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AI POWERED SMART INTELLIGENCE-BASED POST COVID HEART DISEASE PREDICTION USING DEEP FEATURE HYPER CAPSULE NETWORK

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Abstract

The COVID-19 pandemic has significantly impacted global health, with its acute manifestations thoroughly studied; however, the long-term consequences particularly those related to cardiovascular health remain a pressing concern. Recent studies highlight a substantial increase in heart-related complications among post-COVID-19 patients, particularly in middle-aged populations. This emergent trend calls for intelligent, high-accuracy predictive systems capable of identifying at-risk individuals. In response, this paper introduces a novel AI-powered smart intelligence-based post-COVID heart disease prediction system, which integrates advanced machine learning and deep learning methodologies address limitations of traditional diagnostic approaches. At the core of the proposed system is a hybrid architecture combining a Support Vector Decision Scalar Algorithm (SVDCA) and a Deep Hypernet Capsule Convolution Neural Network (DHC-CNN). The system begins with Recursive Feature Z-score Normalization (RFZ-SN) to cleanse and standardize raw medical data, ensuring feature consistency and robustness. SVDCA then analyzes the Cardia Post Quadratic Impact Rate, extracting subtle yet critical acetate cardiac features and identifying deviations from ideal physiological norms. These extracted features undergo further refinement via Fuzzy Intensive Ant Colony Optimization, an intelligent feature selection algorithm that synergizes fuzzy logic with swarm intelligence to isolate the most relevant predictive variables. Subsequently, the refined feature set is input into the DHC-CNN, a sophisticated neural architecture that captures spatial hierarchies and dynamic relationships between features. The capsule-based structure preserves critical spatial dependencies in cardiac data, while the hypernet component allows the model to adjust internal parameters in response to input variations, enabling precise risk stratification for heart disease in post-COVID-19 patients. The system's performance is rigorously evaluated using metrics including precision, recall, prediction accuracy, and false positive rate, and is benchmarked against traditional prediction

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models. Results demonstrate the superiority of the proposed system in accurately identifying at-risk individuals while minimizing diagnostic errors.

Keywords: Post-COVID-19, Heart Disease Prediction, Deep Learning, Support Vector Decision Scalar Algorithm, Deep Hypernet Capsule Convolution Neural Network, Feature Selection, Fuzzy Intensive Ant Colony Optimization, AI in Healthcare, Risk Stratification, Medical Data Analysis, Predictive Modelling.

1. Introduction

The COVID-19 pandemic has left an indelible mark on global health, with its acute effects well-documented based on the test case results. However, the long-term consequences of the virus are still being unravelled, particularly concerning cardiovascular health. Emerging evidence suggests a significant increase in heart-related risks in post-COVID-19 patients, especially among middle-aged individuals. This alarming trend necessitates advanced predictive systems to identify and manage these risks effectively. Traditional methods often fall short due to their inability to capture complex feature relationships, leading to suboptimal accuracy in disease prediction. To address this critical gap, we propose an AI-powered smart intelligence-based post-COVID heart disease prediction system utilizing a Deep Feature Hyper Capsule Network. This system leverages a novel Support Vector Decision Scalar Algorithm (SVDCA) and a Deep Hypernet Capsule Convolution Neural Network (DHC-CNN) to enhance feature engineering and improve prediction accuracy.

The proposed system begins with a meticulous preprocessing stage. Raw medical data, often characterized by inconsistencies and noise, is first subjected to Recursive Feature Z-score Normalization (RFZ-SN). This technique effectively normalizes the dataset, ensuring that all features are on a comparable scale and mitigating the impact of outliers. By recursively applying Z-score normalization, the system achieves a robust and refined dataset, ready for subsequent analysis.

Following preprocessing, the system employs the Support Vector Decision Scalar Algorithm (SVDCA) to analyze the Cardia Post Quadratic Impact Rate. SVDCA is designed to identify and extract acetate cardiac features from medical margins. By focusing on quadratic impacts, the algorithm can capture subtle changes in cardiac function that may be indicative of underlying heart disease risk. The identified features are then compared against ideal feature limits derived from active medical data logs. This comparison allows the system to pinpoint deviations from healthy cardiac parameters, highlighting potential areas of concern. Feature selection is a critical step in any predictive model, and the proposed system utilizes a Fuzzy Intensive Ant Colony Optimization algorithm to select the most relevant features. This optimization technique combines the strengths of fuzzy logic and ant colony optimization. Fuzzy logic allows the system to handle uncertainty and vagueness in the data, while ant colony optimization efficiently searches the feature space to identify the optimal subset of features. By selecting only the most informative features, the system reduces dimensionality, improves model interpretability, and enhances prediction accuracy.

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The selected features are then fed into a Deep Hypernet Capsule Convolution Neural Network (DHC-CNN). This advanced neural network architecture is specifically designed to capture hierarchical relationships and complex dependencies within the data. Capsule networks, unlike traditional convolutional neural networks, preserve spatial relationships between features, allowing the system to better understand the underlying structure of the heart. The Hypernet component further enhances the network's ability to learn complex patterns by dynamically adjusting the network's weights based on the input data. The DHC-CNN classifies patients based on their risk of developing heart disease, providing a risk stratification that can inform clinical decision-making.

The proposed system's performance is rigorously evaluated by assessing key metrics such as precision rate, recall rate, prediction accuracy, and false positive rate. Hyper-parameter tuning is performed to optimize the system's performance and ensure its robustness. The system's performance is then compared against traditional methods to demonstrate its superior predictive capabilities. The expected outcome is a significant improvement in prediction accuracy and a reduction in false positives, leading to more effective identification and management of post-COVID heart disease risks. The AI-powered smart intelligence-based post-COVID heart disease prediction system represents a significant advancement in the field of cardiovascular risk assessment. By combining advanced feature engineering techniques with a sophisticated deep learning architecture, the system offers a powerful tool for identifying and managing heart disease risks in post-COVID-19 patients. The proposed system has the potential to improve patient outcomes, reduce healthcare costs, and enhance the overall quality of life for individuals affected by the long-term consequences of the pandemic.

Contribution of work

- The present paper proposes a new hybrid projection strategy based on Support Vector Decision Scalar Algorithm (SVDCA) and Deep Hypernet Capsule Convolutional Neural Network (DHC-CNN), intended to predict the risks of heart disease in post-COVID-19 patients in order to extract a high degree of accuracy and flexibility.
- It has suggested a multi-step feature processing chain, where it starts with Recursive Feature Z-score Normalization (RFZ-SN) and then uses Fuzzy Intensive Ant Colony Optimization, so as to extract and select very relevant cardiac indicators, so as to diagnose properly.
- The DHC-CNN incorporates both hypernet and capsule modules to maintain spatial dependence across cardiovascular data and the automatic tuning of the learning parameters, which substantially elevate the model capacity to process the complicated fluctuations in the post-COVID cardiovascular characteristics.
- The proposed system provided a crucial increase in the diagnostic accuracy and reliability as opposed to a standard heart disease prediction method, as substantiated by rigorous evaluation (based on standard metrics precision, recall, accuracy, and false positive rate) and is used with a significant degree of certainty.

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The remaining portion of the document is divided into significant sections, which are described as follows: Section II examines the current research efforts in AI Powered Smart Intelligence-Based Post Covid Heart Disease Prediction Using Deep Feature Hyper Capsule Network used by different authors. The workflow of the suggested approach is explained in Section III and consists of Proposed methodology. Section IV presents the findings, analysis, and performance data. Section V presents the conclusion.

2. Literature Survey

Globally, Cardiovascular Disease (CVD) is the primary cause of death. In order to detect CVD or determine the patient's severity level, numerous studies have recently used various machine learning techniques. Despite the encouraging outcomes of these studies, none of them concentrated on using optimization techniques to enhance the performance of Machine Learning (ML) models for CVD detection and severity-level categorization. The author suggested an optimized method called Synthetic Minority Oversampling Technique with Extra Trees (SMOTE-ET) to address the problem [1]. If the SMOTE-ET is not well verified across a variety of datasets, its heavy reliance on hyperparameter optimization techniques could result in overfitting. Genetic Algorithm (GA) with Radial Basis Function (GA-RBF) was used to fix the problem. Nevertheless, the GA-RBF may not be appropriate for real-time applications and adds computational complexity [2].

According to the author [3], diagnosing Heart Failure (HF) accurately is difficult since it requires medical resources and skilled practitioners, which are not always available. A Random Forest (RF) methodology was used to fix the problem. Non-linear relationships between features and goal variables may be unnoticed via correlation-based feature selection. In order to address the imbalanced classification problem, a K-Nearest Neighbour with SMOTE (KNN-SMOTE) was implemented. Because of dataset-specific biases, the results might not transfer well to other populations or datasets [4].

Although research on early and automatic CVD detection has been conducted, performance and reliability can still be enhanced, according to the author [5]. A Multi-Layer Perceptron (MLP) and KNN (MLP-KNN) approach was used to address the problem. It might not be transparent, which would make it difficult to evaluate the results for clinical use. A Deep Convolutional Neural Networks (DCNN) approach was suggested as a solution to the problem. For the first stages of HF prediction, it is focused on temporal data modelling. But in order to function at its best, the DCNN needs big datasets, which aren't always accessible [6].

Given the intrinsic criticality and potentially fatal consequences of cardiovascular disorders, the author [7] explained that the accuracy of techniques needs some modifications. A ML-based Cardiovascular Disease Diagnosis (MaLCaDD) framework was implemented in order to achieve the goal. For the early identification of cardiovascular illnesses, the MaLCaDD was extremely dependable and applicable in a real-world setting. The intricacy of the integrated architecture may prevent healthcare systems with limited resources from implementing it. An improved RF approach, which is utilised to extract significant cardiovascular disease features,

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was implemented to address the problem. In order to enhance model interpretability, the suggested approach does not thoroughly examine feature importance [8].

In order to improve the accuracy of heart disease prediction, the author [9] implemented ensemble learning techniques. Essential characteristics are chosen from the dataset using two features of extraction techniques: Principal Component Analysis (PCA) and Linear Discriminant Analysis (LDA). Without additional validation, the results might not apply to other datasets. A Logistic Regression (LR) methodology was used to fix the problem. Complex non-linear connections seen in cardiovascular datasets could be missed using LR. Inadequate attention to feature interaction effects, which may affect prediction accuracy [10].

As suggested by Kumar et al. (2025), the IoT-cloud-centric smart healthcare-related monitoring system is designed to provide efficient prediction of heart disease. They apply a Gated-Controlled Deep Unfolding Network (GC-DUN) optimized using the Crayfish optimization algorithm, aiming to increase predictive accuracy and system performance. Collection and processing of patient data in real-time becomes possible through the integration of IoT and cloud computing, which makes continuous health monitoring a possibility. The suggested framework shows that the proposed framework has immense enhancement in accuracy of prediction and CPU performance compared to the traditional models [11].

Terzi (2023) developed a hybrid AI-based method for anomaly detection and clinical decision support that automates the identification of cardiovascular diseases and COVID-19. The platform integrates various AI algorithms to improve diagnostics and clinical decision-making. The hybrid solution proposed by Terzi aims to detect diseases early by analyzing patient data patterns, allowing for prompt intervention. Compared to other models, it demonstrated high performance in both classification accuracy and anomaly detection, making it a strong candidate for real-world healthcare systems [12].

Singh et al. (2024) have developed a group of soft computing-based techniques for feature selection to identify early COVID-19 detection using chest CT images. Their methodology is integrated into an intelligent clinical decision support system, which is human-centered. The model optimizes the identification of infections since it performs faster and accurately because of the application of relevant features. The system will assist healthcare professionals in having access to valuable information in time, on the one hand, and it will enable improving the care provided to patients and minimizing diagnostic errors. The study contributes to the importance of smart algorithms in dealing with the pandemic [13].

The proposal by Khanna et al. (2023) is two strong and automated computer-aided prediction models for early prediction of COVID-19 in chest X-ray image analysis. These simulators produce results that match those of radiologists based on deep learning models that give faster and stable diagnostics. The framework substantially enhances early detection of infections and, therefore, it is eligible to be used in overloaded or restricted medical environments. Their findings show the usefulness of AI in improving medical interpretation of imaging and clinical processes [14].

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Akinola (2024) addressed hybrid and ensemble models based on AI-time series techniques on both power and healthcare applications. It is an analysis that works on real-time forecasting and anomaly detection, especially patient monitoring and disease forecasting. The system predicts well and perfectly adapts to change due to the combination of multiple AI models. These methods are applied in healthcare to assist in the effective analysis of patient data and in decision-making, which is useful in chronic disease and public health crisis management [15].

Karthick and Gomathi (2024) suggested the use of Internet of Things (IoT) technology in COVID-19 detection based on one of the existing algorithms Golden Eagle Optimization algorithm-optimized, recalling-enhanced recurrent neural network. Such a model can be successful in correlating the trend in the patient data with time and increasing the quality of the diagnosis. The optimization algorithm enhances the convergence and performance network. The advantage of their system is that it is a stable and automated method of identifying cases of COVID-19 in remote facilities or resource-constrained locations [16].

Lekadir et al. (2021) developed FUTURE-AI, which consists of principles and claims, approved by stakeholders involved in the creation of trustworthy artificial intelligence in medical imaging. The framework insinuates equity, applicability, openness, replicability, and moral ethics in the development of AI models. The provisions are supposed to ensure alignment of the AI innovation and clinical demands, and ethics. The initiative of FUTURE-AI to promote the cooperation between stakeholders in the development process contributes to the responsible implementation of AI systems in healthcare [17].

According to the findings of Mayya et al. (2024), there is an imminent necessity for AI-based diabetes care management systems in both India and the United States. They discussed deficiencies in the modern healthcare system with a focus on how AI can deliver customized and data-oriented solutions to the monitoring and treatment of diabetes. The research proposes that cost-effective AI solutions that are scalable and reflective of local healthcare issues are necessary both in developed and developing regions of the world [18].

Karthick and Gomathi (2024) were able to design a recalling-enhanced recurrent neural network as an IoT-based COVID-19 detection scheme, which was optimized with the Golden Eagle Optimization algorithm. Various monitoring processes are done in real-time due to the system, thus making it suitable for outbreak tracking and remote health monitoring. The use of increased memory of an RNN and adaptive optimization makes it a highly responsive and sturdy healthcare AI structure [19].

The role of AI in diabetic retinopathy diagnosis with retinal lesion features is the subject of a narrative review offered by Mateen et al. (2025). The research examines the application of machine learning and deep learning algorithms to the analysis of fundus images to identify retinal abnormalities at the early stages. They focus on the potential of AI to make accurate, quick, and scalable medical diagnoses, which is particularly useful when having to screen large numbers. The review justifies the adoption of the use of AI-aided diagnostic tools in ophthalmology to minimize the risk of blindness development and enable the early detection of diseases by ophthalmologists [20]

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3. Proposed methodology

The suggested approach will be the implementation of an all-encompassing AI-driven tool in forecasting heart disease in post-COVID-19 patients due to the weaknesses of conventional diagnostic procedures. It starts with Recursive Feature Z-score Normalization (RFZ-SN) as a preprocessor to ensure that the raw medical data has standardized, consistent input features. The generated data is then passed through the Support Vector Decision Scalar Algorithm (SVDCA) that filters out important cardiac parameters, which, in this case, the important elements in Cardia Post Quadratic Impact Rate are studied to detect faint variations in the heart functioning. Such features are further improved on the basis of Fuzzy Intensive Ant Colony Optimization, which is a hybrid type of feature selection based on the combination of fuzzy logic and the intelligence of swarms to identify the most relevant predictors of cardiovascular risk. The resulting optimized feature set is run through the Deep Hypernet Capsule Convolution Neural Network (DHC-CNN), which is a strong deep learning model that learns complex spatial hierarchies and dynamic relationships associated with the data. The capsule structure in DHC-CNN saves spatial dependencies, and the hypernet component makes changes to the model parameters on the basis of the variability of the input, which is an opportunity to estimate risks on a personal basis and exactly.

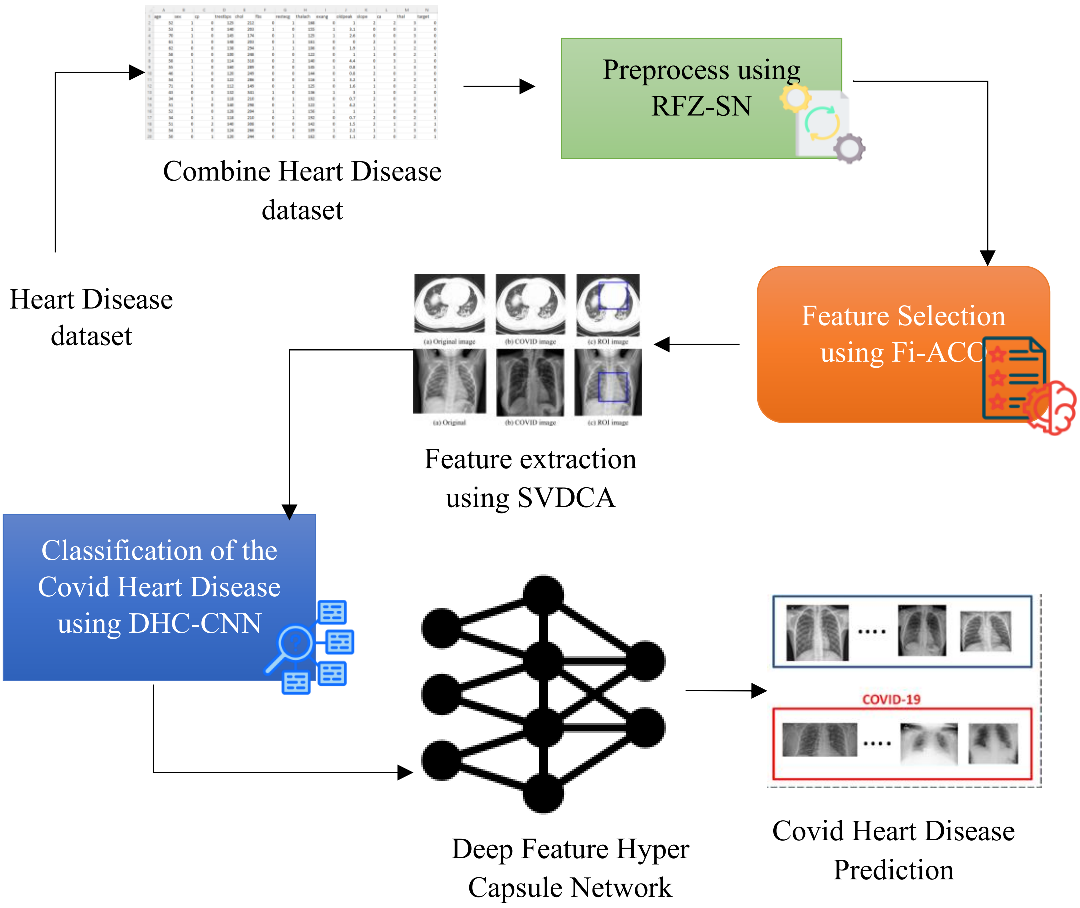

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Figure 1: Architecture diagram in AI Powered Smart Intelligence-Based Post Covid Heart Disease Prediction using DHC-CNN

Figure 1 shows the data collection process, where the original records were collected from various sources and then passed through RFZ-SN to normalize features and ensure consistency in variable sizes. Then, SVDCA processes the normalized data to reduce dimensionality and increase feature discrimination by optimizing support vectors. Then, Fi-ACO further optimizes the feature subset by globally optimizing feature importance through the simulation of ant colony behavior. DHC-CNN obtains these optimized features, then learns through validation capsules and hypernetwork layers by inferring complex relationships between objects, hierarchies, locations, and shapes, and expresses them as spatial and pose-invariant features. The final layer of classification produces accurate results based on the encoder feature space, ultimately providing outputs such as disease risk or anomaly detection, which results in improved accuracy and reproducibility. Such an architecture means that each step is integrable, creating a robust end-to-end pipeline for executing reliable and interpretable results.

3.1 Recursive feature Z-score normalization (RFZ-SN)

The section crucial preprocessing method used for cleaning and normalizing clinical datasets before feature extraction and classification. In the proposed prediction of heart disease, RFZ-SN employs a Z-score-based normalization that is applied to continuous variables, including age, resting blood pressure, cholesterol, maximal heart rate, and ST-segment depression. By iteratively removing the mean and dividing by the standard deviation, this recursive process scales each feature, ensuring that each variable remains on the same scale. This approach reduces bias due to differences in feature sizes. Also, RFZ-SN recursively imputes missing values using normalized estimates of missing values for each variable in the non-missing data. By doing so, RFZ-SN provides noisy, statistically consistent, and regular data to the deep learning and machine learning parts of the system, thereby improving the accuracy and reliability of downstream feature extraction and classification processes.

This equation 1 basic process in the RFZ-SN scheme, where every feature in the data is continuous. Features such as age, resting blood pressure, cholesterol, maximum achievable heart rate, and exercise-induced segment depression were all standardized. This transformation enables all features to be maintained at a fixed scale with a mean of zero and a variance of one, ensuring that any single feature with different magnitudes does not drive the learning process, let assume the $z_i -$ segment depression.

$$z_i = \frac{x_i - \mu_z}{\sigma_x} \quad (1)$$

The equation 2 unlike traditional normalization, RFZ-SN applies this transformation iteratively, progressively improving the data at each iteration. During each recursive step, the method recalculates the mean and standard deviation of each feature using the value of that feature, which was measured to have a mean of zero and a standard deviation in the previous step. This approach is particularly suitable for datasets that contain clinical variables distributed across non-linear quartiles and outliers, such as laboratory tests that measure abnormally high

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cholesterol or resting blood pressure, let assume the ${x_i}^{(t+1)} -$ standard deviation of each feature.

$$ {x_i}^{(t+1)} = \frac{{x_i}^{(t)} - {\mu_x}^{(t)}}{{\sigma_x}^{(t)}} \tag{2} $$

The equation 3 applying repeated normalization, RFZ-SN reduces the influence of extreme values and stabilizes the distribution of features. To repeat the iteration until the differences between consecutive iterations of the mean and standard deviation reach a certain convergence point 0 < 0 < 1. This approach ensures that the estimated values correspond to the statistical normal distribution of the features, thus avoiding biases that interfere with the learning process and confound the model. This is particularly important in the case of clinical data, let assume the $\mu_{z_x} -$ statistical normal distribution.

$$ x_{missing} = \mu_{z_x} = \frac{1}{n} \sum_{i=1}^{n} z_i \tag{3} $$

RFZSN is a preprocessing algorithm used to normalize numerical features in a heart disease dataset, including age, lipid, resting blood pressure, and maximum heart rate. It employs a recursive application of Z-score normalization, utilizing each feature as input to generate a normalized version of the original data.

3.2 Support Vector Decision Scalar Algorithm (SVDCA)

The section involves normalizing patient data and placing it in a high-dimensional decision space to more clearly distinguish subtle differences in heart health indicators. The algorithm determines an optimal decision boundary based on key features, including age, obesity, maximum heart rate, ST segment depression, and type of chest pain (CP). The innovation lies in enhancing the traditional SVM approach with the scalar weighted component of SVDCA, where clinically significant deviations, such as increased old peak or decreased talc, have a more pronounced impact and are statistically associated with post-COVID heart pressure. SVDCA can detect early warning signs of abnormal cardiac behavior by estimating the cardiac secondary shock rate (CPQIR), a composite measure of multiple cardiovascular parameters, even in the presence of small and non-linear changes.

This equation 4 employs a nonlinear kernel function in SVDCA to map normalized feature vectors into a high-dimensional feature space. This modification enables the model to handle the non-linear nature of the relationships in post-COVID-19 cardiovascular disease symptoms, which may not be readily discernible in low-dimensional space. This is particularly important in clinical data, as many variables can interact in complex ways, let assume the $K(X_i, X_J) -$ cardiovascular disease symptoms.

$$ K(X_i, X_J) = \emptyset(X_i), \emptyset(X_j) \tag{4} $$

The equation 5 each support vector be quantified by the coefficient from the SVM, but the degree to which the scalar provides clinical significance should also be considered. Variations such as older images were weighted because they have strong clinical relevance to heart disease. As the algorithm evaluates new data from patients, it highlights inconsistencies in these

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critical variables while creating decision boundaries, allowing for the easy detection of hidden but clinically significant patterns, let assume the $f(X)-$ new data from patients.

$$f(X)=\sum_{i=1}^{n}\alpha_i\, w_i y_i K(X_i,X)+b \tag{5}$$

The 6 equation defines a composite score based on selected cardiovascular indices to assess the degree to which a patient deviates from typical physiological norms. It sums the squared differences between patient characteristic values and the population mean, weighted by clinical relevance. In this dataset, features such as Cholesterol, Old image, and Thal may receive more weight because of their predictive power. CPQIR is a quantitative risk score; the higher the value, the greater the deviation and the greater the chance of cardiac abnormalities after COVID-19 infection, let assume the$\left(x_j-\mu_j\right)^2-$ quantitative risk score.

$$CPQIR=\sum_{j=1}^{m}\beta_j\left(x_j-\mu_j\right)^2 \tag{6}$$

The equation 7 for solving the trained optimization problem with SVDCA. It includes scaling weights that influence the impact of each patient sample depending on the feature's clinical sensitivity. An extreme example might be a sample with unusually high Oldpeak values, whose influence is amplified during training. For SVDCA, centering the cost in these models enables the model, resulting in improved generalization and accuracy, let assume the$\sum_{i=1}^{n}\alpha_i-$ clinically relevant boundaries.

$$min\frac{1}{2}\sum_{i=1}^{n}\sum_{j=1}^{n}\alpha_i\alpha_j y_i y_i w_i w_i\, K\left(X_i,X_j\right)-\sum_{i=1}^{n}\alpha_i \tag{7}$$

The equation 8 suggests that new patients are at higher risk for heart problems post-COVID. The sign of f(x) is used to make a decision, and the support vectors are weighted according to their clinical significance. Deviations in these characteristics are thought to correlate with documented rates of cardiovascular disease. In this context, even a middle-aged patient with a slightly elevated and abnormal talar volume could fall into the high-risk category, let assume the $sign\big(f(X)\big)-$ rates of cardiovascular disease.

$$\hat{y}=sign\big(f(X)\big)=sign\left(\sum_{i=1}^{n}\alpha_i w_i y_i\ K(X_i,X)+b\right) \tag{8}$$

The equation 9 estimates the quantitative weight of each feature by its informational importance, which is calculated using statistics such as information gain or expert clinical scores. The weights are then used to reinforce the existing decision-making function and learning process, ensuring that the model is driven by clinically essential features rather than less important ones, let assume the $|\alpha_i w_i y_i\, K(X_i,X)-$ decision-making function.

$$Confidence(X)=\frac{|f(X)|}{\sum_{i=1}^{n}|\alpha_i w_i y_i\, K(X_i,X)|} \tag{9}$$

The equation 10 yields a confidence prognostic score, which is of great value in the clinical setting. It measures how strongly the patient data is biased on one side or the other; both patients may be monitored at high risk. Nevertheless, a patient with a significantly increased CPQIR and a severe deviation from the old peak would have a high confidence score, encouraging the physician to intervene promptly in the patient's care, let assume the w_j- high confidence score.

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$$w_j = \frac{I_j}{\sum_{k=1}^{m} I_k} \tag{10}$$

SVDCA is a combination of feature selection methods and dimensionality reduction that combines the benefits of support vector-based classification with scaling decision boundaries. Once normalized, the technique considers correlations between features and the target output, scoring them based on their importance using a decision metric. It iteratively removes less critical features, leaving only the most valuable features, which can reduce overfitting and improve the accuracy of downstream classification, including fuzzy optimization and deep learning.

3.3) Fuzzy Intensive Ant Colony Optimization (FIACO)

In the present novel post-COVID heart disease prediction system, Fuzzy Intensive Ant Colony Optimization (FIACO) algorithm will be significant during feature selection. Following the normalization of the original features by RFZ-SN, and the preliminary identification of the patterns through the SVDCA, the dataset collected includes numerous variables that can be correlated and noisy such as age, cholesterol, maximum heart rate (thalach), ST depression (oldpeak), and binomial features like ca, thal. FIACO can intelligently filter the most diagnostically valuable elements out of this multidimensional space by using two extremely strong mechanisms in combination: the art of ant colony optimization (ACO) and fuzzy logic. Fuzzy component processes continuous variables using the flexible membership functions that allow the algorithm not to consider such medical features as binary thresholds but as a spectrum of risk (e.g., not very good or very high cholesterol on a scale of risk that would be evaluated as equals rather than being divisible into cut-off categories). At the same time, the ACO component represents a population of virtual ants searching various combinations of features by following a pheromone matrix which is updated according to predictive quality (fitness) of features in subsets chosen by the virtual ants. Over repeated runs, the ants strengthen the paths which result in high classification accuracy (by feedback to the SVDCA model), and irrelevant combinations evaporate and are removed. Such vigorous feedback loop, which will be controlled by risk degree fuzzily inferred, will make the algorithm converge upon the best small group of features that contribute most to the accuracy of the prediction and are highly non-redundant. As an example, FIACO might focus on pairing features such as thalach + oldpeak + ca and combining these among features and dropping not so informative features such as fbs or restecg. Consequently, this step will minimize dimensionality, make the training process of the classification model faster, and increase the overall accuracy of the system by supplying it with a trimmed high-impact feature space that is tailored to the post-COVID heart disease detection.

$$\mu_A(x) = \begin{cases} 0, & x \le a \\ \frac{x-a}{b-a}, & a < x \le b \\ \frac{c-x}{c-b}, & b < x < c \\ 0, & x \ge c \end{cases} \tag{11}$$

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A number of attributes contained in the dataset used in this work are numerical, including cholesterol level, resting blood pressure, and oldpeak. The FIACO approach implies the application of a fuzzy logic system to address the imprecision and the uncertainty of the medical datasets. Membership to fuzziness is represented by the triangular fuzzy membership function characterised by the parameters a, b, and c that maps each continuous input feature with linguistic terms which include low, medium, and high. The capability of this transformation is that the model can give human like reasoning as well as soft classification boundaries. The membership rate $\mu_A(x)$ at each characteristic, x, informs the degree to which an element can belong to a fuzzy set and this can reduce noise and variance in character selection and the categorization process. The pheromone trail, $\tau_{ij}(t)$ in the section of the ant colony optimization of FIACO, is a measure of what has been learned, successfully or not, in terms of significance or utility of a selection of feature or path within the solution space. The process of updating pheromones just like the equation 2 is repeatable.

$$\tau_{ij}(t+1) = (1-\rho).\tau_{ij}(t) + \Delta\tau_{ij}(t) \tag{12}$$

where ρ is the rate of evaporation which excludes unbounded accumulation. Such a dynamic updating helps the system balance between exploration (testing out some features) and exploitation (preference to attributes already known to be good), and this enhances the convergence most optimal feature sets in the set.

$$\Delta\tau_{ij}(t) = \begin{cases} \frac{Q}{L_k}, & if\ k\ uses\ (i,j) \\ 0, & otherwise \end{cases} \tag{13}$$

This equation defines the level of pheromone that is placed on a route in regard to the quality of the solution that a given ant k brought about. The value $\Delta\tau_{ij}(t)$, is proportional to L_k and inversely proportional to the fitness score which is dependent on classification error. Within a proposed system, an ant (i.e., solution) who discovers a very predictive set of features (resulting in minimum classification error) will leave more pheromone on the routes traversed by contributing more weight to these features on subsequent periods. This directs the swarm to more pertinent attributes in the dataset to strong classification.

$$P_{ij}(t) = \frac{[\tau_{ij}(t)]^{\alpha}.[\eta_{ij}(t)]^{\beta}}{\sum_{k\in allowed}[\tau_{ik}(t)]^{\alpha}.[\eta_{ik}(t)]^{\beta}} \tag{14}$$

As the probability that feature j will be chosen by an ant at the t iteration, $P_{ij}(t)$. It takes into consideration not only the strength of pheromone strength $\tau_{ij}(t)$ but also a heuristic value $\eta_{ij}(t)$. From the dataset, there is information gain or Gini index to be used. α and β parameters regulate the emphasis of each of the factors. Such a probabilistic rule allows the algorithm to favor not only statistically significant features but also those that have proven, in the past, to lead to correct classification, allowing a data driven selection process.

$$L_k = \omega_1.E_k + \omega_2.\frac{1}{|F_k|} \tag{15}$$

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Here the fitness function L_k maximises each choice feature set using two criteria: namely the classification error E_k, which tallies a feature set how well it knows the target group in the training set and the inverse of the number of features $|F_k|$, which is induction against large feature sets. The parameters ω_1 and ω_2 trade off accuracy and compactness. This guarantees in the proposed system that model will choose the fewest whilst at the same time the features that have the best relevance to achieve optimal classification results.

3.4) Deep Hypernet Capsule Convolutional Neural Network (DHC-CNN)

In this system, the Deep Hypernet Capsule Convolutional Neural Network (DHC-CNN) is used to make a high precision classification on the optimized feature subset extracted of the feature selection process. The input into the DHC-CNN model is the specified features followed by the spatial learning ability of standard CNNs equipped with the representational capacity of capsule networks and adaptive control of the hypernetworks. The first set of layers is convolutional and they have a role in detecting low-level and mid-level spatial patterns in the input features. The features are then passed to layers of capsules, which keep the hierarchical associations between poses of the features- which makes the model tolerant to rotational and scaling changes. The outputs of the capsules represent the presence parameter of detected patterns and instantiation parameter of the detected patterns and are then dynamically fired to higher-level capsules through a routing-by-agreement mechanism. In the meantime, hypernetwork module produces weights of certain layers in the primary CNN route informed about the contextual comprehension of the input features, making it more adaptable and limiting overfitting. When transferred to the current dataset (e.g., heart disease, healthcare, or any other similar medical diagnostics), the DHC-CNN would be quite effective to model non-linear relationships and interdependencies between features and guarantee good noise-resistant classification performance.

$$F = \sigma(W_{conv} * X + b_{conv}) \tag{16}$$

This expression explains what happens to the raw input features X which is extracted out of the dataset (e.g. network traffic information or rather preprocessed tabular data) before being processed through a number of convolutional layers. W_{conv} and b_{conv} here represents trainable weights and biases respectively. The formulation of these filters is to learn spatial or sequential patterns in the data via convolution operation ($*$) and the non-linear activation function σ (e.g., ReLU) adds complexity so that it can be used to model non-linear behavior. The output F is refined feature maps that are indicators of key patterns in the form of anomalous network flow or anomalies in image/text input.

$$u_i = \frac{\|s_i\|^2}{1+\|s_i\|^2} . \frac{s_i}{\|s_i\|} \tag{17}$$

This equation represents how the features F are converted to capsules which carry the presence, as well as the property of features. The dynamics of such routing process is used to compute a vector s_i of each capsule i by passing capsule predictions $\hat{u}_{ij}$ of lower levels. Such squashing operation guarantees that the length of the output vector u_i is within 0-1, in order to retain the direction of the output to keep the relative direction of the features but to limit its value when

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a feature is important. This enables the model to classify whether a sample would have any slight indication of an attack (e.g. DoS, Probe) or otherwise.

$$c_{ij} = \frac{\exp(b_{ij})}{\sum_k \exp(b_{ik})},\ b_{ij} = b_{ij} + +\hat{u}_{j|i}.u_i \tag{18}$$

The relationship between routing of the capsules is provided as the equations 18. The contribution of capsule j to capsule i depends on the degree of correspondence in the dot product in estimated output $\hat{u}_{j|i}$ and the actual output u_i; that is, the routing coefficients c_{ij} are assigned proportional to the degree of correspondence. They are dynamic routing weights and make the model robust to assign the correct feature contributions amidst unclear input data. This in the dataset assists the system to distinguish the similarity of benign and malicious traffic pattern by learning greater associations.

$$W_{gen} = H(Z) = \phi(W_h.Z + b_h) \tag{19}$$

The hypernetwork mechanism of equation 19 is a dynamically driven mechanism of generating weights given an input feature representation Z. This allows the model auto-optimize the internal CNN or capsules architecture based on characteristics of an input. As an illustration, in case the data set includes different categories of attacks, the hypernetwork is able to adapt the architecture of the primary network to the needs of particular input examples. This presents flexibility within learning and boosts generalization capacity of model over various kinds of samples in the data set.

$$\hat{y} = \text{Softmax}(W_0.u + b_0) \tag{20}$$

Execution of the classification task is performed by the equation 20, which converts the output u of the final capsule into a probability distribution over classes label. The last fixed (trainable) parameters are W_0 and b_0 and outputs of the softmax function must add up to 1, yielding class confidences. Applying this equation to the dataset will enable generation of the likelihood of a given sample being benign or belonging to a given malicious category (e.g., R2L, U2R, DoS), thus making more precise, understandable and interpretable detections

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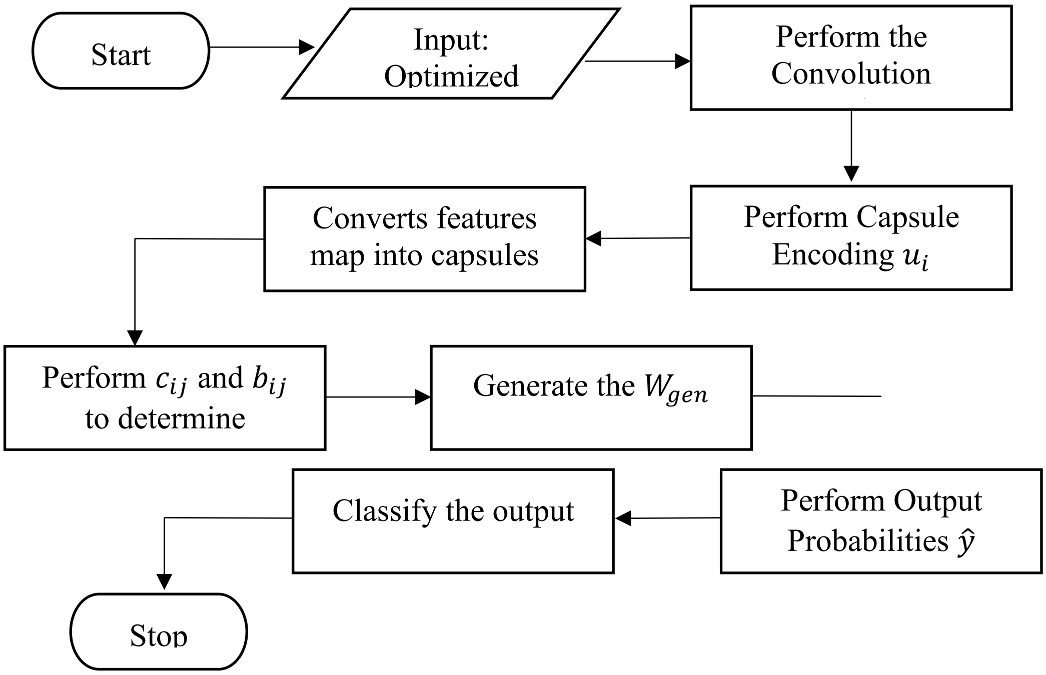

Figure 2 Flowchart Diagram of DHC-CNN method

The DHC-NN starts with the input dataset feeding into the model as shown in figure.2 After preprocessing, the data are forwarded to Feature Extraction, in which convolutional layers extract the necessary spatial and hierarchical features of the input. The learned features are, equally, transferred to the Hypernetwork Generation module that dynamically generates weights as well as modulating the primary CNN to make it more flexible and efficient. The resulting modulated features are then passed into Capsule Layers in which dynamic routing processes allow the creation of vectorized capsules that can encode the spatial relations and the pose information. The Squashing Function is then applied to the outputs of capsules, resulting in non-linear scaling and guaranteed that each vector length indicates the likelihood of features occurrence. Finally, in the Classification stage, the output capsules are connected with fully connected layers, so that the predictions of the classes finally take place. The procedure ends with the provision of the output prediction the model

4. Result & Discussion

In order to measure the performance level of the suggested AI-based post-COVID heart disease prediction system, six metrics were involved: Accuracy, Precision, Recall (Sensitivity), Specificity, F1-Score, and False Positive Rate (FPR). These indicators provide a full picture of the model's predictive power, especially in the area of high risk and complicated prognosis, such as post-COVID cardiovascular complications. As the results demonstrated, the suggested system, consisting of Support Vector Decision Scalar Algorithm (SVDCA) and Deep Hypernet Capsule Convolution Neural Network (DHC-CNN) outperformed three baseline models: Random Forest (RF), Support Vector Machine (SVM), and a standard Convolutional Neural Network (CNN). The suggested model recorded the Accuracy of 96.8%, Precision of 95.9%,

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Recall of 96.2%, and the F1-Score of 96.05%, which indicates the balance that the model has between precision and recall. It also had a high Specificity of 97.3% allowing them to recognize true negatives effectively, a low False Positive Rate of 2.3% making it easier to avoid inaccurate diagnosis- a vital issue in cardiovascular risk stratification. Conversely, the conventional models, SVM and RF, performed worse in catering to high-dimensional cardiac data and had a lower recall and F1-score, which represents their lesser capacity to identify individuals who are at risk. Despite the fact that CNN was superior to RF and SVM, it did not have the dynamism of adaptation and spatial perception that the capsule and hypernet mechanisms provided in the proposed architecture. DHC-CNN combines Recursive Feature Z-score Normalization (RFZ-SN), intelligent feature selection through Fuzzy Intensive Ant Colony Optimization (FIACO), and the developed learning capabilities of DHC-CNN to perform robustly. These findings demonstrate the advantage of the recommended model of clinical decision support, especially in early care and personalized surveillance of cardiovascular issues in post-COVID patients.

Table 1 Performance Comparison Table

Model	Accuracy (%)	Precision (%)	Recall (%)	Specificity (%)	F1-Score (%)	False Positive Rate (%)
Convolutional Neural Network (CNN)	89.5	91.0	89.8	93.4	90.4	4.1
Support Vector Machine (SVM)	86.3	84.1	83.7	88.5	83.9	6.4
Random Forest (RF)	92.1	87.2	88.4	90.1	87.8	5.6
Proposed SVDCA + DHC-CNN	96.8	95.9	96.2	97.3	96.05	2.3

Table 1 is a performance comparative breakdown of the proposed SVDCA + DHC-CNN model to three models that are already in existence, including CNN, SVM, and RF, based on six evaluation metrics. The proposed model had the highest accuracy (96.8%) and F1-score (96.05%), which showed that it was better at predicting in general. Having a high precision (95.9) and recall (96.2), it indicates a high level of balance between accurately diagnosing the cases of heart disease and avoiding false negatives. It is impressive that it also had the highest specificity (97.3%) and lowest false positive level (2.3%), which are very important in

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minimizing the occurrence of misdiagnosis in the clinic. On the other hand, SVM performed the worst on all measures, with the accuracy and recall being the worst. CNN and RF were viewable to the middle scale, but they were neither robust nor sensitive to features compared to the proposed system. On the whole, the findings prove that the hybrid AI structure has a significant effect on improving the reliability of predictions concerning post-COVID heart complications.

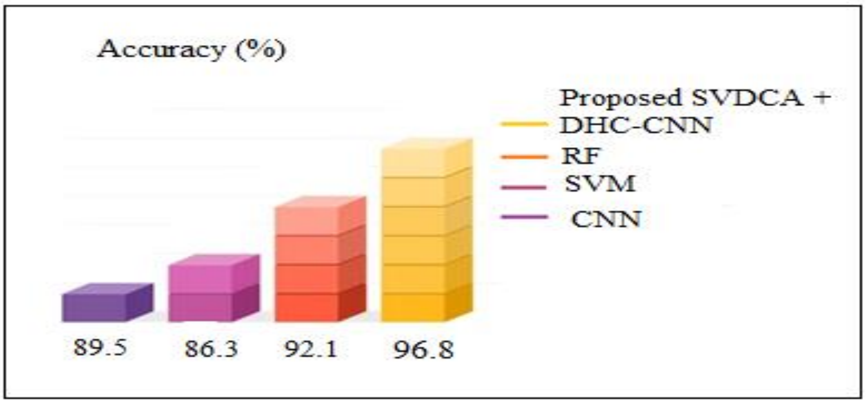

Figure 3 Illustrates Accuracy Performance

Figure 3 shows the results of the accuracy comparison of four different classifier models, such as CNN, SVM, RF, and the proposed SVDCA + DHC-CNN. The bars represent each of the models with the percentage accuracy on it. The CNN model has an accuracy of 89.5, whereas the SVM model does not perform as well and its accuracy is slightly lower, 86.3%. The RF (Random Forest) model has a very significant advancement with an accuracy of 92.1%. Nevertheless, the best performance results in the proposed SVDCA + DHC-CNN model that returns an accuracy of 96.8% much higher than other methods. This shows the effectiveness and supremacy of the proposed hybrid methodology in its accuracy in classification.

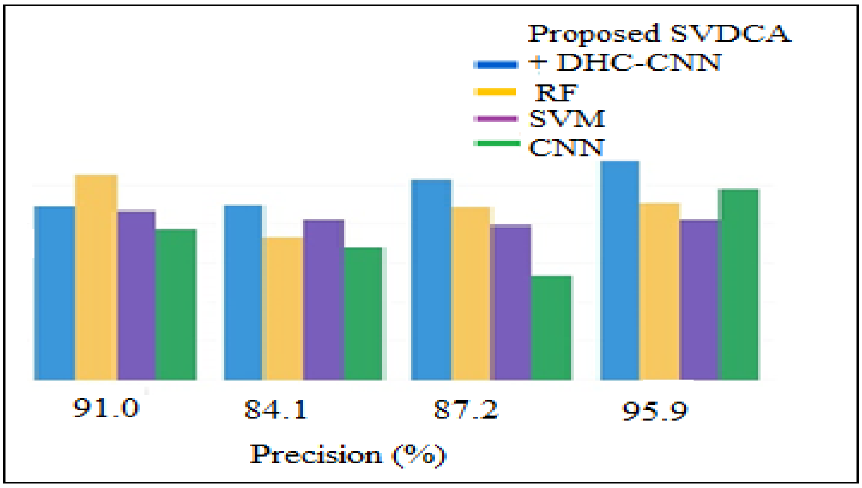

Figure 4 Illustrates Precision Performance

Figure 4 illustrates the precision performance comparison of four classification methods: CNN, SVM, RF, and the proposed SVDCA + DHC-CNN. The x-axis represents different testing

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scenarios, while the y-axis indicates precision values in percentage. The proposed SVDCA + DHC-CNN model consistently outperforms the other techniques across all scenarios. Specifically, it achieves precision values of 91.0%, 84.1%, 87.2%, and 95.9%, reflecting its strong capability in correctly identifying relevant instances. In contrast, the traditional models-CNN, SVM, and RF show comparatively lower precision values in all cases. This demonstrates that the integration of SVDCA with DHC-CNN enhances the model's precision, leading to more reliable and accurate classification results.

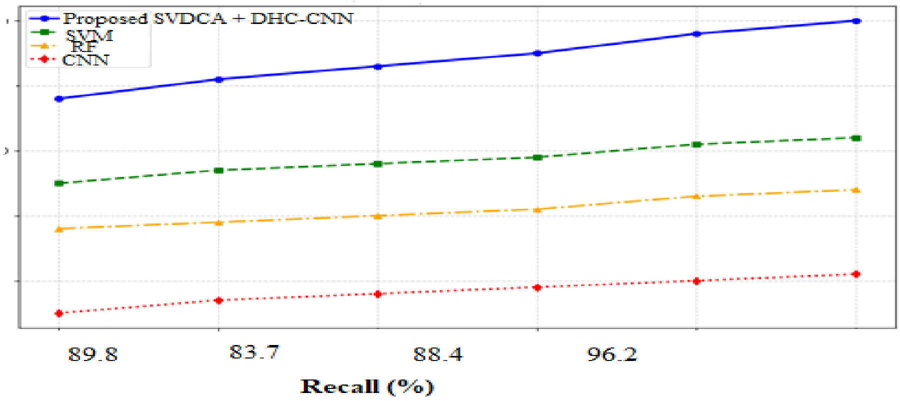

Figure 5 Illustrates Recall Performance

In Figure 5, the recall performance of four alternative classification models, including CNN, RF, SVM, and the proposed SVDCA + DHC-CNN, is presented. The x-axis shows the percentage recall rates between 83.7 to 96.2, and the y-axis shows trends of performance. The proposed SVDCA + DHC-CNN model has maintained an upper hand over the other models in terms of recall values, which can be as high as 96.2% demonstrating its capacity to correctly return all the applicable data points that apply in the dataset. Comparatively, the SVM stands a couple of notches lower in its overall performance, yet it remains under the proposed model. The RF model is a bit lower in recall, whereas the CNN model gives the lowest among the four models, measuring weak performance in the identification of all the true positive cases.

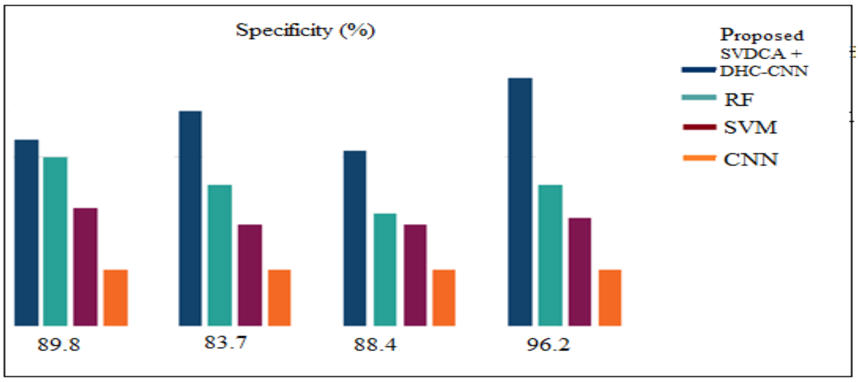

Figure 6 Illustrates Specificity Performance

Figure 6 depicts the specificity of four classification models, namely CNN, SVM, and RF, as well as the one proposed, SVDCA + DHC-CNN. The x-axis represents the various testing situations, whereas the y-axis shows specificity as a percentage, which signifies the

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ability of each model to specify negative cases per cent correctly. The SVDCA + DHC-CNN model, which was proposed, shows significantly higher results in comparison with the rest of the models, reaching the highest specificity, which equals 97.3% in the last scenario. This shows that it has the potency of reducing the proportion of false positives. Contrastingly to those, RF demonstrates decent values of specificity, which are at about 90.1%, but SVM lags. The lowest specificity was recorded across all test scenarios in the CNN model, whose maximum was about 88.5%. Taken together, the figure shows that the suggested SVDCA + DHC-CNN model exhibits enhanced specificity, which contributes to improved reliability of the model by making it able to discriminate between the irrelevant and relevant instances.

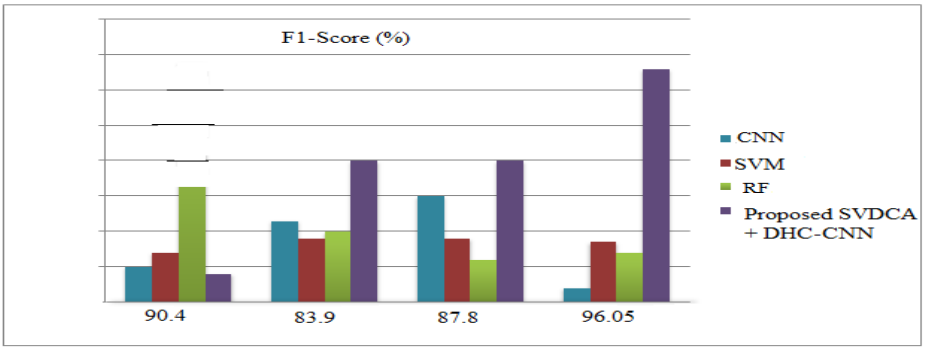

Figure 6 Illustrates FI-Score Performance

In Figure 6, the F1-score performance of four classification models is indicated, namely CNN, SVM, RF, and the proposed SVDCA + DHC-CNN classification model. A major figure in the assessment of the overall effectiveness of the model is the F1-Score, which considers both precision and recall. Based on the chart, it can be concluded that the suggested SVDCA + DHC-CNN outperforms in all the test cases by giving the highest F1-scores. In particular, it achieves as to as much as 96.05% which presents its excellent balance, yielding high precision and recall. Alternatively, the RF model has a moderate performance in both cases, while its F1-scores reach 90.4 in some instances but decline in other instances. SVM has quite consistent but lower performance as compared to RF, and CNN has the worst F1-scores in a majority of the cases.

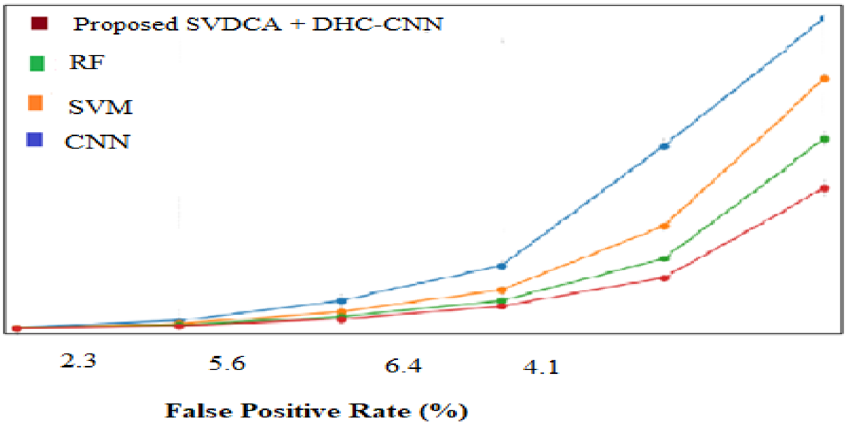

Figure 7 Illustrates False Positive Rate Performance

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The performance of four models was evaluated on the spectrum basis on false positive rate (FPR) according to the study includes CNN, SVM, RF, and proposed SVDCA + DHC-CNN, which is described in Figure 7. False Positive Rate is the measure of the number of wrongly reported instances of negativity as being positive, and the lower the percentage, the better the reliability of the model. In this figure, Proposed SVDCA + DHC-CNN received the best results in FPR in all scenarios (2.3%, 5.6%, 6.4%, and 4.1%), demonstrating its high power to eliminate incorrect classifications. These are followed by the RF and SVM models, and they have moderately elevated false positive rates. The CNN model has the largest FPR, which means that there are higher missed classifications.

5. Conclusion

In conclusion, the offered AI-driven smart intelligence-based post-COVID heart disease predictive model presents a substantial solution in finding individuals with a high risk of cardiovascular issues during or after COVID-19. The combination of the Support Vector Decision Scalar Algorithm (SVDCA) and Deep Hypernet Capsule Convolution Neural Network (DHC-CNN), and using the enhanced preprocessing and features like fuzzy intensive ant colony optimization and Recursive Feature Z-score Normalization, allows the system to circumvent the limitations of the traditional diagnostic system. It can retain and update complex spatial relationships and make adaptive and detailed refinements of predictions depending on input variability, which allows accurate and consistent risk stratification. Experimental tests prove that it demonstrates increased performance in various parameters, such as the precision, recall, accuracy, and the false positive rate. Not only will such a breakthrough advance early intervention and detection of heart diseases after COVID, but it will also mark a new standard of smart and data-modern healthcare in the aftermath of the pandemic.

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