023) to forecast heart disease and derive decision rules for elucidating the correlations between input and output variables. Although the research neglected vital patient medical data that could cause cardiac illness, the model exhibits a low error rate, does not indicate overfitting, and can be generalised to new data.

2.1 Challenges

- While the algorithm has demonstrated its potential to yield optimal solutions, it grapples with the issue of inadequate exploration in the search space. Consequently, this search strategy does not assure convergence, particularly when confronted with highly complex, multimodal scenarios in the context of cardiovascular disease prediction (Khan and Algarni, 2020).
- In ML, the learning models may perform admirably on training data but falter when presented with previously unseen data. This phenomenon, often observed in settings with an abundance of covariates, is known as overfitting (El-Hasnony et al., 2022).
- Convolutional neural networks (CNNs) are typically not initially trained, and relying on pre-trained network weights can assist in addressing various issues related to feature extraction and configuration. However, training very deep networks can be intricate and time-consuming, necessitating considerable computational resources (Hassan et al., 2022).
- During the pre-processing stage, many researchers address missing values by either replacing them with the mean value or the most frequently occurring value for that attribute (Reddy et al., 2021).
- Removing instances with missing values during pre-processing can have repercussions on accuracy. Imputing missing data is a complex task, as it involves exploring a vast solution space that expands exponentially with the volume of data in the dataset (Reddy et al., 2021).

2.2 Motivation

The advancement of a cardiovascular disease prediction model is motivated by the pressing need for proactive healthcare solutions in the face of a growing global health challenge. Cardiovascular disease early detection is crucial for effective intervention and prevention. The integration of the prediction model into healthcare technology offers a promising avenue to collect data on key physiological parameters, enabling timely identification of potential heart-related issues. Such a predictive model has the potential to revolutionise healthcare by providing individuals and healthcare providers with valuable insights into their cardiovascular health, allowing for timely interventions, and ultimately reducing the burden of cardiovascular disease on individuals and healthcare systems.

3 BHO-based SVM coupled deep CNN classifier

The purpose of this research is to develop an advanced methodology for cardiovascular disease detection using sensor nodes, incorporating an optimised SVM-coupled deep CNN classifier. Data from patients is collected through sensor nodes and transmitted to a base station, which is collected from the Heart Failure Prediction Dataset (<https://www.kaggle.com/datasets/fedesoriano/heart-failure-prediction>). The research comprises two main phases: pre-processing and classification. Initially, patient data is gathered from the sensor nodes, followed by a rigorous pre-processing phase where data quality is assessed, irrelevant data is filtered out, and missing data is handled. Subsequently, the pre-processed data is fed into the optimised SVM-coupled deep CNN classifier, which not only categorises and labels data vectors but also fine-tunes its hyperparameters using a hybridised BHO approach inspired by lion optimisation (LO) (Yazdani and Jolai, 2016) and coyote optimisation (CO) (Mohamed et al., 2020). Finally, the sensor-based model, developed through this process, determines the presence of heart-related diseases in patient data, classifying it as normal or diseased based on test data. The proposed model is schematically represented in Figure 1.

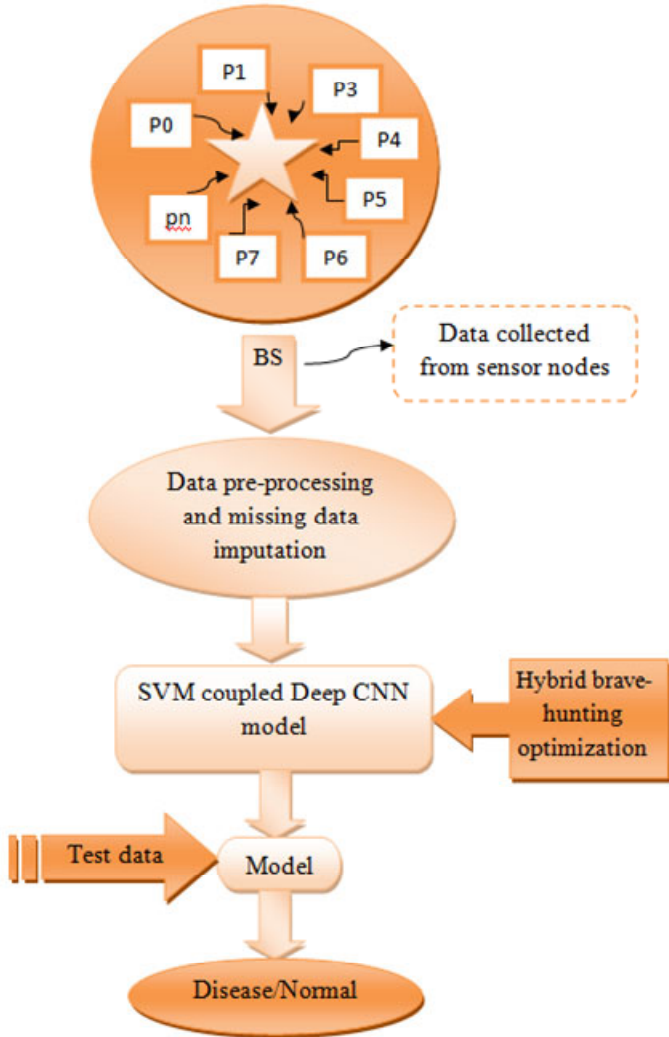
3.1 Input

The Heart Failure Prediction Dataset serves as the crucial input data source for the research. This dataset contains a wealth of information related to heart failure cases, typically including various patient attributes and clinical measurements that can be used to discriminate whether an instance belongs to a healthy or cardiac disease class. The research leverages this dataset as a foundation for training, testing, and validating the cardiovascular disease prediction model. The input data is mathematically mentioned as follows;

$$I = \sum_{i=1}^N H_i \quad (1)$$

where I represents input data, and H_i signifies the quantity of sample contained within the database. The input data is then channelled through the preprocessing phase of the model.

Figure 1 Block diagram of BHO-based SVM-coupled DCNN models (see online version for colours)



3.2 Preprocessing

During the preprocessing stage, data cleaning, normalisation, and handling of missing values are carried out to ensure the dataset's quality and readiness for analysis. Here is an outline of the typical preprocessing steps that may be applied to such a dataset.

- 1 *Data cleaning*: This involves identifying and handling any erroneous or inconsistent data points. Data cleaning may include removing duplicates, correcting typographical errors, and addressing outliers that could skew the analysis.

- 2 *Handling missing data*: Missing data is a common issue in real-world datasets. Various strategies can be employed to deal with missing values, including imputation (replacing missing values with estimates like the mean, median, or mode), removing rows with missing values, or using more advanced imputation methods if appropriate.
- 3 *Splitting data*: The dataset is typically divided into training, validation, and testing subsets. The training data is utilised to train the model, the validation data helps tune hyperparameters and monitor model performance during training, and the testing data is reserved for evaluating the final model's performance.

These preprocessing steps are essential to ensure that the data is in a suitable form for training SVM-coupled deep CNN models and to increase the model's accuracy and reliability. The preprocessed dataset is represented as,

$$I = \sum_{i=1}^N H_i^* \quad (2)$$

where H_i^* is the preprocessed input data. The preprocessed data is then fed to the SVM-coupled deep CNN models.

3.3 SVM-coupled DCNN models:

Utilising an SVM-coupled DCNN model for cardiovascular disease prediction offers several distinct advantages. This hybrid approach combines the strengths of both SVM and deep CNNs. SVMs excel at handling high-dimensional data and are known for their robustness in binary classification tasks, making them compatible for differentiating between cardiovascular disease and non-cardiovascular disease cases (Nguyen et al., 2021). On the other hand, deep CNNs are highly effective in feature extraction from complex data, particularly in scenarios involving spatial data (Li et al., 2019). The SVM component of the hybrid model helps mitigate overfitting, a common challenge in DL, by promoting better generalisation. It enhances the model's capability to make accurate predictions on unseen data, which is crucial in real-world healthcare applications. The integration of deep CNNs allows the model to capture intricate patterns and dependencies within the data, potentially uncovering subtle but critical indicators of cardiovascular disease that might be challenging to identify using traditional methods. The proposed SVM-coupled DCNN architecture is given in Figure 2.

The fundamental operations within a CNN encompass convolution, pooling, and a fully connected layer. Within the convolutional layer, the network extracts various feature maps that highlight specific characteristics within different signals (Nguyen et al., 2021). These feature maps are generated through elements expressed as $\omega_{i,j}[i \leq s, j \leq t]$. Additionally, a bias term, denoted as ω_B , is typically incorporated in each calculation. Therefore, in a general context, the convoluted feature maps denoted as $A_{m,n}$ can be calculated as follows:

$$A_{m,n} = F \left[\sum_{i=0}^s \sum_{j=0}^t \omega_{i,j} X_i + (i, n) + j + \omega_B \right] \quad (3)$$

where $F(\cdot)$ is an activation function, and ω_B is the bias in each calculation. Within the max-pooling layer, the original feature maps undergo segmentation using a non-overlapping window. Let us denote the width and height of this pooling window as ‘ s ’ and the stride as ‘ p ’. In this context, we can represent $s(m, n)$ a novel element within the pooling maps and $a(i, j)$ as a specific value within the feature maps. Consequently, the pooling layer outputs are expressed as follows:

$$s[m, n] = \text{Max}\{A(i, j)\} = \text{Max}\{A[U+1:U+\downarrow S], [V+1:V+\downarrow S]\} \quad (4)$$

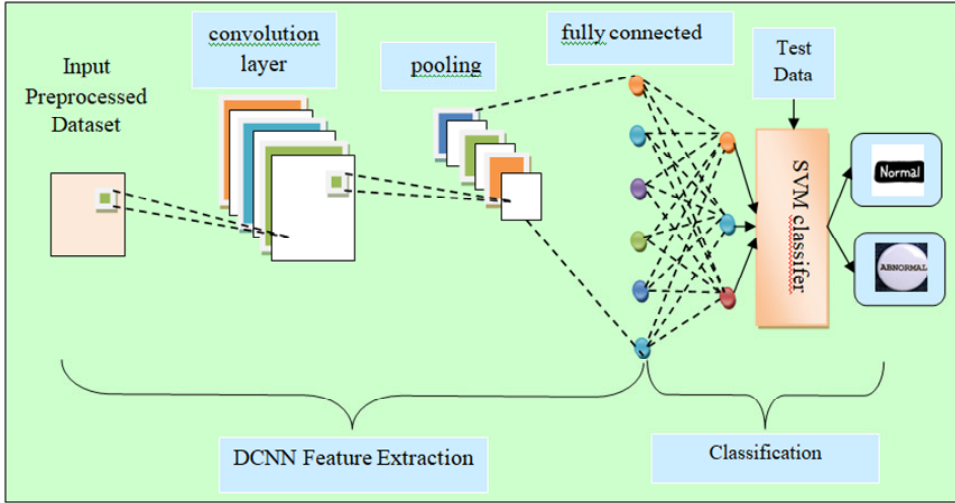
where $U = (m - 1) * p$, $V = (n - 1) * p$. The standard backpropagation algorithm is employed for stochastic learning. During the training phase, weight updates are executed as outlined below:

$$w_L = \left[1 - \frac{j_\tau}{ts}\right] w_{L-1} - \frac{j}{x} \frac{\partial c}{\partial \omega} \quad (5)$$

where ω represent the weight, L the layer number, j the learning rate, τ represent the regularisation parameter, ts represent the training samples, x represent the size of the batch, and c represent the cost function. Furthermore, the biases are adjusted via:

$$B_L = b_{L-1} - \frac{j}{x} \frac{\partial c}{\partial \omega} \quad (6)$$

Figure 2 Proposed SVM-coupled DCNN classifier (see online version for colours)



SVM stands as a robust linear classification technique that transforms multidimensional features into high-dimensional spaces. It achieves this by constructing optimal hyperplanes within datasets while directly maximising the distance (Nguyen et al., 2021). Taking H_i^* the input data intended for classification and C as target or class label belongs to the set $\{-1, 1\}$, the decision function $DF(H_i^*)$ can be formulated as follows:

$$DF(H_i^*) = \omega^T \cdot H_i^* + B, \begin{cases} \omega^T \cdot H_i^* + B \geq 1; C_i = +1 \\ \omega^T \cdot H_i^* + B < 1; C_i = -1 \end{cases} \quad (7)$$

where ‘ ω ’ represents weights and ‘ B ’ denotes bias, the streamlined expression using an inequality constraint, of the above equation is presented in the formula below:

$$C_i [\omega^T + B] \geq 1; \left\{ \left| DF(H_i^*) \right| \geq 1 \right. \quad (8)$$

To widen the gap between class divisions (normal/abnormal), an SVM can attain the optimal hyperplane by minimising the weight parameter while staying within the constraints defined in equation (8).

$$\text{Min}_{\omega, B, \psi} \frac{1}{2} \|\omega\|^2 + R \sum_{i=1}^N \psi_i \cdot s \cdot t \cdot C_i [\omega^T \cdot H_i^* + B] \geq 1 - \psi_i; i = 1..N, \psi_i \geq 0, i = 1..N \quad (9)$$

Here, ψ_i represents a slack variable, and R stands for the regularisation parameter. When instances tend to overlap with other classes, it is possible to minimise the margin to enhance classification accuracy by increasing the value of ψ_i , and conversely, decreasing ψ_i can widen the margin (Nguyen et al., 2021). The pursuit of the optimal solution for the inequality described in equation (9) is tantamount to seeking a solution for the double problem. Consequently, the Lagrange equation is formulated based on the imposed constraints.

$$\text{Max } L[\omega, B, A] = \frac{1}{2} [\omega^T \omega] - \sum_{i=1}^N \gamma_i [C_i (\omega^T \cdot H_i^*) - 1], \text{ s.t. } 0 \leq \gamma_i \leq R \quad (10)$$

In this equation, the variable γ represents the Lagrange multiplier. The maximum or extreme value of this function can be computed concerning both ω and B . Consequently,

$$\frac{\partial L(\omega, B, \gamma)}{\partial \omega} = 0 \text{ and } \frac{\partial L(\omega, B, \gamma)}{\partial B} = 0 \quad (11)$$

Then the classification decision function is represented as,

$$DF(H_i) = \text{SIGN} \left\{ \sum_{i=1}^N \gamma(i) * C(i) [x \cdot \lambda(i) + 1] + B^* \right\} \quad (12)$$

where λ is the training sample in the decision factor of the input data sample.

Optimisation algorithms are an important need in an SVM coupled-DCNN model for heart disease prediction to fine-tune the model parameters and minimise the prediction error. They help the model learn complex patterns within the data, improving accuracy and ensuring the algorithm generalises well to unseen cases. Optimisation enhances the model’s ability to identify subtle correlations in diverse patient datasets, ultimately leading to more reliable predictions in heart disease. Therefore, the weight and biases of the classifier are tuned by the BHO to enhance the models’ performance in heart disease diagnosis. Here, the BHO is used to find the best solutions that make the model detect the diseases efficiently. This optimisation tunes the classifiers by modifying the weight and bias with the solution obtained in each iteration and checks the performance of the model. The process keeps going until it finds the best solution and modifies the weight and bias

based on the attained best solution to detect the diseases more efficiently. The working of BHO is explained as follows.

3.4 *Brave-hunting optimisation*

Heart disease detection can involve searching for the best solution in a global search space with multiple optimal configurations. The development of hybrid optimisation ensures that the process is not stuck in local optima and explores various promising solutions with fast convergence. Therefore, a hybrid BHO is developed by combining the characteristics of LO and CO. LO and CO bring unique search strategies inspired by nature, which can help explore diverse regions of the solution space. This hybrid characteristic can tackle complex and high-dimensional optimisation problems related to fine-tuning the weight and bias of the classifiers used for heart disease diagnosis. Here, the BHO is designed to address quadratic programming (QP) problems encountered in the SVM training process. A QP problem is a type of mathematical optimisation problem that deals with quadratic objective functions and linear constraints. LO and CO operate using different search strategies. LO mimics the hunting behaviour of lions, emphasising a focused and targeted search, while CO models the collaborative hunting behaviour of coyotes (Ali et al., 2017), which involves more distributed exploration. This diversity in strategies can be beneficial for solving complex optimisation problems. LO tends to excel at local optimisation, fine-tuning solutions around a local optimum. In contrast, CO has the potential to explore a broader solution space, which can help discover global optima. Hybrid BHO's ability to explore different regions of the search space can help solutions escape from local optima. Hybrid BHO can capitalise on this feature to avoid getting stuck in suboptimal solutions. The leverages both capabilities, making it suitable for problems with both local and global optima. The combination of LO and CO can make the optimisation process more robust to noisy or uncertain objective functions, as the algorithm's diversity allows it to adapt to changing conditions. By combining two effective optimisation techniques, it increases the likelihood of finding high-quality solutions to the QP problem.

3.4.1 *Motivation*

LO is inspired by the hunting characteristics of lions in a pride, where lions collaboratively capture the prey. LO incorporates a social interaction strategy where the solutions (representing lions) cooperate and share information to find the optimal solution. LO is known for its exploration capabilities and collective intelligence (Yazdani and Jolai, 2016). On the other hand, CO is inspired by the cunning and persistence of coyotes in their pursuit of prey. CO focuses on the exploitation of the search space and the adaptation of solutions to achieve a better fitness value. CO excels in fine-tuning solutions and exploitation of local optima (Pierezan and Coelho, 2018; Abdelwanis et al., 2020; Diab et al., 2020). By combining these standard optimisation techniques, BHO Optimisation aims to strike a balance between exploration and exploitation. It leverages the collaborative and information-sharing aspects of LO while incorporating the adaptive and solution-refinement traits of CO. This fusion results in an optimisation algorithm that can effectively navigate complex search spaces, adapt to changing conditions, and converge to high-quality solutions. Overall, BHO represents a hybrid approach that takes

advantage of the strengths of both LO and CO, making it a promising choice for optimisation problems, with diverse and challenging data.

3.4.2 Mathematical model of BHO

1 Initialisation

Hybrid BHO is an evolutionary algorithm that combines nature-inspired optimisation techniques, LO and CO, to solve complex optimisation problems. The initialisation process in BHO is a crucial step that sets up the initial population of candidate solutions for the optimisation process. Before starting the initialisation process, certain parameters for the algorithm, such as the population size, maximum number of generations, and other control parameters for LO and CO. LO are used as the primary optimisation technique in BHO. LO mimics the hunting behaviour of lions. In the initialisation phase, randomly generate an initial population of potential solutions, represented as a set of lions. CO is used as a supplementary optimisation technique in BHO. Similar to LO, initialise a population of potential solutions, represented as a set of coyotes.

2 Evaluation of cost function

For each candidate solution in the population, which was generated during initialisation or evolved through iterations), apply the objective function to calculate its fitness. These values are used to rank the solutions in terms of how well they perform concerning the optimisation goal. Usually, smaller values suggest superior solutions for minimisation challenges, whereas larger values indicate superior solutions for maximisation tasks. The cost function is evaluated using the condition if $t < t_{\max}$.

3 Selection of search space (if $\$ < 0.9$)

The selection of the search space is crucial to emulate the behaviour of resident male lions in pride. The algorithm aims to mimic the way resident male lions roam within their territory and adapt their positions to find better solutions. The resident male lion starts exploring this selected portion of the solution space. This lion corresponds to a candidate solution in the optimisation problem. As the lion roams, if it visits a new position within the selected territory that is better (according to the optimisation objective) than its present best-known position, it updates its best-visited position (Yazdani and Jolai, 2016). This is similar to a lion marking a new, better position within its territory. The threshold is typically a convergence criterion that indicates when the algorithm should stop searching for a better solution. Here is how the threshold is defined for the optimisation process:

$$Th = d_{\max} - (d_{\max} - d_{\min}) + \frac{(F_{\max} - F_{\min})}{F_{\max}} \quad (13)$$

where $d_{\max}$ is the maximum distance between the territory and the hunter, $d_{\min}$ is the minimum distance between the territory and the hunter, $F_{\max}$ is the maximum fitness of the hunter X_i , and $F_{\min}$ is the minimum fitness of the hunter X_i .

4 Encircling phase (if $\delta < Thr$)

The strategy involves creating a circular-shaped neighbourhood around a target, which could be seen as prey or a point of interest within the search space. The primary purpose of this strategy is to enable hunters or search agents to approach the target from various directions simultaneously. This can potentially increase the efficiency of the search process. Another advantage of this strategy is that it allows solutions to escape from local optima. Local optima are points in the search space where a solution may appear to be optimal but is not necessarily the global optimum. By employing opposite positions, some search agents can explore different regions and avoid getting stuck in local optima. Encircling prey refers to a particular strategy or behaviour inspired by coyotes in nature. Coyotes are known to use tactics like encircling when hunting prey (Ali et al., 2017). They work together to surround and corner their prey, increasing their chances of a successful hunt. The hunter position in the encircling phase is,

$$X^{t+1} = \begin{cases} \frac{1}{2} [rand(2P^t - X^t) + X^* - c_1 c_2], & \text{if } F(X^t) > F_{\max} \\ \frac{1}{2} [rand(P^t - X^t) + c_3 \cdot X^* - X^t], & \text{otherwise} \end{cases} \quad (14)$$

where X^* is the best solution for hunters, c what are the coefficient factors, and P^t is the escape position. This strategy involves creating a circular neighbourhood around a target, enabling multiple search agents to approach the target from various directions, and preventing them from being trapped in local optima by using opposing positions. The coefficient factors in the encircling phase are,

$$c_1 = 2 \cdot d_1 \cdot r - d_1 \quad (15)$$

$$c_2 = 2 \cdot r \quad (16)$$

$$c_3 = [0, 1] \quad (17)$$

where d is the distance between the best solution of hunter X^* and hunter position X^t , and r is the random value $[0, 1]$.

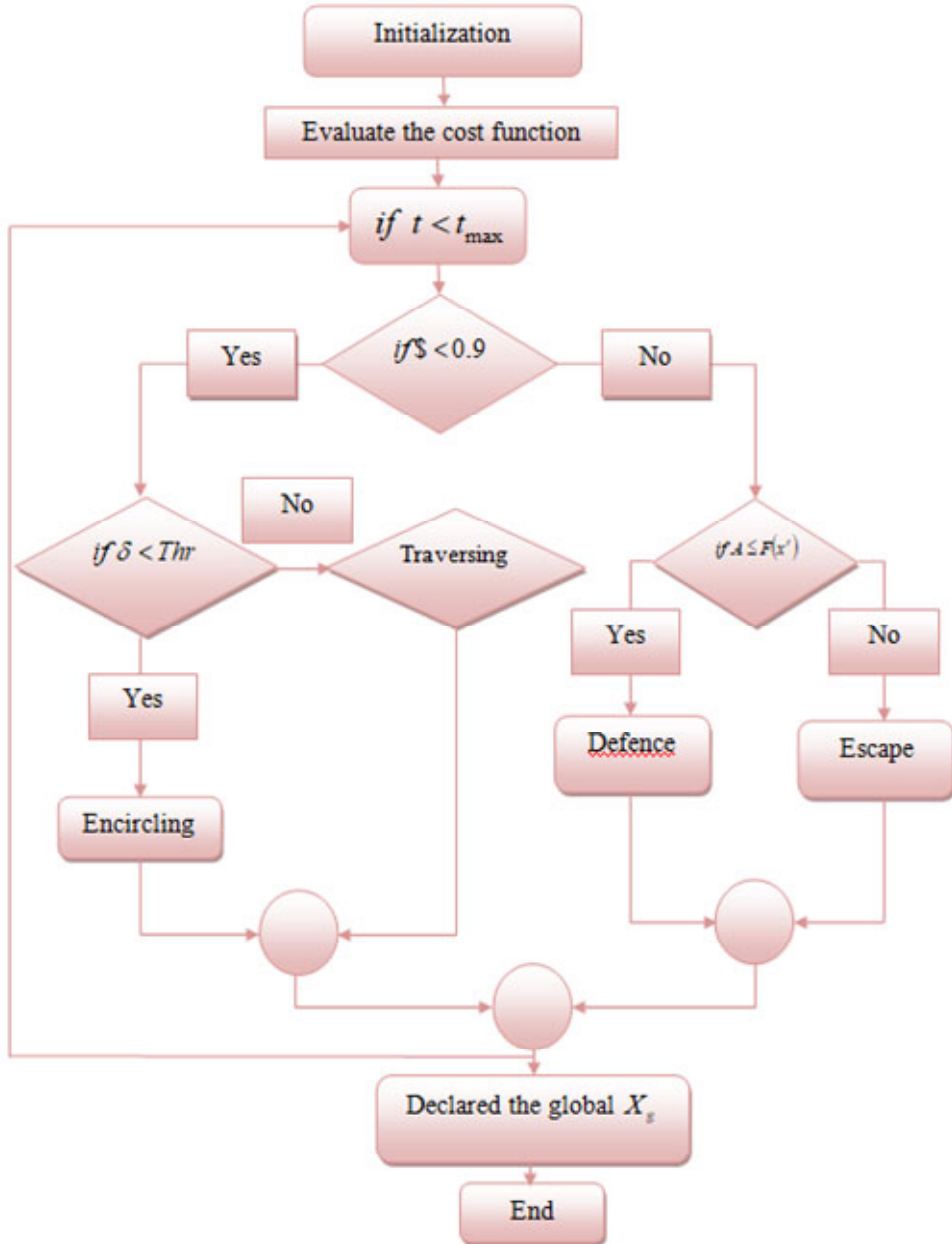
5 Traversing phase

During the traversal phase, lions may use their memory to influence their movement within the search space. They can consider information from past solutions to determine where to explore next. This allows the algorithm to revisit regions of the search space that have shown promise in the past. Lions may adjust their movement based on what they remember. If a particular region of the search space has yielded good solutions in the past, they may focus their exploration efforts in that direction. Conversely, if they remember regions with poor solutions, they might avoid those areas. The ultimate goal of this phase, like any other optimisation algorithm, is to identify an optimal solution within the search space by leveraging the historical knowledge stored in the lions' memory. If they find solutions that are better than what they have stored, they replace their memory with these new solutions. The new updated hunting position in the traversal phase is given as,

$$X^{t+1} = X^t + \text{rand}(X^{t+1} - X^t) + \text{rand}(X_{\text{per}} - X^t) + \alpha \cdot X^{t-1} + \frac{1}{2}\alpha(1-\alpha)X^{t-3} \quad (18)$$

where X_{per} is the personal best, and α is the search order with a value of $[0, 1]$.

Figure 3 Flow chart of the BHO algorithm (see online version for colours)



6 Defence phase (if $A \leq F(x^t)$)

The defence phase refers to the behaviours and strategies employed by male lions to defend their pride from various threats, including challenges from other mature resident males and nomad males. The defence operator is mentioned as part of the LOA, suggesting that this algorithm incorporates aspects of lion behaviour to optimise solutions by retaining powerful individuals as part of the algorithm's process. The hunter's position in the defence phase when the strength of the enemy is less the lion is given as follows:

$$X^{t+1} = \frac{1}{2} \left[\text{Rand} * \exp \left(\frac{X_{\text{worst}}^t - X^t}{X_{\text{max}} - X_{\text{min}}} \right) + P^t + (X^t - X^{t-1}) \right] \quad (19)$$

where X_{worst}^t is the worst hunting position, and P^t is the hunter escape position.

7 Escape phase

An escape phase refers to a phase or mechanism within the algorithm designed to help solutions or search agents escape from local optima. The escape phase is crucial for preventing premature convergence to suboptimal solutions and promoting global exploration, which is specified as follows:

$$P^{t+1} = P^t + \text{rand} * F_I * (P^t - X^t) + r_3 \zeta_1 + r_4 \zeta_2 \quad (20)$$

where F_I is the improvement percentage in the hunter's fitness value, ζ_1 and ζ_2 are the escape factors that decrease from 2, when escape probability is high otherwise $\zeta_1, \zeta_2 = 0$, and $r_3, r_4 \in [0, 1]$. If the global best position is not obtained revert back to fitness function evaluation or else end the process. The flow chart of the BHO optimisation is shown in Figure 3 and the pseudo-code of the BHO optimisation is depicted in Algorithm 1.

Algorithm 1 Pseudo code of BHO optimisation (see online version for colours)

Pseudo code of brave-hunting optimisation	
Initialisation	
Evaluate the cost function	
While $t < t_{\text{max}}$	
do	
if $\$ < 0.9$	
{	
if $\delta < \text{Thr}$	
{	
Encircles and approach the target	
}	
else	
{	
Consider information from the past and find the best solution	
}	

```

    }
else
    {
        if  $A \leq F(x')$ 
        {
            Updates the hunter position in the defence phase
        }
    else
        {
            Escapes from local optima and updates the solution
        }
    }
    }
    Declare the global best solution
    Terminate

```

4 Result

The outcomes obtained while detecting cardiovascular disease with the suggested BHO-based SVM-coupled DCNN classifier are shown within the following categories.

4.1 Experimental setup

The research employs the software Python on Windows 11, operating on a system with 16 GB of RAM, to analyse the heart-failure-prediction dataset (Heart Failure Prediction Dataset, <https://www.kaggle.com/datasets/fedesoriano/heart-failure-prediction>).

4.1.1 Dataset description

Heart Failure Prediction Dataset (<https://www.kaggle.com/datasets/fedesoriano/heart-failure-prediction>): CVDs frequently lead to heart failure, and this dataset encompasses 11 distinct features that can be harnessed for predicting potential heart diseases. For individuals afflicted with CVDs or those facing a heightened CVD risk due to various factors such as diabetes, hypertension, hyperlipidemia, or pre-existing medical conditions, early detection, and effective management are imperative. This extensive cardiovascular disease dataset represents a groundbreaking effort to amalgamate previously disparate datasets. By harmonising data from five distinct sources – Cleveland with 303 observations, Hungarian with 294, Switzerland with 123, Long Beach VA with 200, and Stalog (Heart) data-set with 270 observations – this compilation boasts a staggering total of 1,190 observations. After meticulously addressing duplicates, a total of 272 were identified and subsequently removed. The resultant final dataset, encompassing 918 observations, is available for cardiovascular disease research to date.

4.2 Metrics used

The BHO-based SVM-coupled DCNN classifier is assessed using specific criteria, containing accuracy, F1-score, recall, and precision, as elaborated in the subsequent section.

4.2.1 Accuracy

It is defined as the proportion of correctly identified samples by the DCNN classifier coupled with the SVM algorithm based on BHO when used for cardiovascular disease prediction. Evaluating accuracy is useful for providing a general overview of the model's performance. This measure is expressed as follows:

$$H_{acc} = \frac{H_{TP} + H_{TN}}{H_{TP} + H_{FP} + H_{TN} + H_{FN}} \quad (21)$$

where H_{TP} – true positive value, H_{FP} – false positive value, H_{TN} – true negative value, and H_{FN} – false negative value.

4.2.2 Precision

Precision measures the accuracy of positive predictions made by the BHO-based SVM-coupled DCNN classifier which is crucial in heart disease diagnosis. High precision indicates a low rate of false positives and minimises the chance of misclassifying a healthy patient as having heart disease.

$$H_{pre} = \frac{H_{TP}}{H_{TP} + H_{FP}} \quad (22)$$

4.2.3 Recall

Recall is established by dividing the count of true positives by the total count of positive instances. High recall is crucial in heart disease diagnosis, as it avoids false negatives ensuring that individuals with heart diseases are correctly identified and not missed.

$$H_{recall} = \frac{H_{TP}}{H_{TP} + H_{FN}} \quad (23)$$

4.2.4 F1-score

An ML evaluation metric called the F1-score evaluates a model's accuracy. It merges a model's precision and recall ratings. It provides a balanced assessment of the model's performance, considering both false positives and false negatives. F1-score is valuable in heart disease diagnosis where the high F-score ensures a good balance between identifying actual cases and minimising false positives.

$$H_{F1-S} = \frac{H_{TP}}{H_{TP} + \frac{1}{2}(H_{FP} + H_{FN})} \quad (24)$$

4.3 Performance evaluation

The assessment of the BHO- SVM-coupled DCNN performance across 100 to 500 epochs is examined within the subsequent sections.

4.3.1 Performance evaluation based on training percentage (TP)

Figure 4 shows the performance of the BHO-based SVM-coupled DCNN classifier method for different epochs with varying TP as 40%, 50%, 60%, 70%, 80%, and 90%. In the context with 90% of training, the model is trained on a large portion of the dataset, allowing it to learn intricate patterns and relationships within the data, this can lead to a well-fitted model with high accuracy on a training set. So, the results obtained at TP 90% are described below. At 90% TP, the accuracy of the BHO-based SVM-coupled DCNN model is 91.17%, 91.34%, 91.61%, 94.09%, and 94.80% as shown in Figure 4(a). Likewise, for F1-Score, the BHO-based SVM-coupled DCNN classifier accomplishes the values of 90.17%, 90.24%, 90.71%, 93.25%, and 94.28% at 90% TP as shown in Figure 4(b). At 90% TP, for precision, the BHO-based SVM-coupled DCNN model attains 91.63%, 92.21%, 93.83%, 94.37%, and 94.74% as shown in Figure 4(c). Also, for recall, the BHO-based SVM-coupled DCNN classifier accomplished the values of 72.70%, 88.62%, 88.84%, 89.97%, and 94.75% at 90% TP as shown in Figure 4(d) for varying epochs.

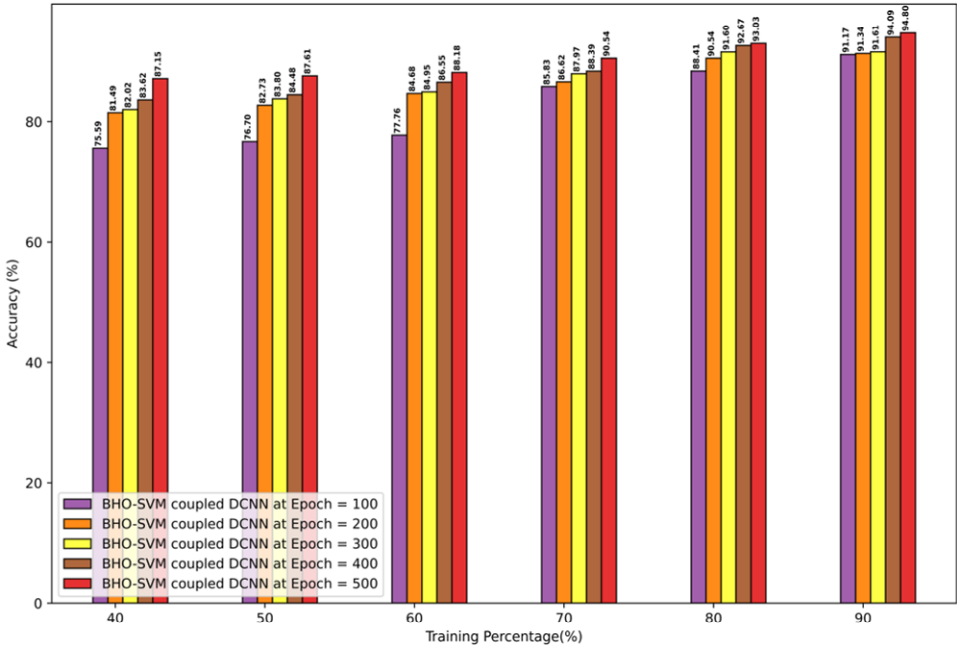
4.3.2 Performance evaluation with K-fold analysis

The performance of the BHO-based SVM-coupled DCNN classifier method for different epochs with different k-fold values 6, 7, 8, 9 and 10 is shown in Figure 5. In a ten-fold cross-validation scenario, the dataset is divided into ten subsets. The model is trained on nine folds and tested on the remaining one, repeating this process ten times with a different fold as the test set each time. This provides a more robust evaluation reducing the impact of dataset variability. The model's performance is averaged across all folds, offering a more reliable estimate of its generalisation ability. This approach helps to determine whether the model performs consistently across different subsets of the data, providing insights into its stability and effectiveness in various scenarios, and the results on ten k-fold are detailed as follows. At ten K-fold, the proposed model attained an accuracy of 76.88%, 83.76%, 90.26%, 93.97%, and 94.69% as shown in Figure 5(a). Similarly, for F1-Score, the BHO-based SVM-coupled DCNN classifier accomplishes the values of 77.59%, 84.98%, 90.62%, 93.40%, and 94.86% at 10 K-fold as shown in Figure 5(b). At ten K-fold, for precision, the BHO-based SVM-coupled DCNN model attains 76.54%, 83.54%, 90.11%, 92.78%, and 94.82% as shown in Figure 5(c). Also, for recall, the BHO-based SVM-coupled DCNN classifier accomplished the values of 77.06%, 84.74%, 90.52%, 91.85%, and 94.71% at ten K-fold as shown in Figure 5(d) for different epochs.

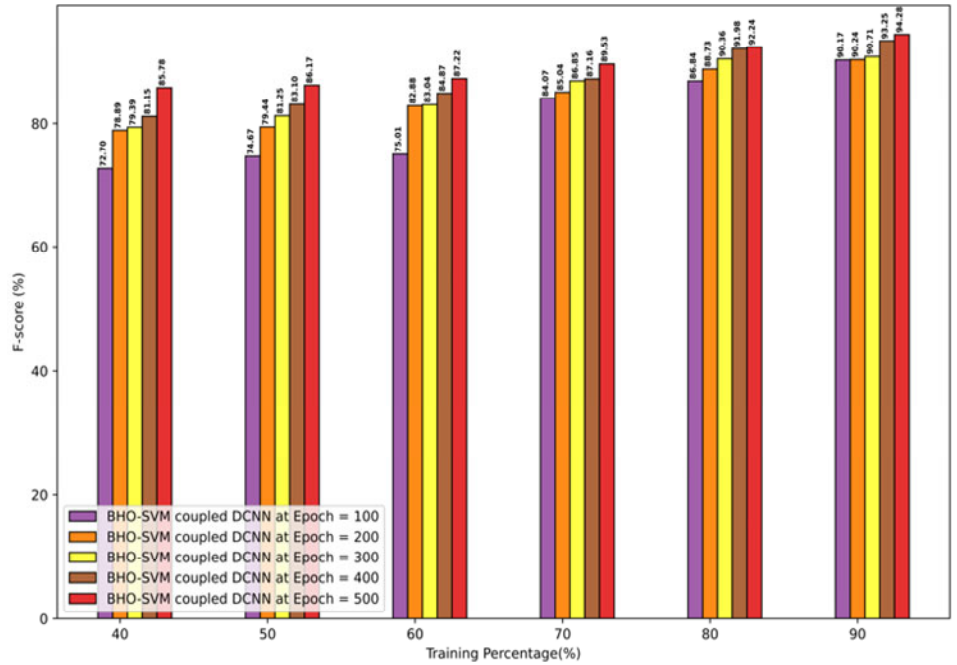
4.4 Comparative analysis for the proposed BHO-based SVM-coupled DCNN

A comparative examination of the SVM-enhanced DCNN utilising BHO Optimisation entails assessing its performance metrics concerning those reported in earlier research studies.

Figure 4 Analysis with TP (a) accuracy, (b) F1-score, (c) precision, and (d) recall (see online version for colours)

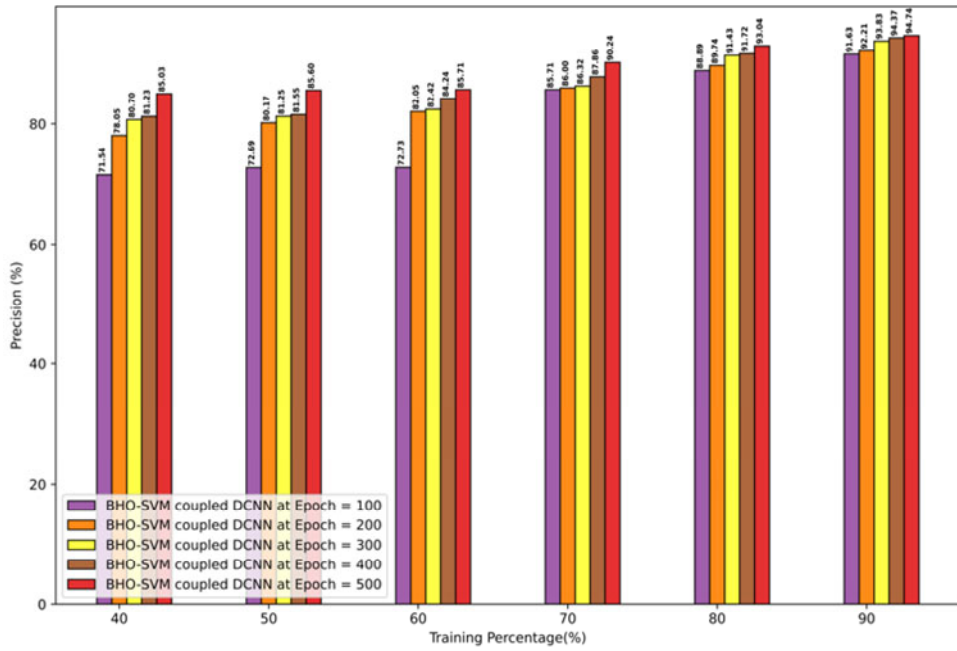


(a)

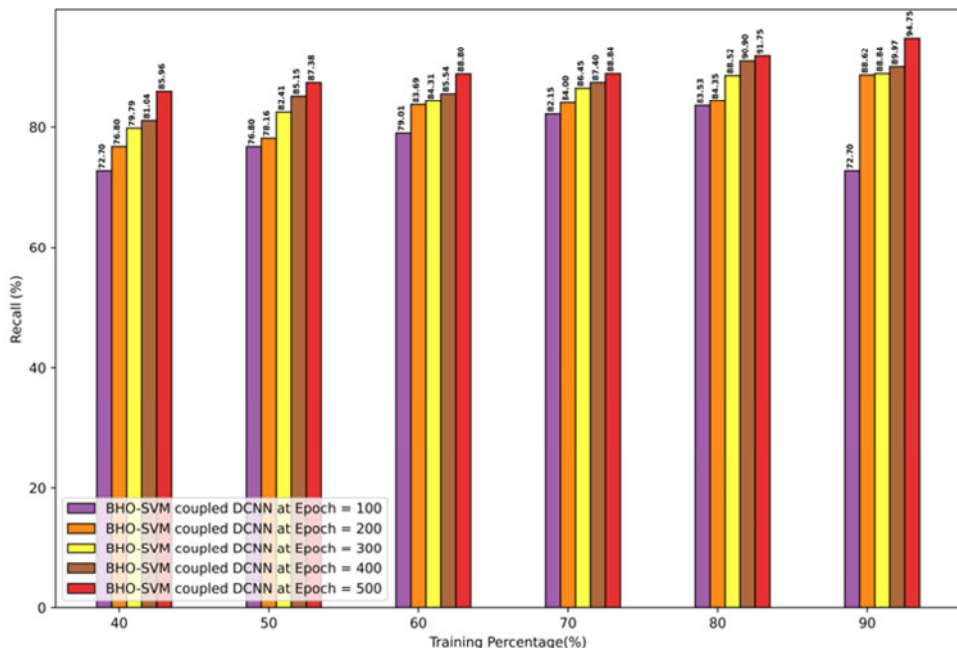


(b)

Figure 4 Analysis with TP (a) accuracy, (b) F1-score, (c) precision, and (d) recall (continued)
(see online version for colours)

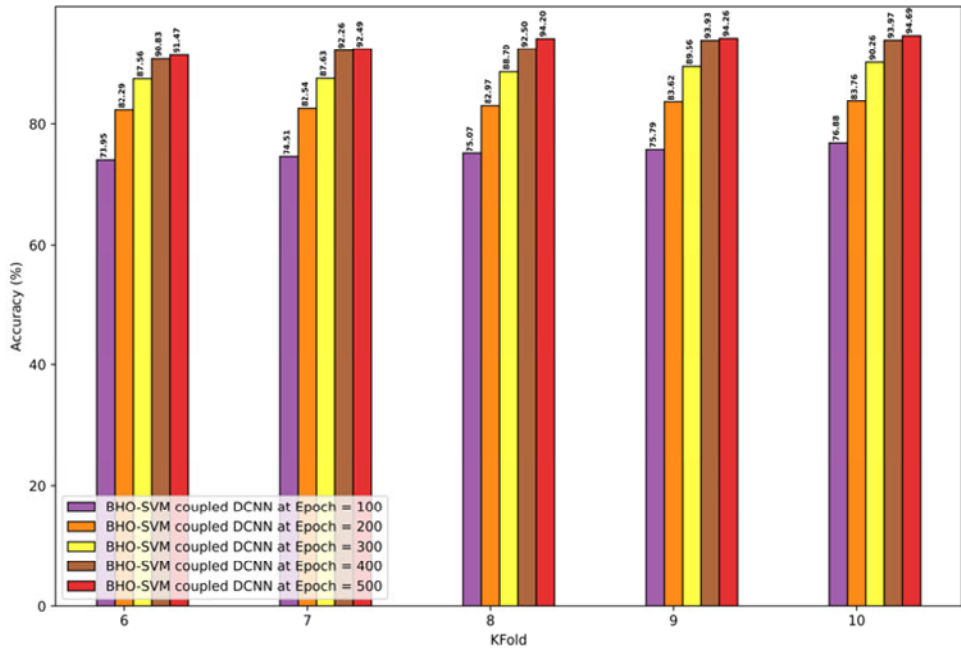


(c)

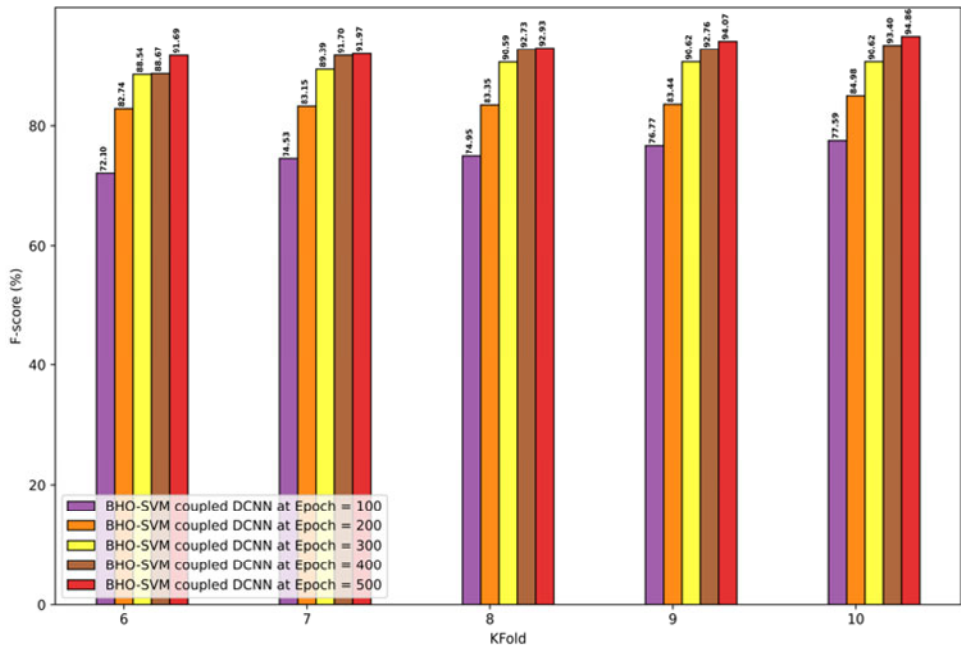


(d)

Figure 5 Analysis with K-fold (a) accuracy, (b) F1-score, (c) precision, and (d) recall (see online version for colours)

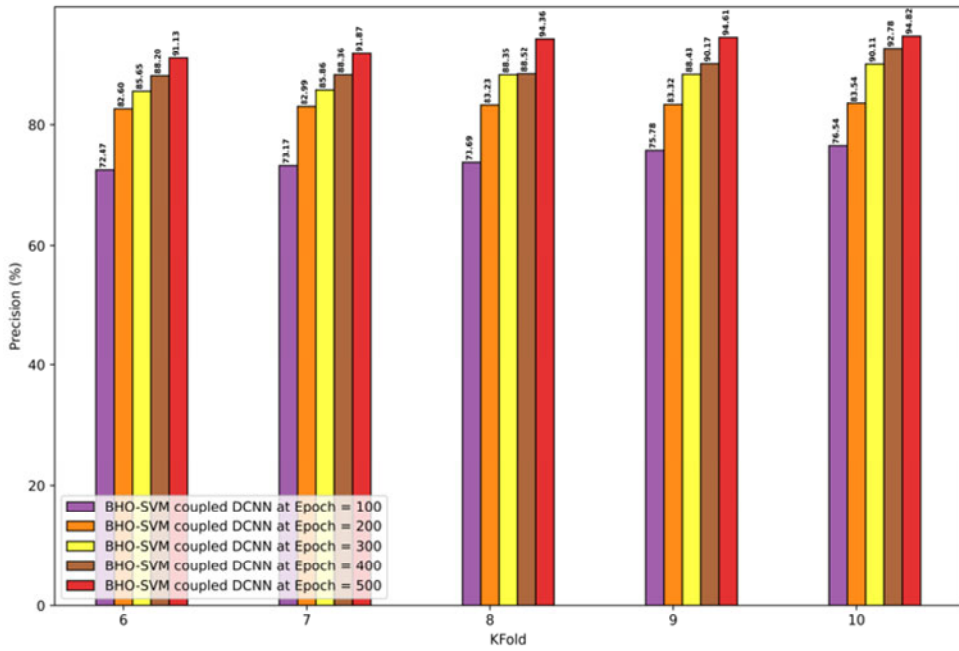


(a)

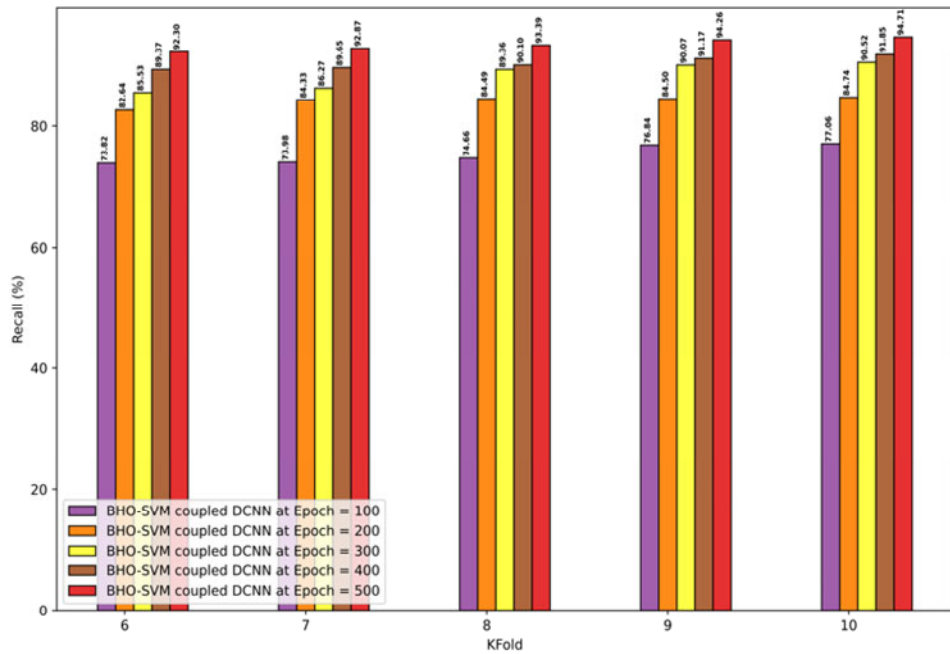


(b)

Figure 5 Analysis with K-fold (a) accuracy, (b) F1-score, (c) precision, and (d) recall (continued) (see online version for colours)

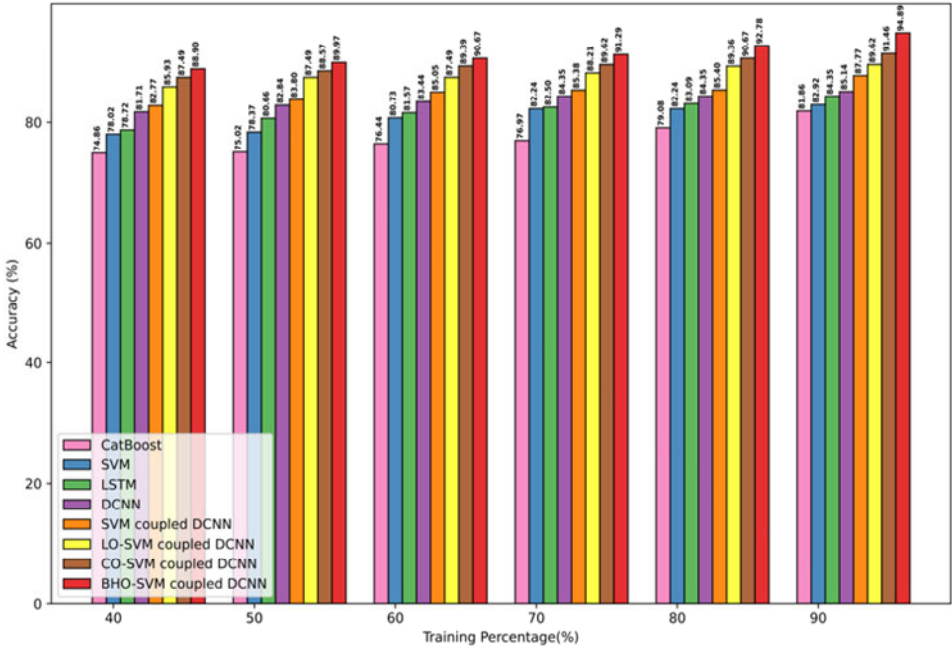


(c)

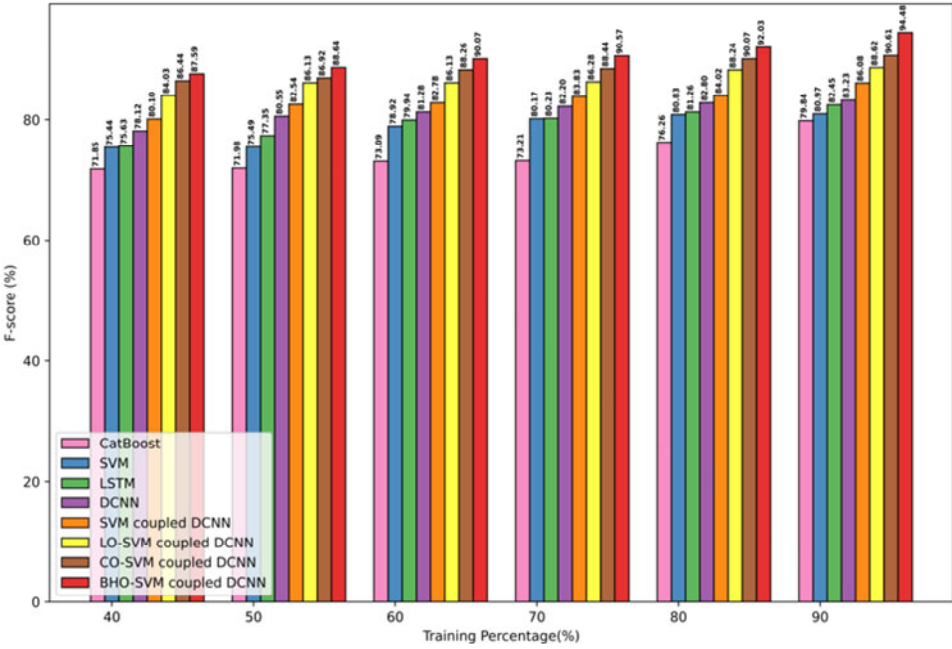


(d)

Figure 6 Comparative analysis based on TP in terms of (a) accuracy (b) F1-score, (c) precision, and (d) recall (see online version for colours)

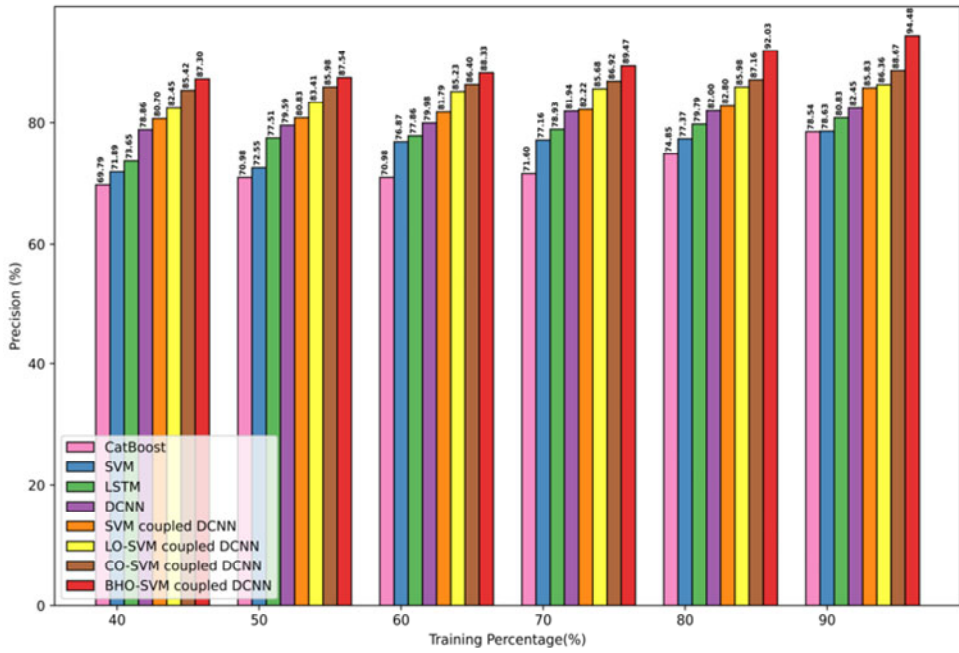


(a)

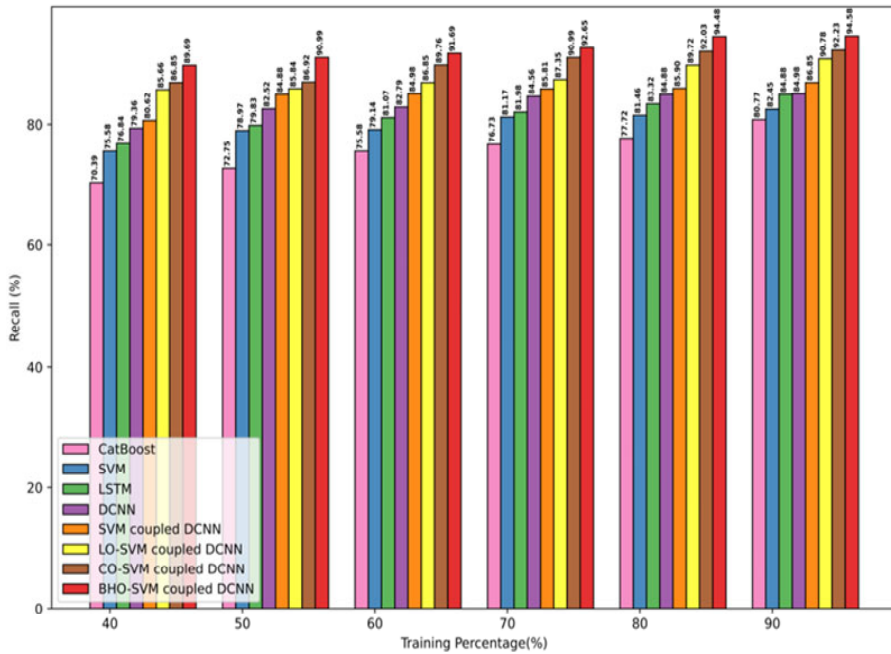


(b)

Figure 6 Comparative analysis based on TP in terms of (a) accuracy (b) F1-score, (c) precision, and (d) recall (continued) (see online version for colours)



(c)



(d)

4.4.1 *Comparative methods*

The BHO-based SVM-coupled DCNN is evaluated with category boosting (CATBOOST) (Dhananjay and Sivaraman, 2021), SVM (Gokulnath and Shantharajah, 2019), long short-term memory (LSTM) (Gemke et al., 2022), DCNN (Arooj et al., 2022), SVM-coupled DCNN (Botros et al., 2022), LO-SVM coupled DCNN (Cherian et al., 2020), and CO-SVM coupled DCNN (Reddy et al., 2022).

4.4.2 *Comparative analysis based on TP*

To ascertain the distinction between BHO-based SVM-coupled DCNN and the previous methods, a comparative analysis is undertaken. This analysis involves a comparison against established methods like CATBOOST, SVM, LSTM, DCNN, SVM-coupled DCNN, LO-SVM-coupled DCNN, and CO-SVM-coupled DCNN, using metrics. Figures 6(a), 6(b), 6(c), and 6(d) illustrate the graphical presentation of this performance comparison based on TP.

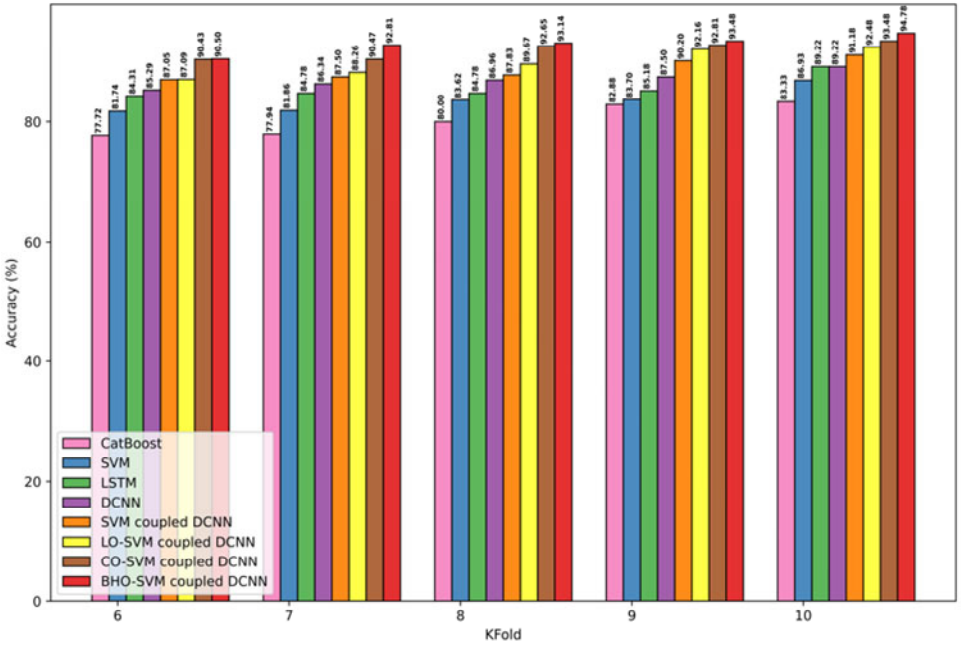
The proposed BHO-based SVM-coupled DCNN classifier method demonstrates an accuracy improvement of 13.03% compared to the existing CATBOOST method and 3.43% compared to the existing CO-SVM-coupled DCNN method, both evaluated on 90 TP. Similarly, when considering F1-score, it exhibits a 14.65% increase compared to the existing CATBOOST method and a 3.87% increase compared to the existing CO-SVM-coupled DCNN method, all based on 90 TP. Regarding precision, it outperforms the existing CATBOOST method by 15.94% and the existing CSO-CO-SVM-coupled DCNN method by 5.81%, again concerning the 90% of training. Finally, concerning recall, it surpasses the existing CATBOOST method by 13.81% and the existing CSO-CO-SVM-coupled DCNN method by 2.34%, using 90 TP.

4.4.3 *Comparative analysis based on K-fold*

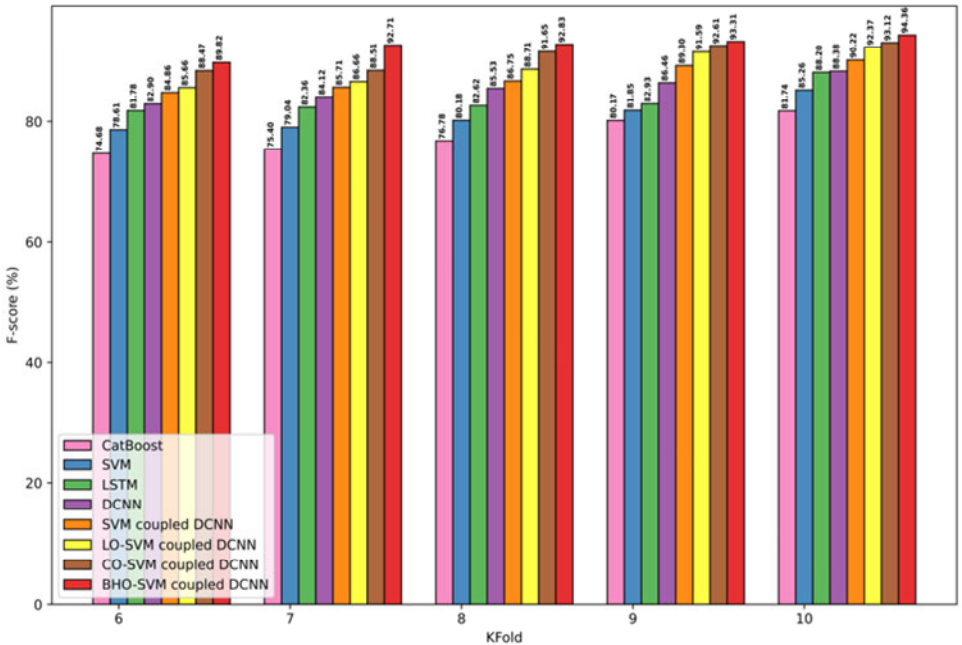
To ascertain the distinction between BHO-based SVM-coupled DCNN and the previous techniques, a comparative examination is undertaken. This analysis involves a comparison against established methods like CATBOOST, SVM, LSTM, DCNN, SVM-coupled DCNN, LO-SVM-coupled DCNN, and CO-SVM-coupled DCNN, using metrics. Figures 7(a), 7(b), 7(c), and 7(d) illustrate the graphical representation of this performance comparison based on k-fold.

The proposed BHO-based SVM-coupled DCNN classifier method demonstrates an accuracy improvement of 11.45% compared to the existing CATBOOST method and 1.30 compared to the existing CO-SVM-coupled DCNN method, both evaluated on ten k-fold. Similarly, when considering F1-score, it exhibits a 12.62% increase compared to the existing CATBOOST method and a 1.24% increase compared to the existing CO-SVM-coupled DCNN method, all based on ten k-fold. Regarding precision, it outperforms the existing CATBOOST method by 20.36%% and the existing CSO-CO-SVM-coupled DCNN method by 5.68%, again regarding ten k-fold. Finally, concerning recall, it surpasses the existing CATBOOST method by 9.87% and the existing CSO-CO-SVM-coupled DCNN method by 0.83%, using ten k-fold.

Figure 7 A comparative assessment using k-fold cross-validation, with a focus on, (a) accuracy (b) F1-score, (c) precision, and (d) recall (see online version for colours)

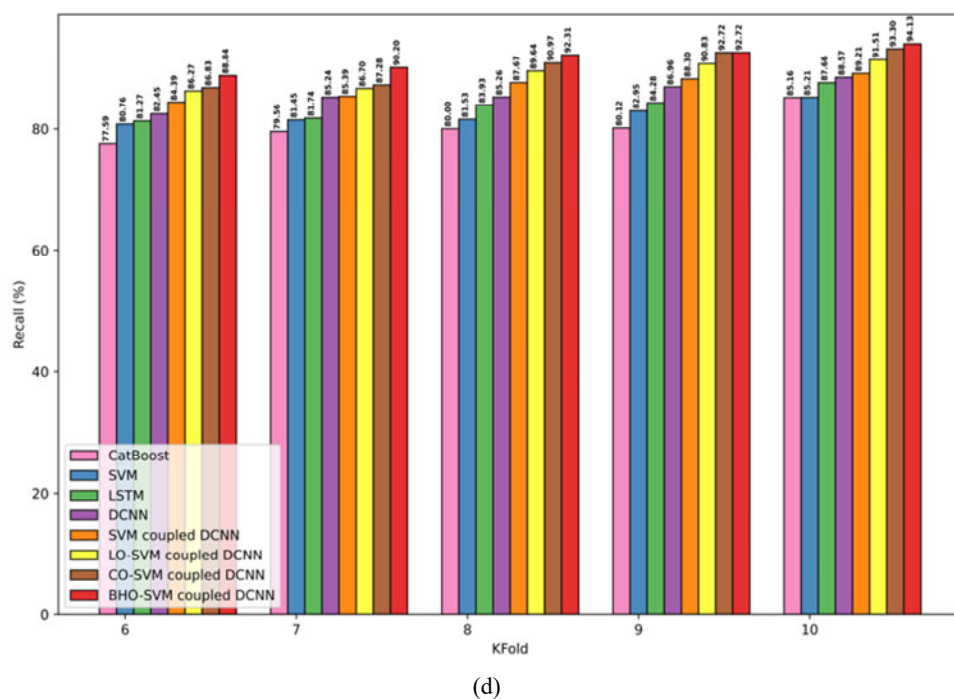
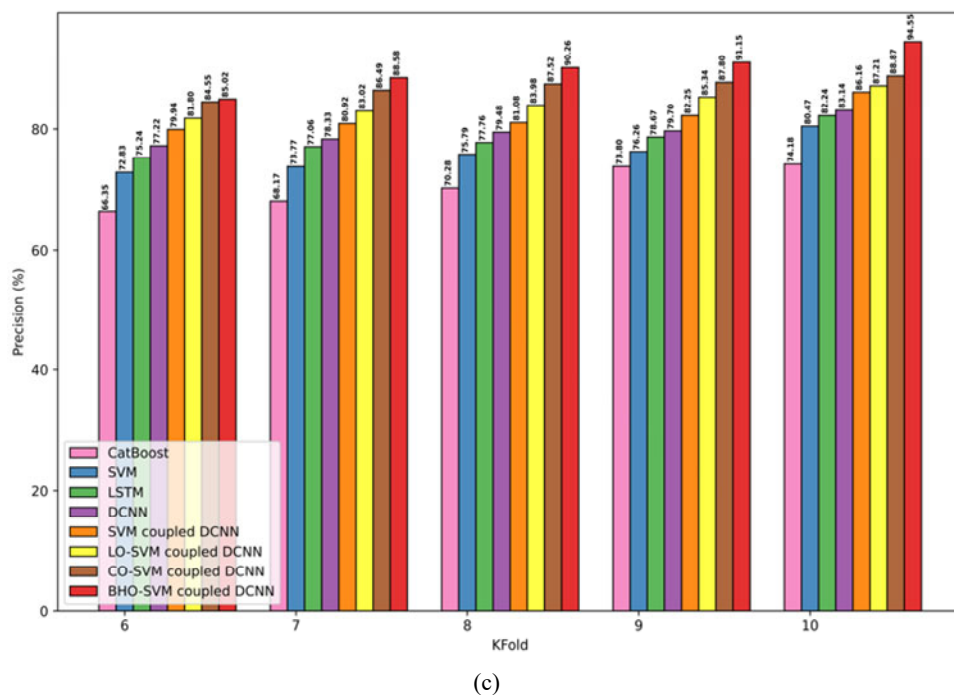


(a)



(b)

Figure 7 A comparative assessment using k-fold cross-validation, with a focus on, (a) accuracy (b) F1-score, (c) precision, and (d) recall (continued) (see online version for colours)



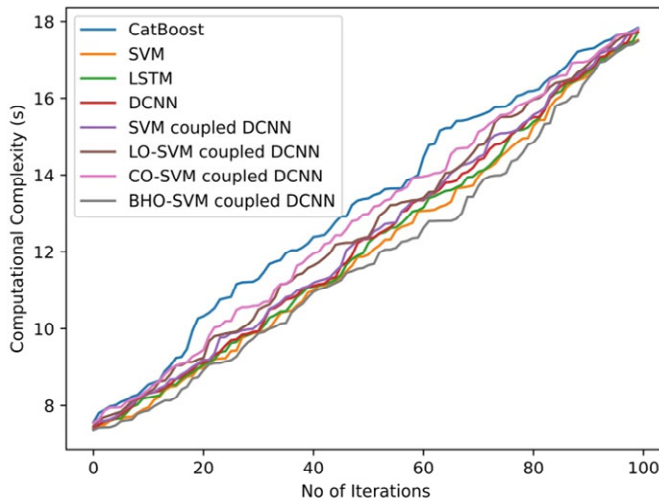
4.4.4 Computational complexity analysis

To demonstrate the effectiveness of the proposed BHO-SVM coupled DCNN method, a computational time comparison between the suggested method and the other current existing approaches is made across several iterations. The outcomes underscore the computational efficiency of the suggested strategy by constantly taking a lot less time than alternative methods. In comparison to other existing approaches, the suggested approach has the lowest computational time of 17.48 ms at iteration 100. This information is displayed in Table 1. The utilisation of the BHO algorithm in SVM-coupled DCNN is responsible for achieving this low calculation time. Utilising BHO to fine-tune the classifier greatly improves operational efficiency and speeds up execution. This suggests that it is the strategy that is most time-efficient among the ones offered, exceeding the alternatives in that regard. The computational complexity analysis of the method is depicted in Figure 8.

Table 1 Comparative analysis based on computational time

<i>Methods</i>	<i>Computational time (ms)</i>
CATBOOST	17.83
SVM	17.51
LSTM	17.71
DCNN	17.71
SVM-coupled DCNN	17.78
LO-SVM coupled DCNN	17.79
CO-SVM coupled DCNN	17.81
<i>BHO-SVM coupled DCNN</i>	<i>17.48</i>

Figure 8 Computational complexity analysis (see online version for colours)



4.5 Comparative discussion

Table 2 presents a comparative investigation relating the existing methods and the BHO-based SVM-coupled DCNN. The proposed method distinguishes itself by employing optimisation techniques and integrating SVM-coupled DCNN classifiers. The effectiveness of the BHO-based SVM-coupled DCNN classifier is illustrated in contrast with different established methods. Distinctively, the BHO-based SVM-coupled DCNN classifier achieves impressive results: an accuracy of 94.89%, an F1-score of 94.48%, a precision of 94.48%, and a recall of 94.58% for a 90 TP. For ten k-fold evaluation, the BHO-based SVM-coupled DCNN classifier had good performance with values of 94.78% accuracy, 94.36% F1-score, 94.55% precision, and 94.13% recall for ten k-fold.

Table 2 Comparative discussion

<i>Methods</i>	<i>Training percentage</i>				<i>k-fold</i>			
	<i>Accuracy</i>	<i>F1-score</i>	<i>Precision</i>	<i>Recall</i>	<i>Accuracy</i>	<i>F1-score</i>	<i>Precision</i>	<i>Recall</i>
CATBOOST	81.86	79.84	78.54	80.77	83.33	81.74	74.18	85.16
SVM	82.92	80.97	78.63	82.45	86.93	85.26	80.47	85.21
LSTM	84.35	82.45	80.83	84.88	89.22	88.20	82.24	87.66
DCNN	85.14	83.23	82.45	84.98	89.22	88.38	83.14	88.57
SVM-coupled DCNN	87.77	86.08	85.83	86.85	91.18	90.22	86.16	89.21
LO-SVM coupled DCNN	89.62	88.62	86.36	90.78	92.48	92.37	87.21	91.51
CO-SVM coupled DCNN	91.46	90.61	88.67	92.24	93.48	93.12	88.87	93.30
BHO-SVM coupled DCNN	94.89	94.48	94.48	94.58	94.78	94.36	94.55	94.13

5 Conclusions

This research addresses the critical issue of heart disease, encompassing various medical conditions affecting the heart and blood vessels, like heart failure, arrhythmias, and congenital heart defects. To improve early detection and risk assessment, a novel hybrid model that combines SVM with a DCNN is introduced. This innovative approach harnesses SVM's classification capabilities and the feature extraction prowess of DCNN to efficiently analyse medical data. Additionally, a unique hybrid optimisation technique called BHO was employed to fine-tune SVM parameters, thereby enhancing its classification performance. Concurrently, a Deep CNN model was utilised to extract intricate and informative features from the medical data. The hunting brave optimisation leverages the strengths of both LO and CO algorithms achieving fast convergence and enhanced solution quality which helps to enhance the detection performance and reduces the time complexity of the model. The BHO algorithm also escapes from local optima. Even though the BHO technique leverages several advantages, setting control parameters

is a difficult process. BHO-based SVM-coupled DCNN achieved an accuracy rate of 94.89%, an F1-score of 94.48%, a precision rate of 94.48%, and a recall rate of 94.58% for a 90 TP. For ten k-fold evaluation, a high level of performance is attained with an accuracy rate of 94.78%, an F1-score of 94.36%, a precision rate of 94.55%, and a recall rate of 94.13%. In comparison to other current models, the computing time required by the suggested model is quite low at 17.48 ms/epoch. These results underscore the effectiveness and promise of this hybrid approach in enhancing cardiovascular disease diagnosis and risk assessment. Implementing the model in diagnostic tools for healthcare professionals leads to earlier and more effective detection of patients with cardiac diseases. The enhanced efficiency of the model contributes to cost effectiveness within healthcare systems. For future work, creating a real-time monitoring system that continuously evaluates a patient's heart health based on data from wearable devices and other sensors could be a valuable application.

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