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Cardiovascular disease risk factors prediction using deep learning convolutional neural networks

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ABSTRACT

Heart disease remains a leading cause of mortality worldwide, prompting healthcare researchers to leverage analytical tools for comprehensive data analysis. This study focuses on exploring crucial parameters and employing deep learning (DL) techniques to enhance understanding and prediction of cardiovascular disease (CVD) risk factors. Utilizing SPSS and Weka tools, a cross-sectional and correlational design was employed to analyze extensive medical datasets. Binomial regression analysis revealed significant associations between age ($p = 0.004$) and body mass index ($p = 0.002$) with CVD development, highlighting their importance as risk factors. Leveraging Weka's DL algorithms, a predictive model was constructed to classify CVD causes. Particularly, convolutional neural networks (CNN) showcased remarkable accuracy, reaching 98.64%. The findings underscore the elevated risk of CVD among university students and employees in Saudi Arabia, emphasizing the need for heightened awareness and preventive measures, including dietary improvements and increased physical activity. This study underscores the importance of further research to enhance CVD risk perception among students and individuals in similar settings.

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1. INTRODUCTION

According to the World Health Organization (WHO), cardiovascular diseases (CVDs) stand as the primary contributor to global mortality, responsible for 31% of all deaths worldwide and claiming over 75% of lives in developing nations. This percentage is particularly high in the Eastern Mediterranean Region, where CVDs are responsible for 54% of deaths. Risk factors for CVDs are categorized as controllable and

non-controllable. Controllable factors include obesity, blood pressure, sedentary lifestyle, smoking, dyslipidemia, diabetes, and hypertension [1]–[4]. Despite the critical need for accurate prediction of CVDs, identifying and monitoring CVD risk factors remains a significant challenge for cardiologists. The general population's prevalence of these risk factors can reach up to 50%. Identifying the specific risk factors contributing to an individual's CVD diagnosis, factors like age, blood sugar levels, and blood lipids contribute to the complexity of the condition. Traditional diagnostic methods, including blood tests, are often time-consuming and expensive [3], [4]. The integration of artificial intelligence (AI), comprising machine learning (ML) and deep learning (DL), into the medical field is rapidly gaining momentum for its prowess in analyzing, classifying, diagnosing, and predicting medical conditions [5]–[7]. In recent years, as the demand for robust dataset analysis has surged, AI algorithms, notably neural networks, have become increasingly prominent due to their capacity to grasp the intricacies of training data distributions and generalize this understanding to unseen data, crucial for effective classification and analysis of medical datasets [6], [7]. This study utilizes artificial intelligence algorithms to analyze, and anticipate CVD based on a curated dataset outlined in study [8].

To our knowledge, there has not been a comprehensive study utilizing deep learning AI algorithms and tools for predicting CVDs on real-world datasets. While there are notable efforts in this area, prior studies have predominantly relied on datasets sourced from KDDnuggets and UCI repository, such as those referenced by Martin-Isla *et al.* [9] for image classification, or conducted meta-analyses [10]–[12], which are not directly comparable to our research. Additionally, the majority of previous analyses were carried out using SPSS or similar tools. Consequently, our objective is to set a benchmark for future studies employing AI and its diverse predictors to enhance our understanding of the risk factors associated with CVDs. This paper will review how AI is used to predict risk factors for CVDs, discussing different machine and DL methods used for this purpose. Additionally, it will investigate the primary determinants of CVD risk factors and deliberate on the advantages and hurdles associated with employing AI within this domain. Additionally, recommendations for future research in this area will be provided. The current study focuses on analyzing key parameters and employs DL through convolutional neural networks (CNNs) to gain insights into and forecast the impact of each risk factor for CVDs.

2. LITERATURE REVIEW

Machine learning classification has been applied to identify several CVDs, revealing a significant increase in mortality rates among smokers [13]. Furthermore, Hsieh *et al.* [14] explored risk factors for CVD among university personnel. In their research carried out in Colombia, it was discovered that although 92% of students were at low risk of CVD, more than half of both university personnel demonstrated at least one risk factor. These factors included being overweight, leading sedentary lifestyles, or having hypertension. A study conducted by Güneş *et al.* [15] in Turkey aimed to assess the awareness of CVD risk factors among university students ($n = 2450$). The research revealed that students recognized smoking (58.7%), stress (71.8%), high cholesterol (72.3%), obesity (64.3%), diabetes (52.7%), physical inactivity (47.8%), hypertension (64.2%), and a family history of CVD (44.4%) as the primary risk factors for CVD disease. Interestingly, the findings indicated a tendency among men to overlook these risk factors. Despite this knowledge, there remains a notable gap in research concerning the prevalence and awareness of CVD disease risk factors among university students and staff, particularly in the Middle East. A review conducted by Damen *et al.* [3] analyzed 212 articles to identify predictive models for CVD disease risk factors in the general population. The majority of these prediction studies were carried out in Europe ($n = 167$, 46%) and focused on fatal and non-fatal coronary heart disease ($n = 118$, 33%), spanning over a period of more than ten years ($n = 209$, 58%). Commonly identified predictors included smoking, age, gender, blood pressure, blood cholesterol, diabetes, body mass index, and hypertension.

In the realm of CVD, several studies have been conducted over the past two decades, leveraging Weka extensively for analyzing diverse datasets, particularly focusing on heart disease. Originating in 1988, the UCI ML repository initially provided four notable datasets dedicated to heart disease research. Various research endeavors have since explored a wide array of ML techniques aimed at predicting the likelihood of heart attacks among patients across different medical institutions. For instance, one study [13] deployed classifiers like k-nearest neighbor (with subpar accuracy) and random forest (yielding the highest accuracy at around 90%). Other research ventures extended beyond the heart disease dataset provided by the UCI repository. For instance, in [16], a convolutional neural network was utilized, achieving an accuracy of 82%, while [17] experimented with various ML algorithms. Additionally, studies [18], [19] employed conventional artificial neural networks, while [20] utilized genetic algorithms and recurrent fuzzy neural networks [21]. Some researchers focused on mitigating overfitting in predictive models through optimization metaheuristics, as evidenced in [22]. Several studies [22]–[34] share similarities with our research approach but utilize

different datasets and ML methods, with references to [35], [36]. Notably, none of the aforementioned studies utilized ML techniques in analyzing real-world datasets, instead focusing solely on those provided by the UCI repository.

3. METHOD

This section provides an overview of the design methodology employed in developing the DL4J predictor. It encompasses a discussion on the tailored neural network architecture optimized for the classification task. In addition, an elucidation of the rigorous dataset processing procedures undertaken, and a detailed exposition of the implementation specifics pertaining to DL4J.

3.1. Classification and Weka workbench

ML operates as a supervised approach, relying on labeled datasets for predictions. In classification tasks, a *training_subset* consisting of pairs of arguments-outcomes is utilized to establish a model for such mapping. By assimilating these observations, the system anticipates future outcomes while minimizing errors. Among various techniques suitable for classifying structured data, artificial neural networks (ANNs) stand out, encompassing CNNs. This study exclusively concentrates on neural networks for consistency and equitable comparison, particularly while implementing DL techniques.

Weka is widely recognized as a powerful free tool equipped with a wide array of procedures and tools tailored for data predictive modeling development. Its user-friendly graphical interface facilitates seamless access to all functionalities. In this study, Weka is harnessed to execute classification and clustering tasks through the integration of the DL4J library, which combines optimization and classification algorithms.

3.2. The DeepLearning4J (DL4J) model

A neural network model must recognize patterns in a dataset to identify specific features of CVD disease instances such as hypertension and cholesterol. Convolutional neural network can detect certain features and extract significant attributes from a data group. DeepLearning4J (DL4J) typically uses a simple feedforward multilayer network (e.g., five layers), a fully connected type of CNN. Since the accuracy of the classification task is all that matters, then we utilize (in some of the models) a combination of deep CNNs with boosting strategy as implemented in study [27]. We realize the optimization algorithm named Adam, which is a gradient-based optimization algorithm of stochastic objective function of the first order which is based on adaptive estimates of lower-order moments. Hence, we are motivated to implement a DL4J that guarantees accuracy through effective parameter tuning and efficient training, while utilizing Adam for speed and robust performance.

Incorporating CNN within DL4J addresses a common issue encountered by traditional neural networks, such as the multilayer perceptron, which relies on a single perceptron per input. When dealing with large datasets or multi-label class attributes, the multilayer perceptron struggles. However, CNN tackles this challenge by utilizing filters or wrappers based on convolutional operations. This allows CNN to analyze the impact of correlated coefficients, such as selected attributes, more effectively in datasets with strong associations, while building subsets based on instances. By passing the entire dataset through several filters, CNN generates feature subsets. These subsets are then subjected to an activation function to determine the presence of specific features at particular positions or correlations within the data. Incorporating additional filtering layers and creating more feature subsets can enhance performance, particularly as CNN architecture deepens. Pooling layers are employed to select the largest values from feature subsets and treat them as inputs for subsequent layers. Specifically, maximum pooling is utilized to identify outliers, ensuring that CNN accurately identifies features.

Within the realm of CNNs, three essential layers play pivotal roles: pooling, convolutional, and fully connected layers. These layers are integral components of CNN architecture, working synergistically to process input data, extract meaningful features, and facilitate accurate predictions. The filter employed to select and assess a subset of features is a crucial parameter. Pooling layers, akin to convolutional layers, perform specific functions such as max-pooling, which selects the maximum value from a subset of filtered attributes, or average pooling, which computes the average value within the filtered subset. These layers are commonly utilized to reduce the network's dimensionality. Fully connected layers are positioned before the CNN's classification output and are utilized to normalize results prior to classification. In summary, CNNs can learn the following: i) in the progression of CNN layers, there is an evolution towards understanding more intricate patterns; ii) initially, the first layer grasps rudimentary features like correlations and significance; iii) as we move through the middle layers, the network delves into detecting subsets of attributes; and iv) finally, in the last layer, the network excels in identifying the most critical and evaluated subset of attributes, drawing from a range of diverse measurements.

The robustness and effectiveness of its fully connected architecture stem from its robust gradient flow, facilitated by implicit deep supervision, parameters, and computational efficiency achieved through strong connectivity. As the number of parameters increases, so does the complexity, resulting in a wider array of diverse features while still maintaining low complexity features. Therefore, in this study, DL4J is employed to classify seven CVD-related diseases, encompassing training, validation, and testing phases. The model is trained using a dataset meticulously curated by the authors, with significant features meticulously chosen. The values of the parameters that perform the best on the validation subset are subsequently utilized for testing purposes. The neural network architecture within the DL4J model comprises the following layers:

- Convolutional layer: preprocessing and feature selection by applying convolution.
- Dense layer: associate all units with all branches of the parent layer. It consists of a collection of DenseBlocks including transition layer (which performs convolution and pooling), classification layer, and dense block layers. It employs two main parameters, hasBias and hasLayerNorm which they activate bias parameters in the model and enable normalization on the layer respectively.
- Subsampling layer: selects from groups of units in the parent layer using various strategies like averaging or selecting the maximum.
- Batch normalization: normalizes activations of the parent layer within each batch.
- LSTM: utilizes long short-term memory approach.
- Global pooling layer: applies pooling across time for recurrent neural networks (RNNs) and pooling across sequences for CNNs.
- Output layer: produces classification or regression outputs.

Trimming down features can enhance a model's effectiveness. These selected predictor variables or features offer optimal predictive capabilities when modeling a dataset. Consequently, feature selection serves to prevent overfitting, decrease model complexity, and enhance interpretability. Figure 1 shows the generic DL4J-based prediction model.

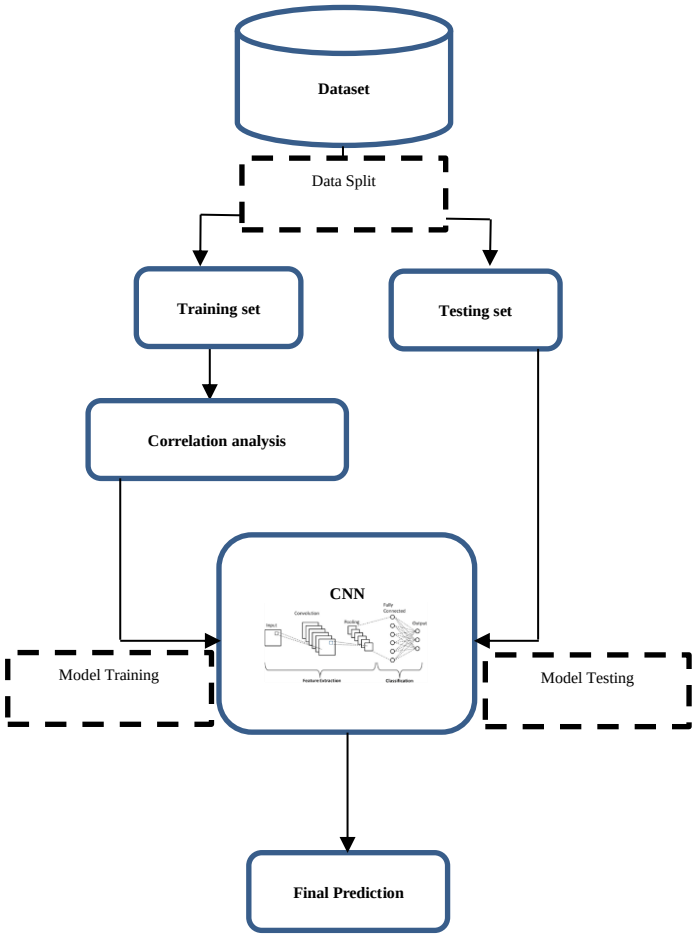

Figure 1. A generic DL4J -based prediction model for CVD risk factors

Figure 1 illustrates the workflow of the generic prediction model leveraging the DL4J framework. Initially, the dataset undergoes a 10-fold cross-validation (CV), dividing it into a 90% training set and a 10% testing set. Next, all attributes from the CVD dataset undergo correlation analysis, employing principal component analysis (PCA) to identify significant influencers of prediction model accuracy. Then, DL4J is applied to the training set, utilizing the identified correlated features. Finally, DL4J validates predictions using the testing set, assessing performance using various evaluation metrics such as accuracy, precision, recall, F-measure, ROC curve, and mean square error.

Through careful experimental design, we established and utilized predetermined parameters and configurations, employing a 10-fold CV testing technique. The rationale behind selecting CV lies in its widespread use for evaluating predictive models. This method involves dividing the dataset into k folds, training models on all but one-fold (used as the test set), and repeating this process to build k distinct models. By averaging the performance of these models, an overall performance estimate is obtained, making CV the gold standard for assessing model performance. While it requires training multiple models, CV offers an objective and reliable evaluation, particularly when the problem is complex or ambiguous. In contrast, the training dataset technique is suitable for descriptive modeling with complete datasets, while the test set approach is more suitable for large datasets, neither of which applies to our experiment with 370 occurrences. Although the percentage split technique provides a quick overview, it may not be suitable for decision-making. Therefore, CV is commonly used as the default method, offering a more accurate estimate of model performance, albeit not ideal for very large datasets. Overall, CV is preferred for its simplicity, providing less biased estimates compared to straightforward train/test splits. Understanding the data and its patterns is crucial before preprocessing or adjusting model parameters, ensuring informed decision-making throughout the analysis process and considering potential differences in significance.

4. RESULTS AND DISCUSSION

This study investigated the effects of a CNN model in predicting CVD risk factors. While earlier studies have generally explored the impact of DL techniques in classifying CVD whether existed or not, they have not explicitly addressed their influence on risk factors for a CVD case. We found that the risk factors (e.g., heart disease and blood pressure) correlates with CVD. The proposed method in this study tended to have an inordinately higher proportion of males with potentials of blood pressure and previously diagnosed heart disease as CVD cases.

4.1. Computational results

In this segment, we delve into the foundational aspects of training and evaluating the predictive model, encompassing its experimental setup, outcomes, and dataset specifications. Our analysis was conducted using Weka version 3.9.4, a Java-based workbench renowned for its analytical capabilities. The subsequent sections delineate the training and testing setup, detail the parameter configurations of the predictive model, and expound on the integration of ML and DL techniques within the model framework.

4.2. Experimental settings

Setting up the experiments are crucial for building the predictive model as well as for results comparisons and validation. Taking into account the specifications of the dataset and the architecture of DL-based methods. Hence, several consecutive steps are considered in conducting the experiments:

a. Dataset gathering comprises the aggregation of pertinent data presented in a tabulated structure. Following the identification of the problem, the compiled data undergoes formatting into a Weka-compatible Arff dataset, with class attributes appropriately annotated for classification purposes. The efficacy of the model hinges on the volume and caliber of the dataset. This stage culminates in the tabular organization of data designated for model training.
b. Data preprocessing involves the meticulous handling and preparation of data intended for training purposes. This encompasses the refinement and refinement of data through the elimination of redundancies, rectification of inaccuracies, treatment of missing values, standardization, and conversion of data formats.
c. Attribute curation involves the deliberate selection of a subset of attributes deemed influential to the model's performance and precision.
d. Selecting a model suitable for classification and regression tasks.
e. We iteratively train the model to optimize its ability to make accurate predictions.
f. To measure its objective performance and allows further tuning.
g. Fine-tuning parameters, also known as hyperparameter tuning, including variables such as the number of training steps, learning rate, and initialization values, can potentially enhance the performance of the model.

h. Using a separate test dataset, with known class labels, to perform predictions and assess the model's performance in real-world scenarios.

Our experimental methodology unfolded across three distinct analytical tiers, each contributing unique insights to our investigation. We initiated the process with predictive modeling using DL techniques, leveraging their advanced capabilities to discern intricate data patterns and anticipate outcomes. Transitioning to the Weka environment, we employed a range of machine learning algorithms for classification and regression tasks, uncovering deeper insights and uncovering patterns within the dataset. Finally, employing IBM-SPSS, we delved into descriptive statistical analyses, meticulously examining measures of central tendency, correlation coefficients, and attribute significance to gain a holistic understanding of the dataset's intricacies. Therefore, we proceeded to explore these measures further using the Weka workbench for both ML and DL model training. DL, a subset of ML employing advanced techniques such as neural networks, enhances the learning process more extensively.

4.3. Experimental datasets

The datasets utilized in this study were obtained through a questionnaire, encompassing a total of 370 participants. Among them, the majority were male, totaling 240 individuals, with approximately 294 participants falling within the age range of 18 to 25, as detailed in Table 1. The dataset was divided into two subsets, namely training and testing, within the "Arff" Weka file, containing a total of 36 attributes, including 7 class attributes. The training set was utilized to train the DL4J model for prediction purposes, while the test set served to evaluate the accuracy of these models using new data. As per experimental design, the training set was split into 70%, with the remaining 30% allocated to the test set. Table 2 provides a summary of labels and their corresponding counts for each class attribute. In comparison to well-known UCI heart disease datasets, our dataset comprises 76 attributes, which have been condensed to 14 significant attributes pertaining to a single class (e.g., heart disease).

Table 1. Sociodemographic characteristics of the participants ($n = 370$)

Characteristics	Frequency	Percentage
Gender		
Male	240	64.9
Female	130	35.1
Total	370	100.0
Age		
18 - 25	294	79.5
26 - 40	27	7.3
> 40	49	13.2
Total	370	100.0
Employment status		
Employed	76	20.5
Unemployed	294	79.5
Total	370	100.0
Marital Status		
Single	168	45.4
Married	202	54.6
Total	370	100.0
Nationality		
Saudi	304	82.2
Non-Saudi	66	17.8
Total	370	100.0

In contrast, our dataset comprises 36 attributes, which have been condensed to a select set of significant attributes (2-5 attributes) associated with 7 classes, extending beyond heart disease diagnosis. Predicting a class becomes easier, quicker, and more precise when using a smaller set of attributes. With seven classes in our dataset, we can diagnose seven different CVDs related to heart disease. Moreover, our dataset contains no missing values, unlike the UCI heart disease datasets, simplifying processing and enhancing comprehension. Several significant attributes, such as age, gender, cholesterol, fasting blood sugar, and blood pressure, are shared between our dataset and the UCI datasets, enhancing the validity of our dataset. The dataset comprises numerical readings of CVD indexes and related diseases, including fasting blood sugar, low and high blood lipids, triglycerides, cholesterol, body mass index, blood pressure, demographics, and certain smoking and eating habits. These readings reveal distinct features of heart disease cases, notably associated with other features such as blood pressure and fasting blood sugar, well recognized by medical experts and therapists.

Table 2. Dataset class attributes and labels

Class	Label	Count
Heart disease (HD)	Yes	112
	No	258
Blood pressure (BP)	Yes	132
	No	238
Low blood lipids (LBL)	Normal	237
	BroadlineHigh	62
	High	71
High blood lipids (HBL)	Normal	192
	BroadlineHigh	86
	High	92
Triglyceride (Tri)	Normal	190
	BroadlineHigh	68
	High	112
Cholesterol (Cho)	Normal	218
	BroadlineHigh	42
	High	110
Fasting Blood Sugar (FBS)	Excellent	233
	Good	33
	Acceptable	57
	Poor	47

4.4. Experimental results

Here, we summarize the obtained accuracy results of ML and DL predictive models. First, we have implemented several popular ML algorithms with the same experimental settings and configuration for the classification task, e.g., data preprocessing, testing mode, and attribute selection method. Then, we implemented a DL algorithm "DL4JMlpClassifier" in four different configurations to demonstrate its accuracy over other ML algorithms with different attribute selection methods and compare them against each other. The classification task in DL4J is carried out using a CNN approach, which entails at least three layers of nodes: input, hidden, and output layers. CNN is preferred for its supervised training process, employing a non-linear activation function and backpropagation. These features enhance the model's flexibility in defining relationships. In summary, the CNN algorithm operates as follows:

a. Forward pass (input layer): Inputs are passed into the model, where each input undergoes convolution with various filters to produce the model's calculated output.
b. Loss calculation (activation function/hidden layer): After processing a sample data (e.g., a record in a dataset), the model generates a predicted output. Subsequently, backpropagation computes the gradient of the loss concerning all learnable parameters in the model.
c. Backward pass (output layer): During model training, backpropagation computes the loss gradient, and optimization techniques (e.g., Adam) update the weights based on the information gathered from backpropagation.

In DL techniques, hyperparameters and setups are experimentally predetermined and applied, including the use of 10-fold CV test mode. The rationale for employing this testing mode, "CV", is outlined below to justify its suitability for our experiments. One of the techniques used for evaluating predictive models is CV, which involves splitting the dataset into k-folds. This method trains a model on all folds except one, which is held out as the test set. This process is repeated k times, with each fold taking turns as the test set. The average performance of all k models is then calculated. Although creating multiple models incurs a computational cost, CV is widely regarded as the gold standard for evaluating model performance. The technique of training on the entire dataset is primarily employed for creating descriptive models rather than predictive ones, aiding in a better understanding of the problem. This approach is facilitated by software such as IBM-SPSS. Conversely, using a separate test set is typically reserved for very large datasets, which is not applicable to our experiment with a dataset size of 370 instances. Percentage split techniques offer a quick performance assessment but may not be suitable for decision-making purposes due to their impracticality. Therefore, CV is the preferred option when there is uncertainty about the problem's description. It generally provides a more accurate performance estimate compared to other evaluation techniques. However, CV is not recommended for very large datasets. Common values for k in CV are 5 and 10, depending on the dataset size.

In summary, CV is widely used because it offers a straightforward approach and typically provides a less biased or optimistic estimate of model performance compared to other methods, such as a simple train/test split. Establishing the baseline accuracy of each class attribute using the ZeroR rule-based ML algorithm is essential as it serves as a benchmark for predictive model performance assessment. ZeroR typically predicts the most prevalent class attribute, for instance, by calculating the proportion of instances belonging to the majority class. For example, based on the observations from Table 3, in the case of heart

disease prediction, if 258 instances out of 370 belong to the heart disease class, the accuracy would be 69.72%. This baseline accuracy serves as a reference point to evaluate the performance of predictive models. However, the true indicator of a highly accurate model, which avoids overfitting, is the receiver operating characteristic (ROC) area under the curve in Table 3. For instance, consider DL4JMlp-1, which achieves an accuracy of 96.75% and an ROC of 0.989 for the heart disease class. On the other hand, DL4JMlp-3, despite having a higher accuracy for the fasting blood sugar (FBS) classification, falls short in ROC (0.743) compared to DL4JMlp-1. Implementing ZeroR is valuable in comprehensive empirical studies, particularly when comparing results against software like SPSS.

This observation may be attributed to the relatively small size of our dataset, where the attributes may not offer sufficient information. Hence, it is crucial to thoroughly understand the data and its patterns to support the baseline classifier (ZeroR) before preprocessing the data or fine-tuning a model's parameters. It is important to consider whether these small or large differences are likely to be significant, particularly in our case. For instance, in the case of the heart disease (HD) class, DL4JMlp-1 exhibits a small significance slightly larger than 1% compared to DL4JMlp-2, and relatively high significance compared to MLP (4%), and very high compared to the baseline accuracy (27%). This highlights the importance of scrutinizing differences and their potential significance in our analysis.

Table 3. Predictive DL models for each class

Model		HD	BP	LBL	HBL	Tri	Cho	FBS
ZeroR	AC	69%	64%	64	51	51%	58%	62%
RF	AC	95%	72%	69%	42%	67%	54%	61%
	ROC*	.97	.76	.93	.081	.90	.83	.68
J48	AC	95 %	71%	69%	37%	65%	48%	60%
	ROC*	.98	.80	.90	.12	.91	.72	.90
MLP	AC	94%	70 %	66%	38%	61%	51%	61%
	ROC*	.96	.73	.75	.46	.70	.51	.73
MLPBP	AC	95%	74%	65%	45%	56%	48%	59%
	ROC*	.98	.79	.75	.54	.67	.53	.72
DL4JMlp-0	AC	95%	67%	67%	44%	65%	52%	59%
	ROC*	.98	.72	.78	.50	.71	.54	.74
DL4JMlp-1	AC	96%	68%	71%	45%	68%	54%	57%
	ROC*	.98	.73	.80	.47	.74	.51	.71
DL4JMlp-2	AC	95%	68%	66%	44%	67%	52%	62%
	ROC*	.98	.73	.78	.46	.71	.54	.73
DL4JMlp-3	AC	96%	72%	71%	61%	70%	55%	58%
	ROC*	.98	.76	.80	.72	.73	.55	.72

Notes: *Weighted average; MLP: Multilayer perceptron function-based classifier; MLPBP: Multilayer perceptron using backpropagation function-based classifier; DL4JMlp: Java version of DL MLP function-based classifier. RF: Random Forest based decision tree; J48: Java version of the decision tree C4.5.

Initially, we implemented default parameter settings of the predictive model DL4J, including training and testing mode. Table 4 presents the parameters settings for the well-known MLP and MLPBP classifiers, as well as four versions of the DL4JMlp. In addition, a fifth version named DL4JMlp-b is considered in the experiments as it presents the enhancement of the previous four versions in terms of parameters tuning. The accuracy, efficiency, and overall performance may improve by further investigating the optimization algorithm's impact by employing more advanced metaheuristics. Table 4 presents differences between the classification models. We compared our DL4J model with other traditional ML and DL models, which outperformed all other models. Our study suggests that higher heart disease and blood pressure levels indicate an imminent CVD case. In addition, those two risk factors are not associated with poor performance in DL4J as in the case of other traditional models. The proposed DL4J model may benefit from DenseNet, and search method without adversely influencing its accuracy.

Table 5 and Figures 2 to 5 illustrate the accuracy of the top-performing classifier. The DL4JMlp-b model exemplifies them while concerning all 7 class attributes. Beyond the metrics outlined in Table 5, various other critical measures and rates are detailed as follows:

a. Accuracy: This metric reflects the overall correctness of the classifier, indicating the percentage of test instances correctly and incorrectly classified. However, it has limitations such as lack of chance correction and insensitivity to class distribution, making the ROC Area a preferred measure.
b. Matthews's correlation coefficient (MCC): MCC assesses the quality of binary classifications, considering true and false positives and negatives. It is a balanced measure suitable for classes of varying sizes.
c. True positive rate (TP): TP denotes how often the model predicts "Yes" when the actual class is "Yes", representing correctly classified instances.

d. False positive rate (FP): FP indicates how often the model predicts "Yes" when the actual class is "No", representing incorrectly classified instances.
e. Precision: it measures the accuracy of positive predictions, calculated as the ratio of correctly classified instances to the total instances predicted as positive.
f. Error rate: it reveals the frequency of classifier errors if it always predicted the majority class. It serves as a baseline for performance comparison, particularly in numeric prediction tasks.
g. Cohen's Kappa: it quantifies the classifier's performance relative to chance alone, providing a chance-corrected agreement measure between classifications and true classes.
h. Recall: akin to the true positive (TP) rate, it indicates the proportion of instances correctly classified as a specific class relative to the actual total instances in that class.
i. F-measure (or F-score): it offers a balanced assessment of precision and recall, calculated as the weighted average of the two. It provides a combined measure of the model's ability to make precise predictions and retrieve relevant instances.

Table 4. Hyperparameter settings and neural network configuration for DL4JMlp models

Parameter	MLP	MLPBP	DL4JMlp				
			0	1	2	3	b
Activation fn.	ApproxSigmoid	Softplus	Softmax				
#layers	3						
#inputs	35						
Hidden layers	18		36				
#outputs	2						
Learning rate	0.3		0.1				
Momentum	0.2						
Epoch	50	100	10	100			
Instance iterator	Multilayer		Conv.				Recur.
Bias updater	-		Sigmoid = 0.001				
Optimizer	Steepest descent heuristic		Stochastic gradient descent				
Updater	-		Adam				Sigmoid
Test mode	Cross-validation = 10 folds						
Attribute selection	-		Csf	PCA	Wrapper		Wrapper
Search method	-		BestFirst	Ranker	Greedy		Genetic
DenseNet	Activation fn. = Softmax || Epochs = 90 || Learning rate = 0.1 || weight decay = .00004 || momentum = 0.9						

Table 5. Enhanced DL prediction model using Weka and its best selected subsets of attributes

Class attribute	Selected attributes	DL4JMlp-b (accuracy)
Heart disease	11	98.64%
Blood pressure	11	92.97%
Low blood lipids	10	81.89%
High blood lipids	6	75.67%
Triglyceride	6	72.97%
Cholesterol	12	79.45%
Fasting blood sugar	10	80.0%

With a dataset comprising 370 instances, Table 3 indicates that all classifiers achieved highly accurate classifications. Notably, both DL4JMlp-1 and DL4JMlp-3 models, along with several others, attained the highest accuracy compared to the baseline accuracy across all classes. While some achieved excellent or acceptable accuracy, others demonstrated poorer performance. Notably, certain models exhibited signs of overfitting, such as MLP. The DL4JMlp models demonstrated stability without either overfitting or underfitting the data. Indicators of this stability include Kappa, precision, recall, F-measure, and the confusion matrix. These metrics collectively affirm the models' robustness and reliability in accurately classifying the dataset.

The optimal experimental configurations for the best performing DL4JMlp-1, DL4JMlp-3, and DL4JMlp-b models are detailed in Table 5. These configurations consist of 36 hidden layers, a learning rate of 0.1, and a momentum of 0.2 for weight updates. The training process involves 100 epochs, with CV employed as the testing mode. Additionally, the models utilize either a convolutional or recursive instance iterator and employ the Softmax activation function. The LossMCXEN serves as the loss function, with a maximum number of epochs set between 5 and 30 for detecting improvements. Further enhancements include the use of a bias updater and attribute selector. These meticulously chosen configurations aim to optimize the models' performance in accurately classifying the dataset. Activation function, instance iterator, maximum epochs, number of epochs, and bias updater are significant improvements for the default model DL4JMlp-0 towards DL4JMlp-b. Even more significant improvement is contributed by the attribute selector,

e.g., wrapping subsets evaluation rather than classifying features subsets evaluation, and genetic algorithm search rather than best-first search method. A wrapper subset evaluator employs a genetic algorithm to estimate the accuracy of the learning scheme for a subset of features using CV. Utilizing a genetic algorithm involves navigating through a training data space to identify pertinent features. Inspired by the principles of natural evolution, this approach operates with a population of subsets. Through a generational process, potential subsets are generated utilizing crossover and mutation mechanisms. Subsequently, a selection mechanism is employed to choose the most optimal subsets, typically those with the highest rankings, to proceed with further analysis.

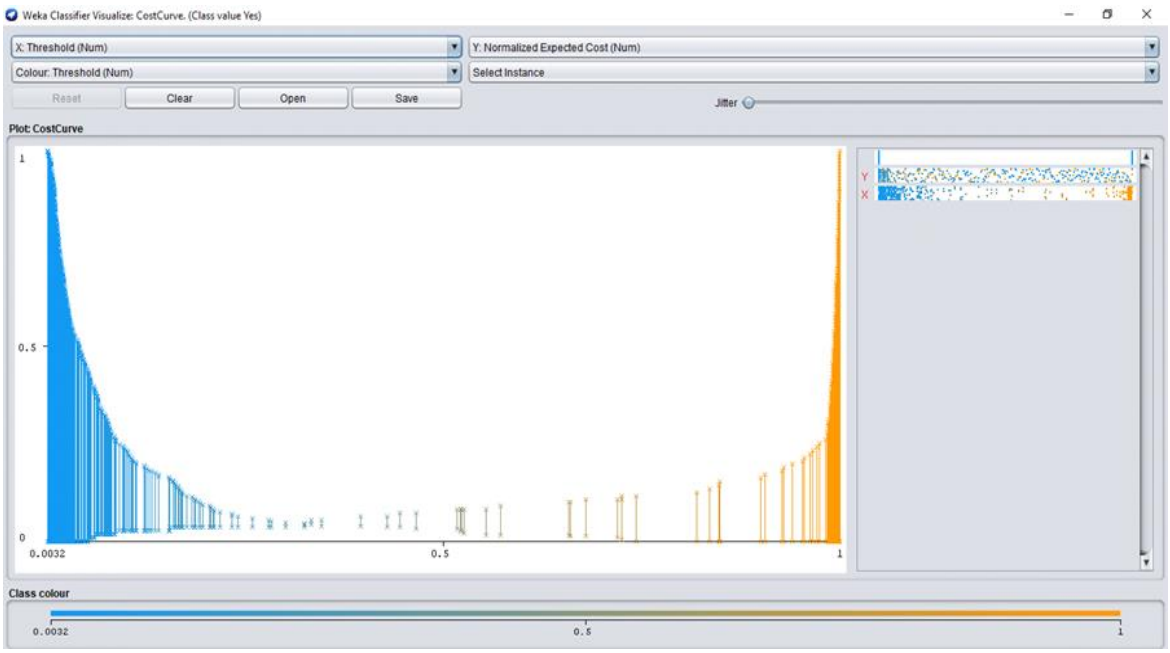

Figure 2. CostCurve-HeartDisease

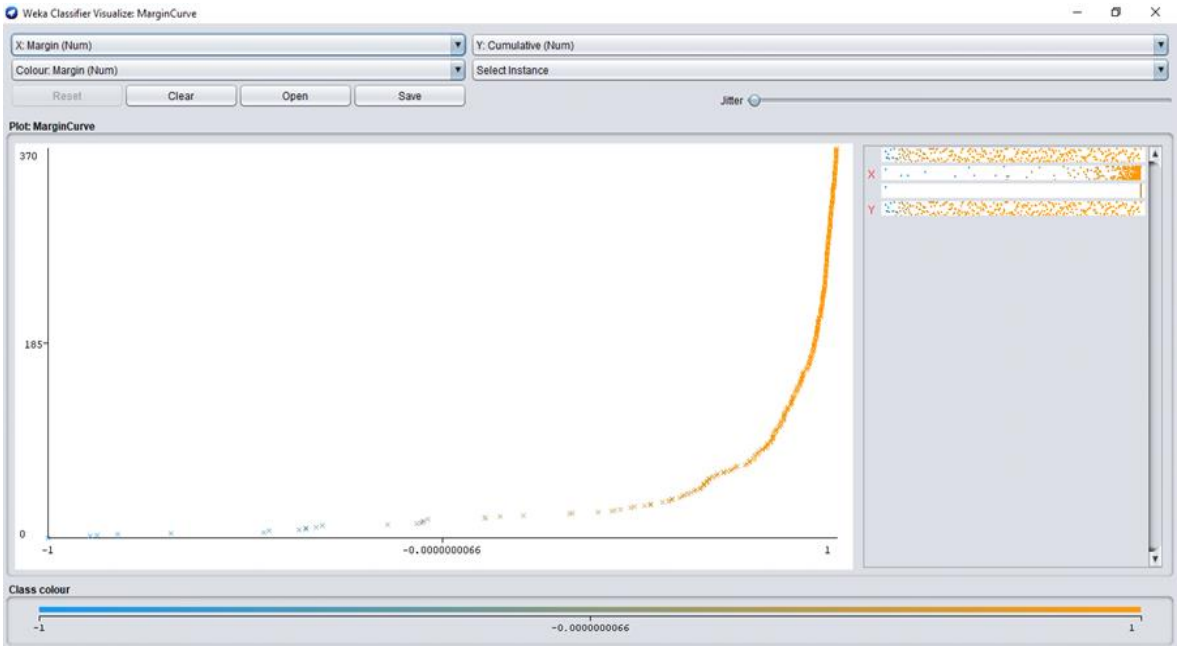

Figure 3. Margin curve progression

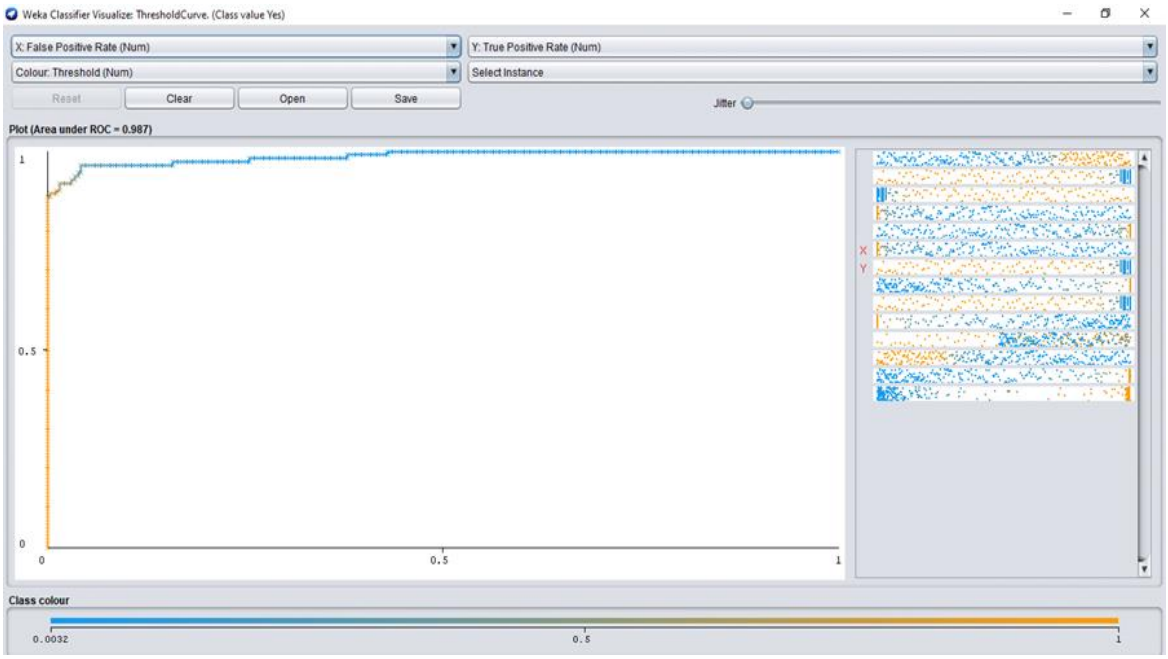

Figure 4. ROC curve-HeartDisease

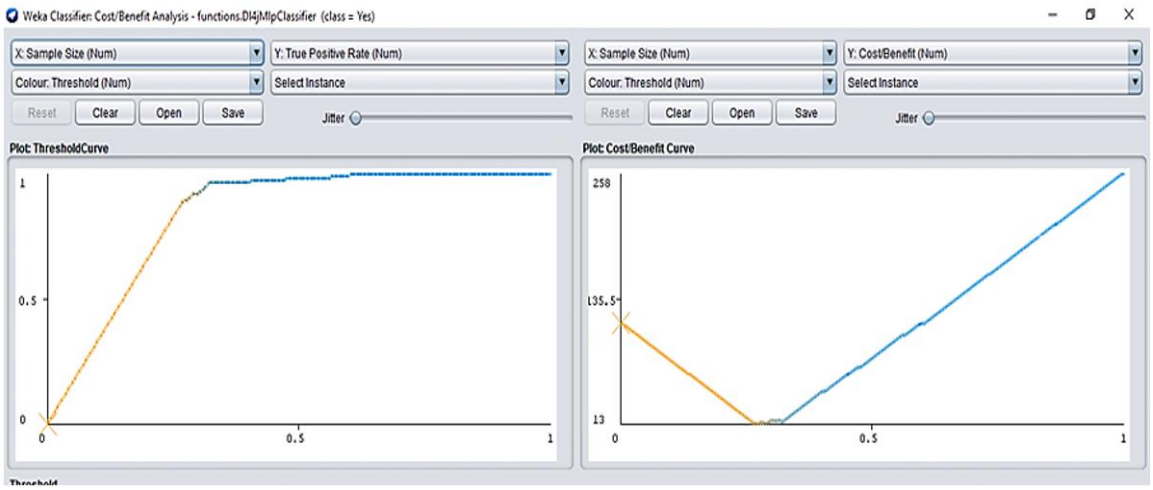

Figure 5. Threshold and cost-benefit analysis–HeartDisease

Generally, the NN for the heart disease class attribute has a subset of attributes selected by the classification attribute subset evaluator filter, where six possibly significant attributes are the model's inputs towards hidden layers (the size of the number of attributes plus the number of classes) configured into inputs towards the output layer with two labels. The DL4J model is highly accurate for some class attributes. DL4J models are clearly powerful, e.g., for the class Heart disease DL4JMlp-b model demonstrates that by the percentage of incorrectly classified instances (1.36%) and the smallest absolute mean error (0.0724) among all models presented in table 5 for the same class attribute. Figures 2 to 5 present the performance of the DL4J-Mlp-b model over the class attribute "heart disease". This class attribute is selected for presentation among seven others to summarize the performance and efficiency of the model. Figure 2 shows the cost curve of the model, where it represents the sigmoid function. The sigmoid is biased towards absolute one, which indicates a normal distribution of the data and a consistent performance. Figure 3 shows the margin curve for the model, where it represents the Epoch progression during the training process.

Figure 4 displays the receiver operating characteristic (ROC) curve, showcasing the diagnostic capability of the model by varying the threshold on the class probability estimate in each instance. Weka adjusts these thresholds to yield appropriate distributions, ensuring reliable classifier performance. On the

other hand, Figure 5 provides a more detailed depiction of the ROC area, focusing on thresholds and cost-benefit analysis. The ROC curve's independence from class distribution renders it particularly valuable for disease predictions, elucidating the trade-off between sensitivity and specificity. Notably, Figure 4 demonstrates a discernible convergence of the curve towards the 90-degree diagonal of the ROC space, indicating the model's high accuracy.

The ROC curve serves as a widely employed visualization tool, offering a comprehensive overview of a classifier's performance across various threshold levels. It is constructed by plotting the TP rate against the FPR while adjusting the classification threshold. Our endeavors have focused on refining the accuracy and overall performance of the predictive model. Table 5 showcases the superior classification accuracy achieved by the DL4JMlp-b model across all 7 class attributes, indicating enhancements made over the preceding DL4JMlp-3 model, including parameter tuning and other improvements. The enhancements primarily focused on implementing two key modifications:

a. Utilizing an improved feature selection technique aimed at selecting attributes highly correlated with their respective classes, such as heart disease. This was accomplished by employing the WrapperSubsetEval as an attribute evaluator and utilizing the genetic algorithm as a search method. Additionally, a class balancing technique was implemented to address the skewed distribution of certain class attributes, like cholesterol and fasting blood sugar. This involved activating a cost matrix within the cost-sensitive classifier embedded within the DL4JMlp-b model, enabling the penalization of misclassified instances.
b. Implementing an enhanced learning strategy to effectively manage bias, convergence, and mitigate overfitting. This entailed employing a Softmax activation function, utilizing 100 epochs for training, employing a recursive instance iterator, utilizing a sigmoid updater, and incorporating a non-improvement criterion every five epochs. These measures were implemented to ensure better control over the learning process and enhance the model's performance.

The DL4JMlp-b model has showcased remarkable accuracy across all seven classes, outperforming previous classifiers detailed in Table 5. This notable improvement stems from a deliberate effort to encapsulate highly correlated features within subsets, a process guided by insights from medical professionals using IBM-SPSS. These carefully selected attributes, as outlined in Table 5, play a pivotal role in training, testing, and validating the DL model. By leveraging significant correlation coefficients with their respective class attributes, the model effectively learns to make precise predictions, particularly evident in cases such as heart disease. Consequently, the model achieves superior accuracy compared to baseline metrics and other classifiers, notably in predicting attributes like fasting blood sugar.

4.5. Discussion

The results highlight several key factors influencing the classification accuracy within the DL4JMlp-b model are described as follows. The number of hidden layers, including DenseNet layers within DL4J, correlates with the testing mode, which encompasses both the number of attributes and the number of classes. This relationship underscores the importance of appropriately configuring the model architecture to accommodate the complexity of the dataset. In addition, CV emerges as the preferred testing mode over percentage split and training evaluation methods for all class attributes. This preference may be attributed to the size of the training dataset, indicating that CV provides a more robust evaluation framework. Moreover, the utilization of the Adam optimization algorithm significantly influences model’s performance. Adam offers advantages over traditional stochastic gradient descent methods by facilitating rapid convergence towards local minima. This optimization technique plays a pivotal role in iteratively updating network weights based on training data, contributing to the overall efficiency and effectiveness of the DL4JMlp-b model.

Identifying attributes with significant influence on the classification task is pivotal for ensuring accurate predictive models. Our emphasis was on selecting sizable and independent features to bolster validation outcomes, prioritizing the integration of medical observations and demographic data for comprehensive predictions. However, the choice of the optimal algorithm hinges on several factors, including data types and size, time constraints, and specific prediction objectives. In medical decision-making processes, the DL4JMlp-b model has showcased remarkable accuracy, rapidity, and cost-efficiency. Its adeptness in handling test datasets has been consistent, surpassing various classifiers such as the baseline classifier, RF, J48, MLP, and MLPBP. The model's accuracy has been progressively enhanced through the fine-tuning of a relatively small number of parameters, with the optimization algorithm, stochastic gradient descent, playing a pivotal role in this refinement process. Additionally, attribute selection has emerged as a crucial factor in achieving a robust and effective predictive model. Addressing major issues in classifier modeling, such as redundant attributes and overfitting, has been paramount to the success of the DL4JMlp-b model. Redundant attributes can lead to skewed predictions, while retaining irrelevant attributes may result in overfitting, where the model becomes too closely aligned with the training data and loses predictive accuracy

on new datasets. Overfitting is a common modeling error that limits the model's applicability beyond the initial dataset, highlighting the importance of robust modeling techniques in ensuring accurate predictions across various datasets.

To mitigate overfitting and ensure the development of accurate and reliable models, it is crucial to address redundant and irrelevant attributes within the dataset prior to classifier evaluation. This process should ideally be integrated before the data preparation phase. Feature selection, a pivotal step in this regard, involves identifying and retaining only the most relevant attributes that effectively represent the data to the predictive model. By selecting a subset of pertinent attributes from the raw data, the predictive model's accuracy on unseen data can be significantly improved. Attribute selection encompasses two main components: attribute evaluator and search method. The process is iterative and tailored to the specific problem at hand. Different importance metrics and selection techniques are iteratively utilized to categorize potential attributes into subsets. These subsets are subsequently assessed for their influence on model accuracy using unseen or test data. This iterative approach enables the enhancement of attribute selection strategies until an optimal subset is achieved. In our study, the feature selection phase utilized both filter and wrapper methods to identify a subset of attributes significantly correlated with classification accuracy. Techniques such as cost-sensitive principal components and Chi-square were employed to gain deeper insights into the data, including its patterns, correlations, and significance. By employing the CsfSubsetEval attribute evaluator and Best-First Search method, we generated several attribute subsets, each tailored to individual class attributes. However, while these subsets led to highly accurate predictions, they proved to be insufficient and lacked robustness to fully support the classifier. Despite their effectiveness, this approach was time-consuming and unable to adequately rank all features within the search space.

The Chi-square test presents comparable constraints in its application. Although it expedites training, its accuracy remains moderate, hindered by limitations in classification and the ineffective differentiation of correlated predictors. Primarily employed to pinpoint statistically significant attributes within the demographic section of our dataset, we chose to incorporate Chi-square through IBM-SPSS before integrating Weka into our analytical framework. PCA is valuable for condensing data into fewer dimensions via orthogonal projection ranking searches. However, its accuracy is moderate, primarily due to challenges in determining variances and selecting significant and robust subsets. PCA excels at attribute extraction from raw data, although it does not construct new attributes, making it less suitable for our dataset. As an unsupervised learning algorithm, PCA is primarily employed for dimensionality reduction, lossy data compression, and feature extraction, making it particularly beneficial for large datasets. In contrast, Laplacian scores or statistical tests focus solely on determining the independence of a single attribute from the response, offering an estimate of its usefulness.

Hence, to overcome the limitations observed in previous feature selection techniques, we opted for WrapperSubsetEval as the attribute evaluator and genetic search as the search method. WrapperSubsetEval assesses subsets using a predefined classifier and employs 10-fold cross-validation for robustness. Meanwhile, the genetic search method utilizes a well-established genetic algorithm to explore attribute subsets comprehensively. This strategy allowed us to identify significantly correlated and robust subsets, resulting in superior classification accuracy. Leveraging genetic search facilitated thorough exploration of potential subsets, permutation, and ranking, ultimately pinpointing the top-performing attributes. Utilizing the same classifier with a wrapper for attribute selection helped alleviate attribute redundancy. Overall, this approach enhances flexibility, simplicity, accuracy, and efficiency while mitigating overfitting and reducing training time. The predictive model's implementation and evaluation hinge upon meticulously curated attribute subsets tailored to each class attribute. These subsets are strategically utilized within the DL4J framework, where parameter settings and configurations are finely tuned to optimize classification accuracy. This approach ensures that the model operates efficiently and effectively, yielding reliable predictions across all target classes.

This study explored a comprehensive parameter tuning of the DL4J model with three main parameters (e.g., search method, DenseNet, and activation function). However, these three factors could be the limitations of our model where they may possess a potential influence on the results. Hence, further and in-depth studies may be needed to confirm its performance in terms of speed and accuracy, especially regarding model’s overfitting. Our study demonstrates that DL4J are more resilient than e.g., MLP in terms of parameters tuning. Future studies may explore other risk factors and tune other potential parameters with feasible ways of producing highly accurate predictions without overfitting the model and in less running time. Recent observations suggest that only the parameter tuning may be an effective strategy of producing highly accurate prediction models for CVD. Our findings provide conclusive evidence that this phenomenon is associated with the type of risk factors regarding CVD (aka. attributes), not due to elevated numbers of risk factors.

5. CONCLUSION

This work aimed at investigating vital parameters of a DL model (e.g., CNN) with an attribute selection process to better understand and the effect of CVDs risk factors. In general, the predictive model consists of three main phases including data-preprocessing using filters, attribute selection using optimizers, and prediction using classifiers. A variety of five predictive models, namely DL4JMlp-0 to DL4JMlp-b with different parameter settings, has been tested on a real-world dataset with seven class attributes. All models have been evaluated by comparing them to some well-known ML models (e.g., random forest) where they showed a high accuracy in most cases. In addition, the DL4JMlp-b model with best configuration of parameter settings among the five DL4JMlp models has demonstrated its superior ability to classify CVD cases with high accuracy 98.64% and outperformed all models including decision trees and neural networks. Generally, the performance of the DL4JMlp-b has been improved by tuning some vital parameters, such as: learning rate, momentum, number of hidden layers, epoch, and training time. However, the most influential parameters are the instance iterator and the optimization algorithm within the CNN. The predictive model showed a better performance when triggering a recursive iterator rather than the convolution iterator. Also, the predictive model showed a better performance when employing a stochastic gradient descent optimization rather than the steepest descent heuristic. The predictive model has effectively utilized the attribute selection mechanism using a wrapper subset evaluator and a genetic search method for a reduced space of attributes that have a potential impact on the accuracy. However, this highly performed predictive model came at a great cost of running time, and the limitation of the search convergence in the optimizer. This could be achieved in future research by applying better learning or search strategies such as a deterministic heuristic rather than a stochastic gradient heuristic which may narrow the search space of attributes.

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