Classification of Chronic Kidney Disease Based on Gfr in Internet of Medical Things Environment Using Graph Neural Network Based Deep Q Learning (GNN-DQL)

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CLASSIFICATION OF CHRONIC KIDNEY DISEASE BASED ON GFR IN INTERNET OF MEDICAL THINGS ENVIRONMENT USING GRAPH NEURAL NETWORK BASED DEEP Q LEARNING (GNN-DQL)

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Abstract

The identification of Chronic kidney (CK) disease in the medical field is still acts as a challenging scenario in the recent years. Precise recognition of CK disease possess a significant aspect in rendering effective treatment to the patients. Various forms of approaches have been developed for the exact classification of CK disease, but still there emerges certain forms of demerits including, improper selection of features, necessity of high storage space, requirement of effective learning model, less accurate, high complexities with respect to time and cost. The presence of these drawbacks adversely decreases the overall model performance. Hence to overcome these complexities, a graph neural network based deep Q learning (GNN-DQL) approach is proposed for the effective classification of five different stages like normal, mild, moderate, severe and end. Initially, the data are gathered from different people with the help of biomedical sensors through Internet of medical things (IoMT). The data are pre-processed through Handling Missing Values, Categorical Data Encoding, Data Transformation and Outlier Detection to eradicate the unwanted distortions. The Glomerular Filtration rate (GFR) is calculated with respect to age and serum creatinine level. Then, GNN-DQL technique is adopted for enhancing the classification accuracy. The parameters are optimized through Adaptive Mayfly Optimization (AMO) method. The classification performance is analysed with respect to accuracy, precision, recall, specificity, F1 score, confusion matrix and so on using PYTHON simulation tool. The classification accuracy of 99.93% is attained in the CK disease classification of five different stages regarding the collected data.

Keywords: Deep learning, GNN-DQL, GFR, Classification, IoMT, Optimal features, Parameter optimization, AMO.

1. Introduction

The CK disease is a severe illness all over the world, mainly in developing countries [1]. Timely identification of chronic diseases and also tracking of risk factors slow down the continuation of diseases and may exclude dangerous events in the everyday patient's life. An unidentified CK disease results in various problems that put patients in high-risk circumstances [2]. A quick creation of renal disease in patients with hypertension may cause

worse events. CK disease is a heterogeneous breakdown that mainly affects kidney function and structure. The major reasons of the CK disease are heart disease, diabetes, and HB (high blood) pressure [3]. Diabetes is also known as blood sugar that can harm the blood vessels in human kidney. HB pressure also can harm the blood vessels in human kidney [4]. Heart disease is also related with kidney disease which is severe than all other disease.

Symptoms of the CK disease are chest pain, feeling tired, loss of appetite, shortness of breath, weight loss, muscle cramps, trouble concentrating and sleep problems [5]. Human body temperature placed a vital role to the well-being of the patients. The patient's health can be routinely monitored to reduce the risk of their life. Hence, biomedical sensors have the capability to handle medicine. The usage of the biomedical sensors for detecting the early-stages of CK disease was identified by comparing breath samples of patients to analyse the breath samples of healthy controls [6]. A typical BM (Biomedical sensor) device consists of small battery-operated board with a memory, a microprocessor, and a radio frequency transceiver. DM (data mining) is a process by combining information from biomedical sensor devices, storing information, and successfully send information to the patients [7].

Some of the common features of DM process are flexibility, robustness, trade-off energy efficiency, etc. The simple reasoning of health identifying device in biomedical sensor readings like calculating the sleep hours or the number of processes each day to the better levels of information processing in order to provide correct data to the patients [8]. Nowadays, healthcare services have mainly focused on deeper DM tasks to provide better services for the well beings of human [9]. The DM approach consists model data learning, extraction and identification, and information pre-processing [10]. Various features including meta-data and expert knowledge to identify the operations such as detection, prediction, and DM (decision making). Pre-processing techniques helps to filter unusual information from the input data to remove high frequency noise [11].

The main purpose of extraction is to identify the features of an information set which are characteristics of the original information. ML (machine learning) models can be classified into unsupervised and supervised methods, also called descriptive and predictive, respectively [12,13]. Supervised learning methods, including face recognizers over images, medical diagnosis systems and spam classifiers of e-mail for patients, where the training information can be taken the collection of (u, v) pairs, the prediction "u" and a query "v" [14]. Several supervised methods include support vector machines, kernel machines, decision trees, logistic regression, decision forests, Bayesian classifiers and neural networks. ML can achieve significant task, but it still falls short of replicating HI (human intelligence) [15]. These drawbacks can be rectified by using DL (deep learning) which is a subcategory of ML.

DL is evaluated by the way of classifying, clustering, and predicting things by using a NN (neural network) that has been trained on huge amounts of information [16]. It has its roots in NN that consists of algorithms, modelled loosely after the brain of human, that are mainly designed to find patterns. The main aim of DL models is to bring together impactful and novel research work on deep learning for medicine based on the IoMT, thereby expediting research in this field [17,18]. BMs are used all over the world, which used to measure the blood level and help patients cope with diabetes [19,20]. Such sensors are specifically implanted under the skin. It offers continuous monitoring and measurement of

blood levels in patients. In order to overcome the above-mentioned ML problems, a new deep learning technique is proposed in this research.

A novel methodology is adopted in the proposed research work for the precise classification of five various stages of CK disease. Some of the prominent contributions for enhancing the performance of classification accuracy are given as follows.

- To generate the CK disease data throughBMs on several people and thereby gathering the data using IoMT.
- To initiate data pre-processing by Handling Missing Values, Categorical Data Encoding, Data Transformation and Outlier Detection for eradicating the unwanted distortions.
- To classify different stages of CK disease through the evaluation of glomerular filtration rate based on age and serum creatinine level.
- The generated data are precisely classified using Graph neural network with deep Q-learning technique (GNN- DQL) classifier.
- The parameters are optimized through Adaptive mayfly optimization (AMO) approach for precise classification outcome.

The structure of the proposed research work is organized in to various sections. Section 2 describes the literature survey of CK disease classification done by various researchers in learning methodologies. Section 3relates with the description of proposed methodology in CK disease classification. The simulations implemented for determining the performance outcome of proposed method are discussed in Section 4 using PYTHON simulation tool. Finally, the conclusion and future workof the proposed research is delivered under Section 5.

2. Related works

Based upon the CK disease classification, most of the researchers have undertaken several techniquesto achieve precise outcomes. Some of the significant classification techniques adopted by several authors are surveyed below.

Singh *et al.* [21] performed a deep NN for early prediction and detection of CK disease. HB (high blood) pressure and diabetes are the common reasons of CK disease. The patients with CK disease have a higher possibility of dying young age. This project presented a novel DL approach for the early prediction and detection of CK disease. This model created a deep NN and compared its operation to that of other ML models. The NN optimum devices were attached by running multiple trials and building the parameters. The characteristics were determined by RF (recursive feature) elimination process. Specific gravity, cell count of red blood, Haemoglobin, serum creatinine, packed cell volume, and hypertension were considered as important structures in the RF elimination. The deep NN model outperformed the other classifiers Logistic regression, KN (*K*-nearest) neighbour, SV (support vector) machine, NB (naive bayes) and Random Forest classifier to achieve the 100% precision. It used for nephrologists in detecting CK disease. However, there is limitations on how much information required to train the correct model to calculate about deep structures.

Liao *et al.* [22] identified data augmentation with generative adversarial networks by improving stage classification of CK Disease. To identify the stage classification of CK

disease, this model provides an auxiliary diagnosis system with DL technique for renal ultra-sound images. It used the MobileNetV2 pre-training model and ACWGAN-GP model. The generated images by the original images and the ACWGAN-GP technique were concurrently input to the MobileNetV2 pre training technique for better training. The technique evaluated a precision of 81.9% in the four phases of CK disease classification. The forecast outputs permitted a bigger stage acceptance, then the accuracy could be achieved by up to 90.1%. DL method solved the problem of inadequate data samples and imbalance during training model for an automatic process. This model enhanced the prediction of CK disease diagnosis process. This technique requires a hugeamount of training information to accelerate the forecastaccuracy-based classifier.

Sabanayagam *et al.* [23] implemented a DL technique to identify CK disease from photographs of retina in community-based persons. The information related from cross-sectional, multi-ethnic studies in China and Singapore. SEED (Singapore-epidemiology-eye-diseases) process worked to progress (5188 persons)and validate (1297 persons) using DL technique. There are three models were trained: Image DL technique, RF (risk factor) and hybrid DL technique combined with RF and image. DL technique were evaluated usingthe receiver characteristics. It used CNN (convolutional-neural-network) based DL for CKdisease from retinal images. It has many challenges that it does nothave data on albuminuria for every patient, so it cannot perform an albuminuria usingprediction DL approach. It does not know what characteristics were used bythe DL technique to obtain CK disease because of heat-maps specified changes of vessel andun-usual lesions.

Navaneeth *et al.* [24] developed a dynamic pooling using CNN model to detect CK disease. This model analysed the attention of urea in the saliva sample to identify the disease of patients. Novel discovery and DL model were used to find the disease using saliva samples from patients. Hybrid DL model consists of SVM (support vector classifier) and CNN which helped to rectify the difficulties obtained by the CDC (convolutional data classification) technique. It analysed the urea concentration in the sample of saliva to identify the illness of patients. This technique obtained sensitivity (97.5%), specificity (97.83%) and an accuracy (97.67%). The drawback in this model that the evaluation was continued ten more times until the total information set was calculated.

Kriplani *et al.* [25] analysed the prediction of CK diseases using deep artificial NN model. This model analysed 224 documents of CK illness maintained on the UCI (University of California, Irvine) ML repository named CK diseases dating back to 2015. The deep NN predicted the appearance (or) non-appearance of CK disease with a precision of 97%. The automatic CK disease process helped to minimize the damage of kidney, but for the detection of CK disease at starting stage was essential to attain the better output. Deep NN was made of number of layers that were built with number of neurons. The cost function is identified using convex shape. The chronic and non-chronic diseases were obtained and compared with other classification models. Deep NN achieved 97.7679 % accuracy that was the perfect prediction of the CK disease. The limitation was that, Deep NN model required large amount of information to analyse the better output. Table 1 signifies the analysis of various existing approaches with its respective merits and demerits.

Table 1: Analysis of existing classification approaches

Author name and Reference	Technique used	Objective	Merits	Demerits	Performance (%)	Dataset used
Singh *et al.* [21]	Deep NN	Early prediction and detection of CK disease	Improved efficiency in selection of features	Lower model performance due to testing over small datasets	Precision-100	UCI-CKD
Liao *et al.* [22]	MobileNet V2 and ACWGAN-GP	To provide an auxiliary prediction model with DL	Imbalance and insufficient data problems are solved	Requires huge amount of training data	Accuracy-90.1 Precision-81.9	Kidney ultrasound image (KUI)
Sabanayagam *et al.* [23]	CNN-based DL	To recognize CK disease from retinal images	High potentiality can be attained in CK disease identification	Specified variations of vessel and un-usual lesions	AUC- 93.8 (SEED) AUC- 81.0 (SP2) AUC- 85.8 (BES)	SEED, SP2 and BES
Navaneeth *et al.* [24]	Hybrid DL (SVM+CNN)	To analyse the urea concentration in the saliva sample	High robustness can be attained	Evaluation processing time is high	Accuracy-97.67 Specificity-97.83 Sensitivity-97.5	Real time dataset
Kriplani *et al.* [25]	Deep NN	To classify the CK and non-CK disease efficiently	Overfitting issues can be solved	Requires large amount of information for output prediction	Accuracy-97.76	UCI-CKD

When undergoing survey over the existing approaches with respect to CK disease classification, there emerges certain drawbacks which widely affects the performance of the

overall system. The limitations like lower performance model due to the utilization of smaller datasets, requires larger amount of training data for promoting effective classification process,Quantified variations of vessel and un-usual lesions degrades the output performance. Also, high processing time is needed for the performance estimation. Due to the existence of these complexities, accurate classification CK disease stages cannot be obtained. In order to conquer these limitations and promote the classification accuracy, an effective deep learning technique is proposed in this research work.

3. Proposed methodology

CK disease is found to be highly threatening as it adversely affects the working conditions of kidney. When it is not detected in the early stages, the affected people may enter severe conditions. Most of the patients are left in to critical stages due to improper or wrong prediction of diseases. Even though so many CK disease classification techniques are in practice, precise results cannot be attained. Hence in the proposed research work, GNN-DQL model is adopted for the precise classification stages of CK disease. The overall architecture for accurate CK disease classification with different stages is illustrated in Figure 1.

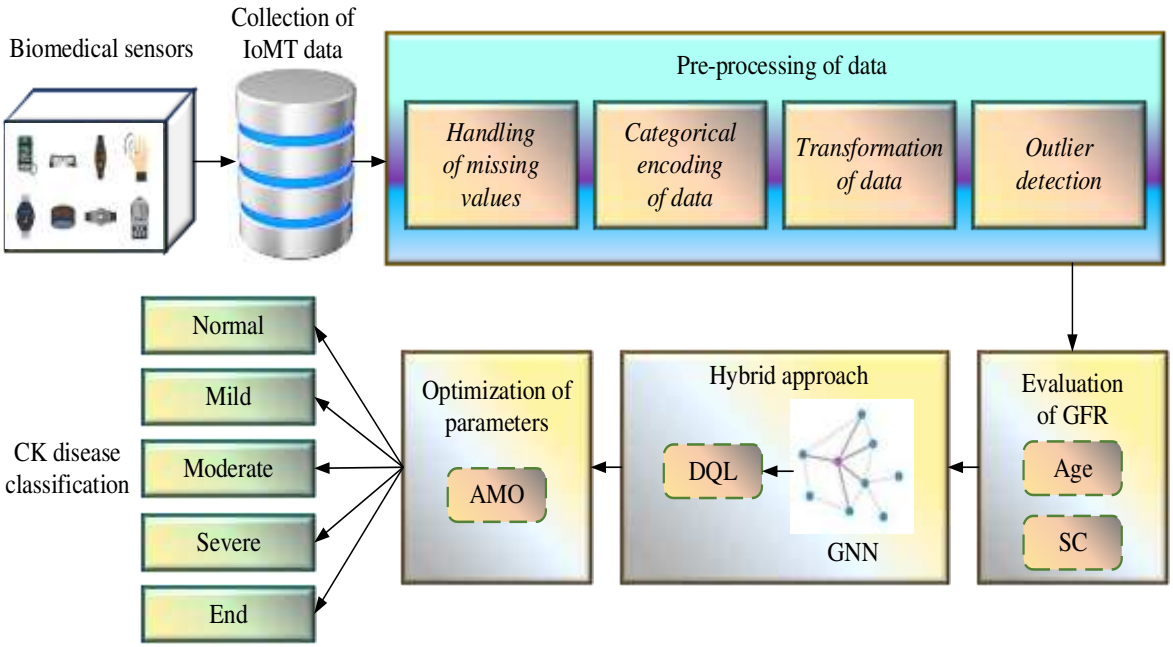


Figure 1: Overall architecture of CK disease classification

Initially, the BMs are used to evaluate different factors of CK disease such as serum creatinine, sugar, red blood cells (RBC), white blood cells (WBC), potassium and so on. The gathered data from the BM sensor are collected by the data centre through IoMT. To improve the quality of data, pre-processing is the first step undertaken to eradicate the unwanted distortions present in the data. The glomerular filtration rate (GFR) is evaluated, GNN- DQL model is utilized to classify and predict several stages of CK disease including normal, mild, moderate, severe and end stage. The parameters of the neural network are then optimized through AMO approach. The steps involved in the proposed research work are described as follows.

3.1 Data pre-processing

The evaluation of missing values and the eradication of noises including outliers as well as the validation and normalization of instable data are the pre-processing stages that are undertaken. During the patient assessment, some of the estimations are found to be incomplete or missing. To compensate that, several pre-processing steps are carried out in the proposed research work which are labelled as follows.

3.1.1 Handling of missing values

The modest method to work with the missing values are neglecting the records but however it is not possible among the smaller datasets. During the process of data generation, the dataset is examined to confirm whether any attribute values are missing. Through the adoption of statistical method of mean imputation, the missing values for numerical structures are evaluated. The mode method is used for missing value replacement of insignificant features.

3.1.2 Categorical encoding of data

As most of the deep learning procedures only consider numerical values as input, the category values must be encoded in to arithmetical values. The characteristics of categories including yes and no are represented by the binary values 0 and 1.

3.1.3 Transformation of data

The process of converting numbers over the small scale so that the domination of one variable over the others does not happen is called to be data transformation. Or else, the learning approaches observe bigger values as advanced and smaller values as lesser regardless of the weight unit. The data alterations modify the values in a dataset and so they can be treated further. To enhance the accuracy of deep learning approaches, this research undergoes a data normalization method. The data is converted between the ranges from -1 and +1 where as the transformed data possess the standard deviation as 1 and mean as 0.

The standardization can be stated as,

$$s = \frac{\left(v - \bar{v}\right)}{\sigma} \qquad (1)$$

From the above equation, s denotes the standardized score, observed value is represented as v , mean is denoted as $\bar{v}$ and σ signifies the standard deviation.

3.1.4 Outlier detection

Outliers are considered to be the observation facts which are inaccessible from the rest of the data. An outlier can be created in the experiment by variability estimation or the signal error. The learning process of deep learning algorithm can be distorted and mislead by the outliers. The presence of outliers directs the process to longer training time, poorer result generation and less model accuracy. Before the data transferring to the learning algorithm, this research utilizes Interquartile range (IQR) foundedmethod to eliminate the outliers.

The IQR is the evaluation of variability on the basis of dividing dataset in to quartiles. The values that divide every part are termed to be first, second and third quartiles that are denoted as V_1 , V_2 and V_3 . The formula to calculate IQR is given as follows.

$$IQR = V_3 - V_1 \tag{2}$$

where, V_1 denotes the middle value in the first half of the ordered data set whereas V_3 denotes the second half. V_2 denotes the median value in the dataset.

3.2 Estimation of Glomerular filtration rate

The GFR is highly crucial to most of the characteristics including public health, medical care and research. The clinical laboratories render a significant role in GFR assessment and chronic kidney disease diagnosis. In the GFR evaluation, serum creatinine measurement along with the estimated GFR is recommended as the initial step. From the gathered data, the GFR is estimated to classify the five different stages of CK disease and here the filtration rate is estimated on the basis of age and serum creatinine (SC) level. The equation for estimating the GFR for age greater than or equal to 18 years can be mathematically expressed as,

$$GFR = 142 \times \min\left(SC/k,1\right)^{b} \times \max\left(SC/k,1\right)^{-1.200} \times 0.9938^{Age} \times 1.012 \tag{3}$$

From the above equation, k = 0.7 for females and 0.9 for males, b = -0.241 in case of females and -0.302 for males. SC denotes the SC level in mg/dL and Age is represented in years. Table 2 shows the equation to estimate GFR from SC level.

Table 2: GFR estimation values

Age	Gender	SC mg/dL	GFR
≥18	Female	≤0.70 or <0.71	$=142\times\left(SC/0.7\right)^{-0.241}\times 0.9938^{age}\times 1.012$
		> 0.70	$=142\times\left(SC/0.7\right)^{-1.200}\times 0.9938^{age}\times 1.012$
≥18	Male	≤0.90 or <0.91	$=142\times\left(SC/0.9\right)^{-0.302}\times 0.9938^{age}$
		> 0.90	$=142\times\left(SC/0.9\right)^{-1.200}\times 0.9938^{age}$

3.3 Graph neural network with deep Q learning technique

GNNs are the framework to gather the node dependency in graphs through passing of messages between the nodes. The GNN performs on the graph to describe the data from its neighbourhood with random stages. This creates GNN as an appropriate tool to utilize for the wireless networks that holds compound features which cannot be taken in a closed form. In the proposed research work, the GNN based approach in accordance with the relationship of cell and entities between the nodes.

Two adjacent matrices are defined for the given network comprising a set of P cells and Q entities. The graph between cells is represented as $R_{cl} \in \{0,1\}^{P\times P}$ and the graph between entities and cells are denoted as $R_e \in \{0,1\}^{P\times Q}$. The mathematical expression can be given as,

$$R_{cl}(u,v)=\begin{cases}1 & if\ e_{f_u^{cl}}, e_{f_v^{cl}} \in \varepsilon^{cl} \\ 0 & Otherwise\end{cases} \tag{4}$$

$$R_e(u,v)=\begin{cases}1 & if\ e_{f_u^{cl}}, e_{f_v^{cl}} \in \varepsilon^{e} \\ 0 & Otherwise\end{cases} \tag{5}$$

A L-layer GNN is considered which calculates on the graph and the fundamental nodal characteristics of the cells and the entities are defined as $Y_{cl,1}^{(0)}$, $Y_{cl,2}^{(0)}$ and $Y_e^{(0)}$ correspondingly.

The initial nodal characteristics are the functions of cell data rates and the reportednetwork capacities and entities. The channel capacity matrix $C \in Z^{P\times Q}$ is defined with the elements $c\left(f_u^{cl}, f_v^{e}\right)$and user rate matrix $Z \in Z^{P\times Q}$ with elements $\frac{c\left(f_u^{cl}, f_v^{e}\right)}{\left|C\left(f_u^{cl}\right)\right|}$ for an assumed cell-entity connectivity graph. The input features can be calculated as,

$$Y_{cl,1}^{(0)}=\left[R_{cl}Z1_P \| Z1_P\right] \in Z^{Q\times 2} \tag{6}$$

$$Y_{cl,2}^{(0)}=\left[R_e Z^T 1_Q \| C1_P\right] \in Z^{Q\times 2} \tag{7}$$

$$Y_e^{(0)}=\left[C^T 1_Q \| Z^T 1_Q\right] \in Z^{P\times 2} \tag{8}$$

From the above equation, the vector concatenation operator is denoted as $[.\|.]$. All-ones vector of size 1_P and 1_Q is denoted as P, Q. Each of the latent features gather either the sum rate of nearby cells or node or channel capacity in case of entities. These are chosen as the features as they gather relevant data regarding to make better decisions.

At each layer, the GNN evaluates a d dimensional latent feature vector for every node $f_u^{cl}, f_v^{e} \in V$ in the graph G. At L layer, the later feature estimation can be expressed as follows.

$$H_{cl}^{(L)}=\sigma\left(Y_{cl,1}^{(L)} w_1^{(L)}\right)+\sigma\left(Y_{cl,2}^{(L)} w_2^{(L)}\right) \in Z^{P\times d} \tag{9}$$

$$H_e^{(L)}=\sigma\left(Y_e^{(L)} w_3^{(L)}\right) \in Z^{Q\times d} \tag{10}$$

$$Y_{cl,1}^{(L+1)}=R_{cl}H_{cl}^{(L)} \in Z^{P\times d} \tag{11}$$

$$Y_e^{(L+1)}=R_e^T H_{cl}^{(L)} \in Z^{Q\times d} \tag{12}$$

$$Y_{cl,2}^{(L+1)} = R_e H_e^{(L)} \in Z^{P\times d} \tag{13}$$

From the above equations, the neural network weights are represented as $w_k^{(0)} \in Z^{2\times d}$ and $w_k^{(L)} \in Z^{d\times d}$ for $L > 0, k = 1,2,3, etc$, the layer index of GNN is represented as L and $\sigma(.)$ denotes the non-linear activation function. The sum of hidden features of cell to cell and cell to entity graph connectivity is represented by the auxiliary matrices $H_{cl}^{(L)}$ and $H_e^{(L)}$. The L layer in GNN effectively replicates the above estimation for $L = 0,1,....l-1$. By this, the nodal features are directed to other nodes and will get combined at distant nodes. Every feature comprises of data regarding l hop neighbours whereas the embedding is undertaken L times.

In the last layer of GNN, the feature vectors are integrated to attain a scalar valued score for G. The output layer of GNN is combined over cells, the score estimation $H_{cl}^{(l-1)}$ invariant to nodes before transforming to the single fully connected neural network layer. The network score of the graph G is expressed as follows.

$$S(G) = \sigma\left(1_P^T H_{cl}^{(l-1)} w_4\right) w_5 \tag{14}$$

All-ones vector of size P is denoted as 1_P^T, the weight matrix of the fully connected neural network is represented as $w_4 \in Z^{d\times d}$ and the vector to combine the output of neural network is represented as $w_5 \in Z^{d\times 1}$. Once the evaluations of GNN are over, the scores of G, $S(G)$ will be adopted to choose the best connection graph. The optimal weights of GNN are learned by the deep Q learning algorithm.

The Q-function is learned from the cell and entity placement instances through deep Q learning approach. The major merit of Q- function is to establish GNN scalable over various sizes that can gather limited network features with different number of cells and entities. To generate the optimal selection, the right Q function has to be learned. When the Q function is gathered through GNN, this renders to learn the GNN parameters which is done by sequential accumulation of new cell entity connections over partly connected graph. The state, action and the reward in deep Q learning approach are provided as follows.

The state S_T is defined as the present graph G_T holding the cells and linked entities at iteration and also the input features of corresponding nodes $Y_{cl}^{(0)}$ and $Y_e^{(0)}$. The beginning state can be contemplated as the partlylinked network with linked and unlinked entities. The ending stateis attained when the entire network entities are associated. The action $A_T = G_T \cup e_{f_u^{cl}, f_v^e}$ in step T is to link a separate entity to one of the cells. The reward $R(S_T, A_T)$ at S_T state after choosing the action A_T can be expressed as,

$$R(S_T, A_T) = U\left(G_T\right) - U\left(G_{T-1}\right) \tag{15}$$

The reward is described as the variation in the network utility function after linking a new entity. The deterministic greedy policy can be expressed as $\delta(A_T | S_T) = Arg\max_{A_T} Q\left(S_T, A_T\right)$

with ε greedy examination during the training process. Here $Q(S_T, A_T)$ is denoted in equation (14) with $G_T = S_T \cup e_{f_u^{cl}, f_v^e}$.

At first, the parameters are initialized in deep Q learning approach that are defined for every deployment. At every T step, one entity $A_T = e_{f_u^{cl}, f_v^e}$ is linked by pursuing the greedy policy $\delta(A_T | S_T)$ where the exploration rate is denoted as ε. The number of stages T is provided by the end state S_T. The graph G_T is updated and so the following step S_{T+1} is attained. Every time when the graph is being efficient, the new input features called $Y_{cl}^{(0)}$ and $Y_e^{(0)}$ are estimated. For every chosen action, the reward $R(S_T, A_T)$ is evaluated and the l layer GNN evaluation renders the score for every action and state pair. To enhance the classification accuracy, the GNN with DQL parameters are optimized through the adoption of AMO approach.

The may flies that are separated to male and female would update the velocities randomly. The individual velocities are updates from the weighted present velocities with some other weighted distance among them and the global finest individuals. The weighted distance of either parts can be found through the following expression.

$$J_o = K_m e^{-\lambda r_n^2} (U_n - U_m) \tag{16}$$

When U_n is far away from U_m, the velocities are updated with a lower amplitude. When they are near, the velocities are updated with a higher amplitude. But these situations cannot be acceptable probably because when the individuals are distant away, the velocities should be reorganized with larger rates and should attain lower rates when they are nearby. Hence the equation (16) can be updated to optimize the parameters of GNN-DQL as,

$$J_o = K_m e^{-\frac{\lambda}{r_n}} (U_n - U_m) \tag{17}$$

Where J_o denotes the composited velocity, K_m and λ are constants, U_n denotes the male fly, U_m represents the female fly and r_n describes the Cartesian distance. Through the implementation of the proposed research, the classification accuracy can be greatly improved. The evaluation time for conducting this research is low and the overall system performance is enhanced.

4. Results and discussion

The performance outcomes of the proposed method are conferred in this section. The experiments are analysed and implemented using the PYTHON simulation tool. The performance outcomes of the proposed technique are compared with the recent existing techniques. The performance metrics including accuracy, F1 score, recall and precision of the proposed method are compared with the existing approaches like Linear Regression (LR), Nearest Neighbour (KNN), Support Vector Machine (SVM), Decision Tree (DT) and Naive Bayes (NB). The metrics like specificity, Mathew's correlation coefficient (MCC), Kappa, Balanced score (BS) and AUC are compared with the existing techniques like DT, SVM,

KNN, LR, Adaboost (ADB), Stochastic Gradient Descent (SGD), Multilayer Perceptron (MLP) and Gaussian Naive Bayes (GNB). In accordance to this, some of the methods such as SVM, Multi-Kernel Support Vector Machine (MKSVM), Hybrid Kernel Support Vector Machine (HKSVM), and Fuzzy Min-Max GSO Neural Network (FMMGNN) are also adopted for comparing Positive predictive value (PPV), Negative predictive value (NPV), False positive rate (FPR) and False negative rate (FNR). The mean absolute error (MAE) performance is compared with the techniques like Random Forest (RF), NB, SVM, neural network (NN), DL, KNN, DT and Auto-MLP. The error rate (ER) performance is compared with NB, SVM, Artificial neural network (ANN), NB-Hybrid Filter Wrapper Embedded-feature selection (NB-HFWE-FS), ANN-HFWE-FS and SVM-HFWE-FS.

4.1 Dataset description

The proposed CK disease classification approach is performed by utilizing the gathered CK disease data. This dataset comprises of 400 instances, 76 parameters and 25 attributes. Butthe data may subject to noisy data and numerical missing values that has been retrieved systematically through pre-processing. For analysing the results, the dataset has been splitted into training and testing sets as 80% and 20%. The download link of the gathered dataset is https://www.kaggle.com/mansoordaku/ckdisease/activity.Moreover, different kinds of features include age, anemia, bacteria, albumin, appetite, blood urea, blood pressure, blood glucose random, diabetes mellitus, coronary artery disease, hypertension, haemoglobin, pus cell clumbs, pus cell, packed cell volume, potassium, RBC, pedal edema, serum creatinine, WBC count, specific gravity, sodium, sugar and RBC count.

4.2 Performance metrics

The description of each performance metric considered for the performance evaluation of the proposed method and its mathematical expression are explained as follows.

(a) Accuracy

The overall count of precise predictions over the whole amount of predictions is termed as accuracy. The accuracy can be mathematical expressed as,

$$Accu = \frac{D+E}{D+E+F+G} \tag{18}$$

Where D signifies true positive, E denotes true negative, F defines false positive and G signifies false negative.

(b) F1 score

The harmonic means of PPV and Recall or TPR (True positive rate) is termed as F1 score. It can be mathematically represented as,

$$F1S = 2\,\frac{PPV \times TPR}{PPV + TPR} \tag{19}$$

(c) Recall

The measure of positive outcomes over the entire count of samples that are actually positive and is also called as Recall. Recall can be mathematically expressed as,

$$R = \frac{D}{D+G} \tag{20}$$

(d) Precision

Precision is represented as the availability of predicted positive that are actually positive. The mathematical expression of precision can be denoted as,

$$P = \frac{D}{D+E} \tag{21}$$

(e) Specificity

The number of negative outcomes over the entire number of samples that are truly negative. The specificity rate can be mathematically represented as,

$$S = \frac{E}{E+F} \tag{22}$$

(f) MCC

MCC is described as the combination between true and projected decisions by undertaking the correlation coefficient evaluation formula that can be expressed as,

$$MCC = \frac{(D*E)-(F*G)}{\sqrt{(E+G)(E+F)(D+G)(D+F)}} \tag{23}$$

(g) Kappa

The steadiness of prediction and employment of probabilistic evaluations amongst the predictable scores in case of disagreement and agreement is determined in Cohen's Kappa Score (CKS). It can be expressed as,

$$K = \frac{\beta_0 - \beta_f}{1-\beta_f} \tag{24}$$

From the above equation, β_0 represents the score agreement between predicted and actual values and β_f describes the score disagreement between actual and predicted ones.

(h) Balanced score

The arithmetic mean of sensitivity and true negative rate is termed as the balanced score that can be mathematically expressed as,

$$BS = \frac{1}{2}\left(\frac{D}{D+E} + \frac{E}{E+F}\right) \tag{25}$$

(i) AUC

The capability of the technique to differentiate between the aimed classes is signified by AUC. It is also termed to be area underneath the receiver operating curve. The performance of AUC is evaluated by mapping the graph for true positive rate (TPR) over FPR.

(j) Positive predictive value

The probability that intends with a positive screening test showing the presence of actual disease is analysed in PPV that can be expressed as,

$$PPV = \frac{D}{D+E} \tag{26}$$

(k) Negative predictive value

The amount of the cases providing negative test outcomes that are really positive is analysed in NPV that can be expressed as,

$$NPV = \frac{E}{E+G} \tag{27}$$

(l) False positive rate

The ratio between the quantity of negative results that are wrongly categorized as positive is analysed in FPR which can be represented as,

$$FPR = \frac{F}{F+E} \tag{28}$$

(m) False negative rate

FNR refers to the proportion of important tests which failed to eradicate the null hypothesis when it is indeed false. It can be mathematically expressed as,

$$FNR = \frac{G}{D+G} \tag{29}$$

(n) Mean Absolute error

The prediction error between the predicted and actual values is termed as MAE. High values of error tend to minimize the CK disease classification accuracy. The formulation of MAE can be expressed as,

$$MAE = \frac{\sum_{v=1}^{m} \left| x_v - y_v \right|}{m} \tag{30}$$

From the above equation, x indicates the predicted value, y represents the actual value and m denotes the total amount of data samples.

(o) Error rate

The proportion of the number of erroneous data units over the entire amount of data units transmitted in a process is termed as error rate. It can be expressed as,

$$Err = \left| \frac{V_a - V_e}{V_e} \right| \tag{31}$$

where V_e denotes the expected value, V_a represents the attained actual value and Err denotes the error percent.

4.3 Performance analysis and comparison

The significant performance metrics adopted for estimating the comparison of proposed and existing approaches including accuracy, F1 score, recall, precision, MCC, Kappa, BS, AUC, PPV, NPV, FPR and FNR are analysed with its description and graphical representation that are explained as follows.Table 3 describes the proposed results in terms of various performance metrics.

Table 3: Performance analysis of proposed work

Technique	Performance metrics	Performance outcomes
Proposed (GNN-DQL)	Accuracy	99.93
	Precision	99.861
	Sensitivity	99.86
	F-measure	99.869
	MCC	99.901
	Specificity	99.911
	BS	99.88
	AUC	99.89
	Kappa	99.72
	FPR	0.011
	FNR	0.013
	NPV	99.3
	PPV	99.20
	Error rate	0.115
	MAE	0.86

Table 4 represents the performance outcomes of proposed and existing methods [26] in terms of accuracy, F1 score, recall and precision.

Table 4: Performance outcomes of proposed and existing techniques

Techniques	Performance outcomes (%)			
	Accuracy	**F1 score**	**Recall**	**Precision**

LR	99	99	100	98
KNN	92	92	88	98
NB	95	95	92	100
SVM	92	92	87	96
DT	97	97	95	100
Proposed	**99.93**	**99.86**	**99.86**	**99.86**

Table 5 signifies the performance results of proposed and existing techniques [27] in terms of specificity, MCC, Kappa, BS and AUC.

Table 5: Result analysis of proposed and existing methods

Techniques	**Performance outcomes (%)**				
	Specificity	**MCC**	**kappa**	**BS**	**AUC**
DT	93	88	87	94	94
SVM	95	91	91	97	96
ADB	95	93	93	97	97
KNN	85	76	76	89	89
GNB	91	88	87	95	95
SGD	84	81	79	92	92
MLP	98	95	94	97	97
LR	99	96	96	98	98
Proposed	**99.91**	**99.90**	**99.72**	**99.88**	**99.89**

Table 6 demonstrates the performance comparison of proposed and existing techniques [28] in terms of PPV, NPV, FPR and FNR.

Table 6: Performance comparison of PPV, NPV, FPR and FNR

Techniques	**Performance outcomes**

	PPV	NPV	FPR	FNR
HKSVM	98.49	95.99	0.029	0.030
SVM	96.70	82.37	0.050	0.160
FMMGNN	89.94	85.49	0.062	0.040
MKSVM	99.00	96.30	-	0.032
Proposed	**0.992**	**99.3**	**0.011**	**0.013**

The performance comparison of MAE and error rate is described in Table 7.

Table 7: Performance comparison of MAE and error rate

	Techniques used								
Performance	RF	NB	SVM	NN	DL	KNN	DT	Auto-MLP	**Proposed**
MAE	0.91	3.8	6.31	3.48	1.96	28.44	4.58	3.78	**0.86**
Performance	**Techniques used**								
	ANN-HFWE-FS	NB-HFWE-FS	SVM-HFWE-FS	NB	ANN	SVM	**Proposed**		
Error rate	13.33	14.77	6.67	33.33	30.00	26.67	**0.115**		

Confusion matrix

The significance of the proposed CK disease model in classifying the five different stages including normal, mild, moderate, severe and end. Figure 2 describes the confusion matrix using training data for the proposed model of CK disease classification.

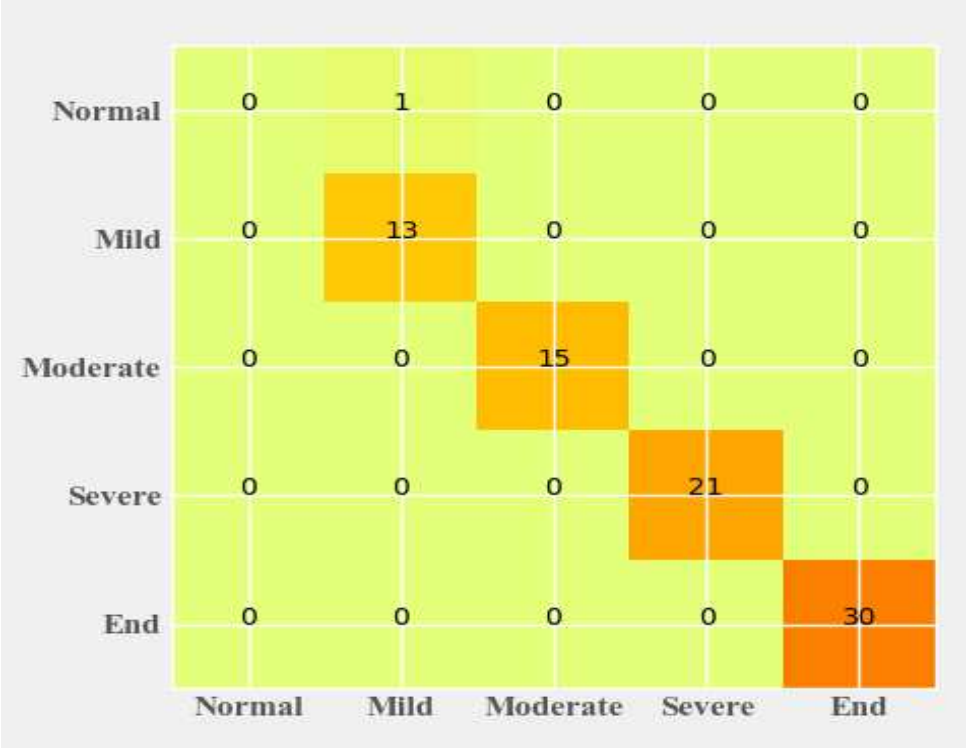


Figure 2: Confusion matrix

Here the data collected from different people for classifying the five stages of CK disease are considered. From the figure, it can be clearly analysed that the proposed model accurately classifies the stages of CK disease with improved accuracy which are represented in the diagonal format. The remaining values represent the number of wrong predictions made with respect to each stage. For example, 1 normal person is wrongly predicted as mild stage. The mild, moderate, severe and end stages are precisely classified with no error and hence the accuracy of the proposed model is widely enhanced.

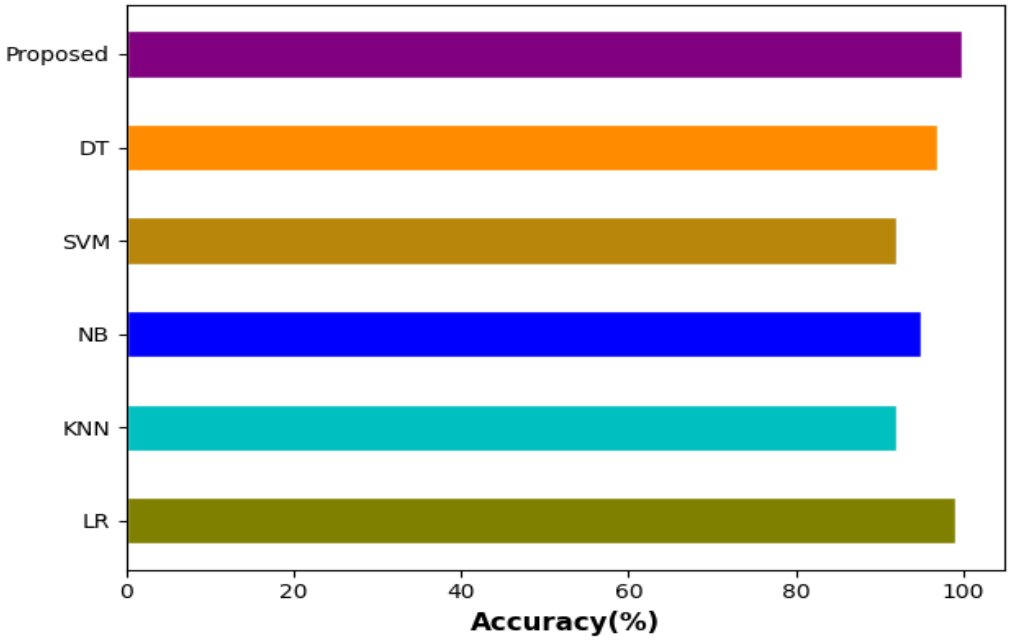


Figure 3: Accuracy comparison

Figure 3 provides the graphical representation of the performance measures in terms of accuracy. From the figure, it is clear that the accuracy attained by the proposed model is found to be highly accurate when compared to the existing models like LR, KNN, NB, SVM and DT. The overall accuracy of the proposed model is attained to be 99.93%. the existing models obtained lower accuracy due to larger accumulation of datasets, degraded system performance and increased complexities. Higher rate of accuracy insists that the technique accomplishes better classification performance.

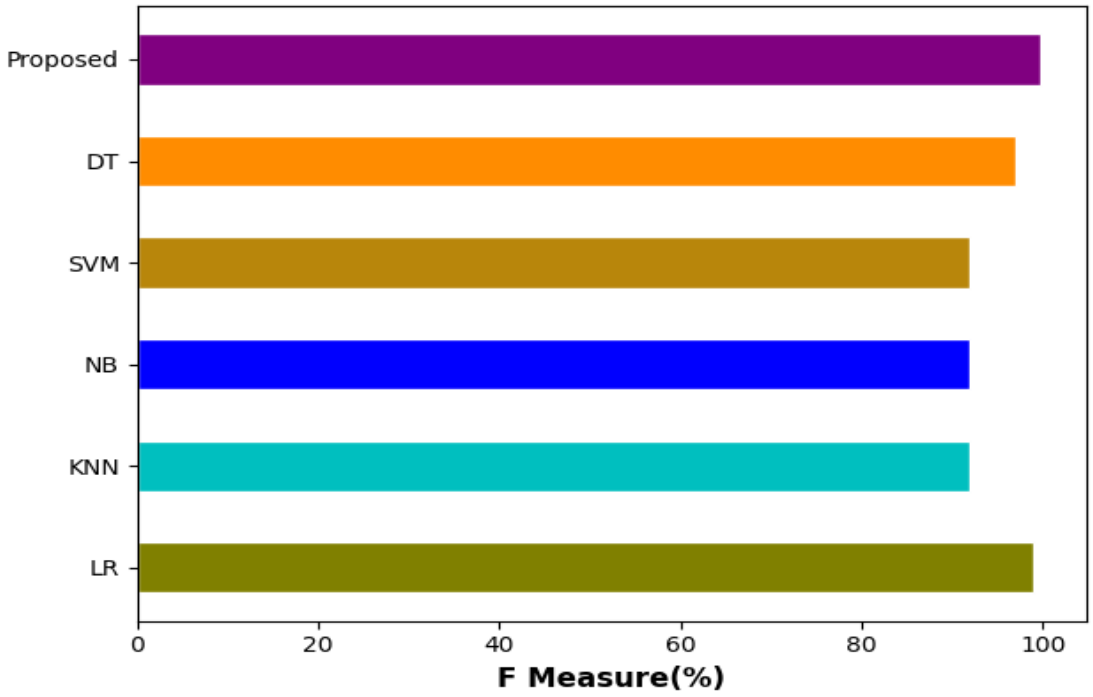


Figure 4: Performance comparison of F1 score

Figure 4 illustrates the graphical representation of F1 score in terms of proposed and existing techniques. It is made clear that the proposed method attains more capability to classify the CK disease depending on the input parameters when compared to the existing techniques. The value of F1 measure is attained to be 99.86% in the proposed method whereas the existing approaches like LR obtained 99% of F1 score, KNN as 92%, NB as 95%, SVM as 92% and DT as 97%in classification performance. In the proposed method, F1 measure shows better results in classifying the different stages.

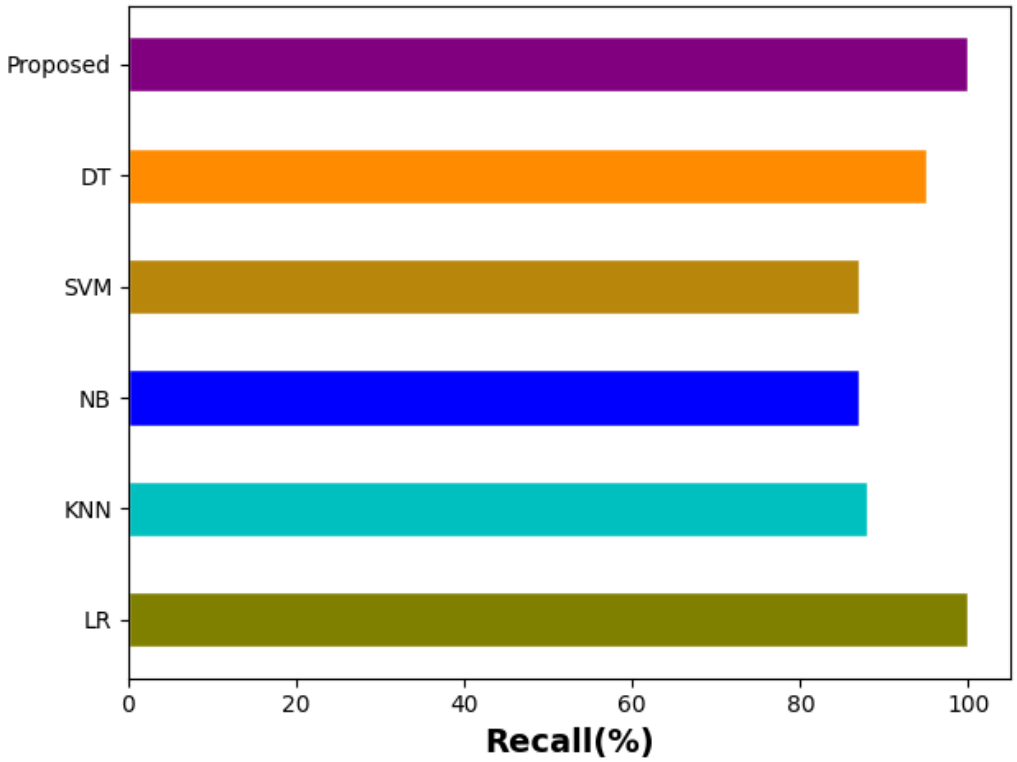


Figure 5: Performance comparison of Recall

The graphical representation of recall on the basis of proposed and existing approaches is presented in Figure 5. 99.86% of recall is obtained while assessing the performance of the proposed technique in contrast to the existing approaches. The existing learning algorithms has accomplished100%, 88%, 92%, 87%, 95% with respect to LR, KNN, NB, SVM and DT. Due to high complexities of time and storage, the existing approaches tends to offer lower performance other than LR approach when compared to the proposed method.

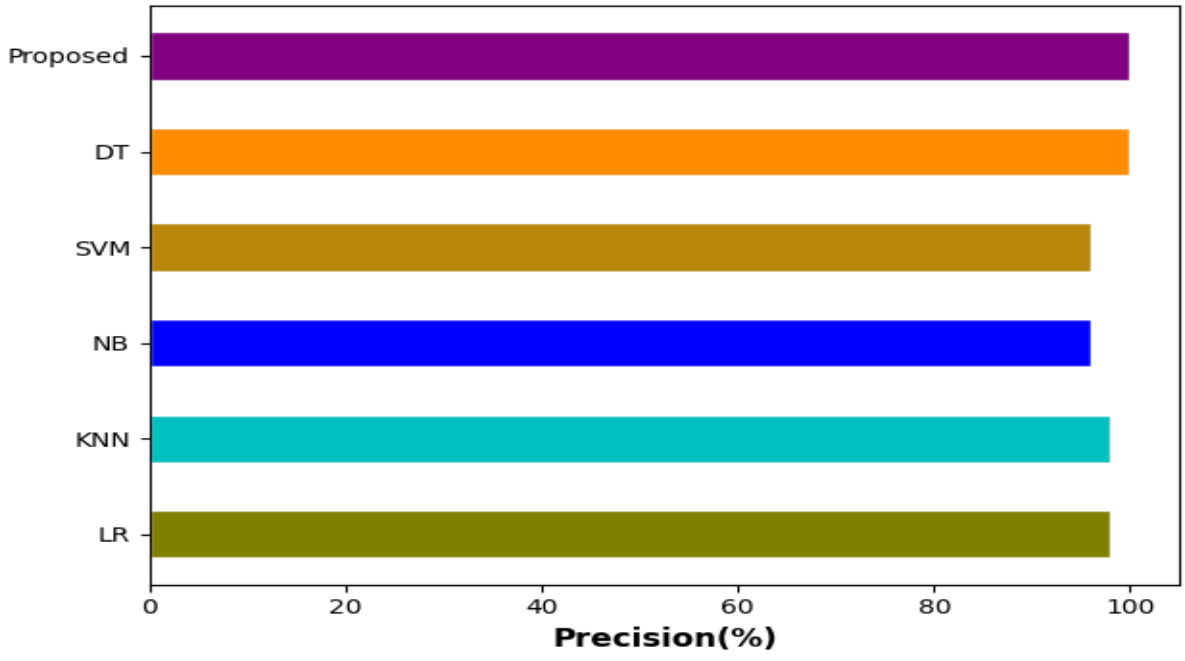


Figure 6: Precision performance

The graphical representation of precision in terms of proposed and existing approaches are shown in Figure 6. Precision is one of the prominent metrics to be measured for gathering the effectiveness of outcomes. The proposed GNN-DQL method has attained 98% of precision and showed a better result in reducing the false detection rate. While the existing learning methodologies other than NB and DT has achieved lower results when compared to the proposed approaches. Finally, from the figure, it is estimated that the proposed technique outperforms well than the existing methods due to higher ability in data handling process.

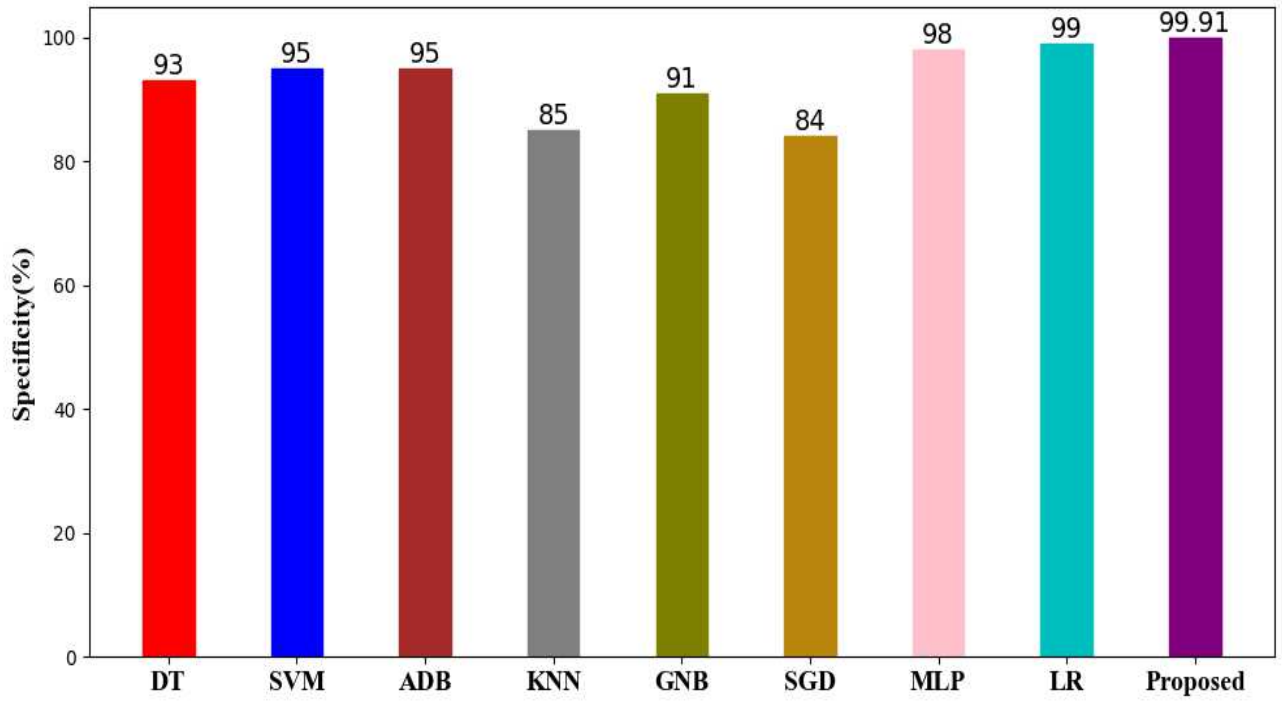


Figure 7: Specificity performance

Figure 7 presents the performance values obtained over the experiments in terms of specificity for proposed and existing approaches. The results illustrates that the proposed model performed better in classifying the various stages of CK disease effectively than the other compared models. The overall specificity performance of the proposedmethod is found to be 99.91%. The proposed method has improved the classification performance high specificity. The selection of optimal features helped in optimally predicting the outcomes based on the input attributes. Whereas the performance attained in the existing methods like DT, SVM, ADB, KNN, GNB, SGD, MLP and LR are 93%, 95%, 95%, 85%, 91%, 84%, 98% and 99% respectively.

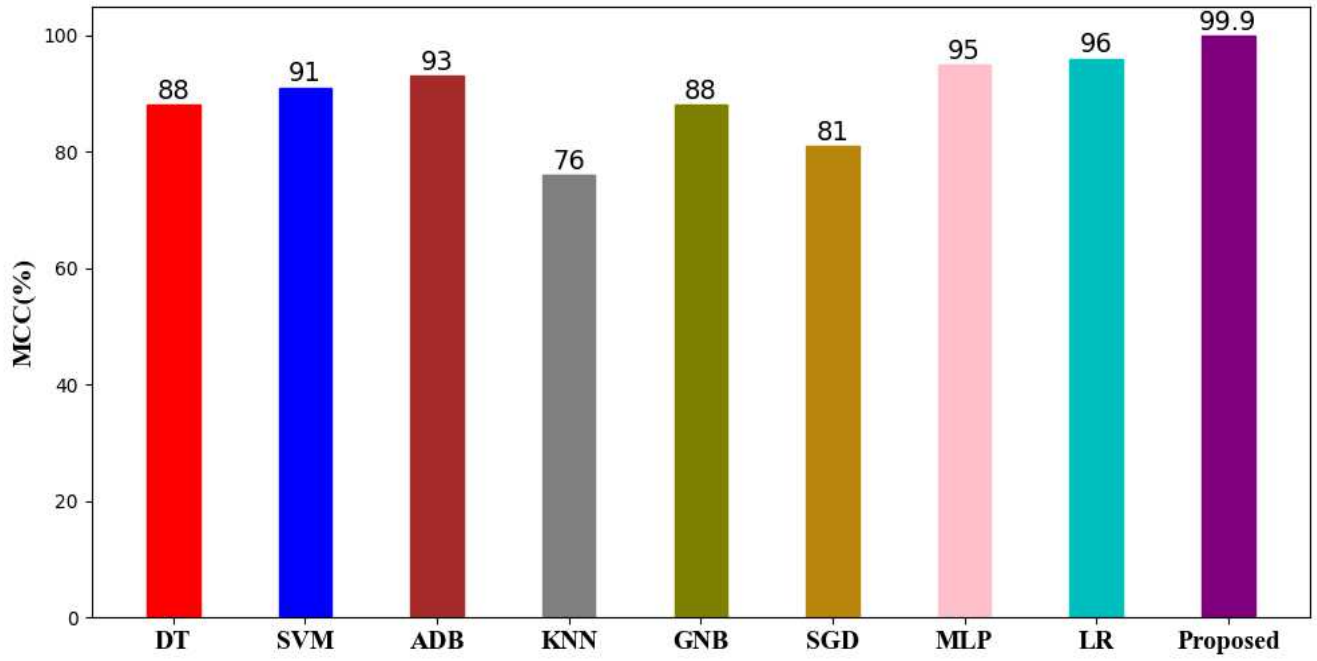


Figure 8: MCC performance

The performance of MCC for the proposed technique is analysed with existing methods and the attained outcomes are portrayed in Figure 8. In the figure, it is clearly shown that the proposed technique has gained improved correlation between true and predicted decisions than the existing methods. This obviously exposed that the proposed method has established minimum false rate and superior to CK disease classification stages. MCC attained by the proposed method is 99.90% whereas, the existing methods like DT, SVM, ADB, KNN, GNB, SGD, MLP and LR are88%, 91%, 93%, 76%, 88%, 81%, 95%and 96% respectively.

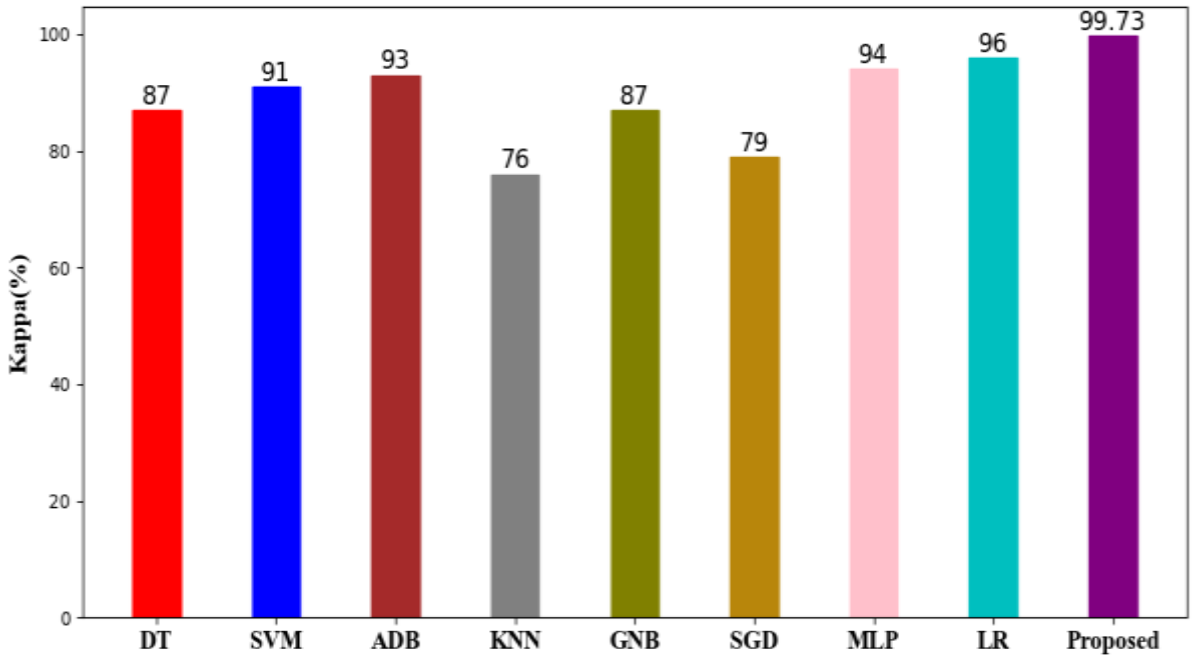


Figure 9: Kappa performance

Figure 9 represents the graphical illustration of kappa performance in CK disease classification. High kappa values are obtained in the proposed approach as 99.72% which shows better outcomes when compared to the existing approaches. When compared to the existing methods of DT, SVM, ADB, KNN, GNB, SGD, MLP and LR, the kappa performance of the proposed method tends to be highly superior in classifying the CK disease. Efficient performance can be attained in testing the data reliability gathered for CK disease classification. The performance of kappa among the existing method are found to be low because of larger accumulation of information from the datasets.

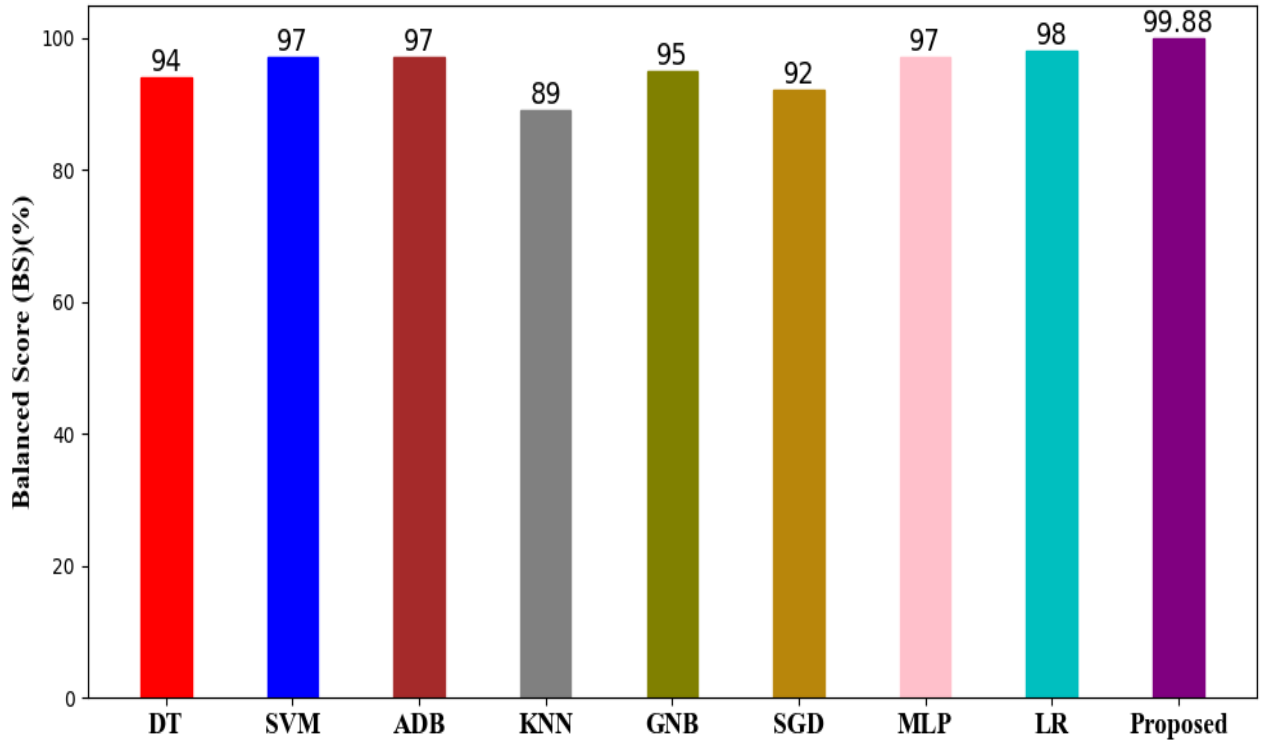


Figure 10: Performance of BS

Figure 10 signifies the BS performance of proposed and existing methods. The proposed model has attained 99.88% because of limited redundant features and false rates. The result of BS is analysed with other existing methods like DT, SVM, ADB, KNN, GNB, SGD, MLP and LR which have obtained 94%, 97%, 97%, 89%, 95%, 92%, 97% and 98% respectively. On this performance evaluation, it is found that the proposed method is highly efficient in CK disease classification.

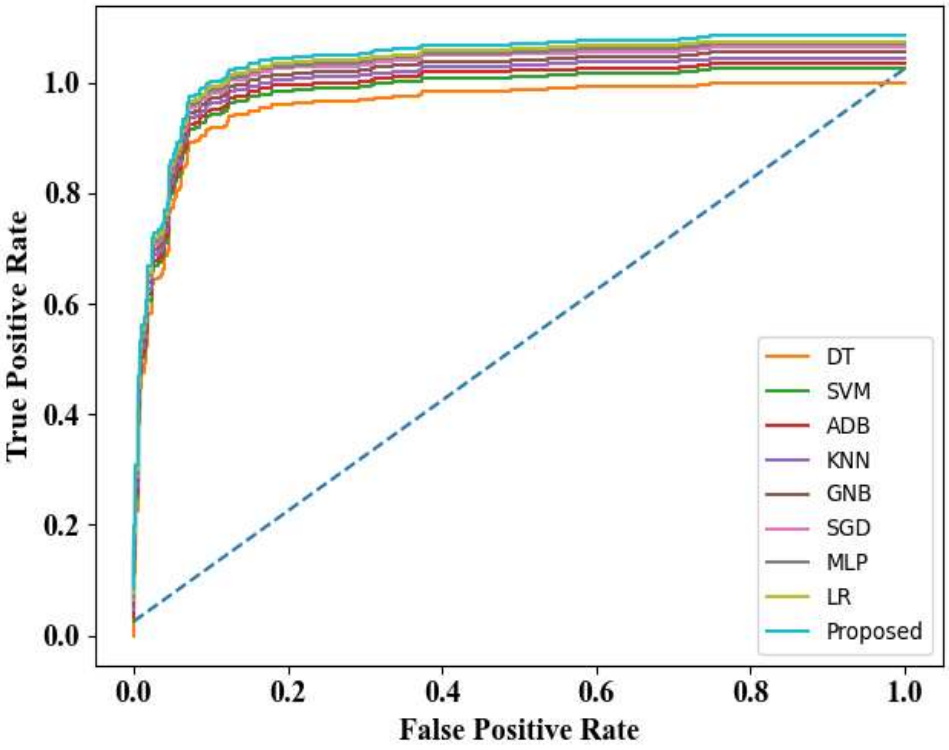


Figure 11:AUC analysis

Figure 11represents the AUC comparisonin terms of proposed and existing approaches. The proposed method possesses better ability to differentiate between the target classes. The graph has plotted between FPR and TPR to establish the AUC value. The proposed method has attainedthe AUC value of 99.89%, that is superior than the other state-of-art techniques since, it has improved the capabilityin CK disease classification on the basis of input parameters.

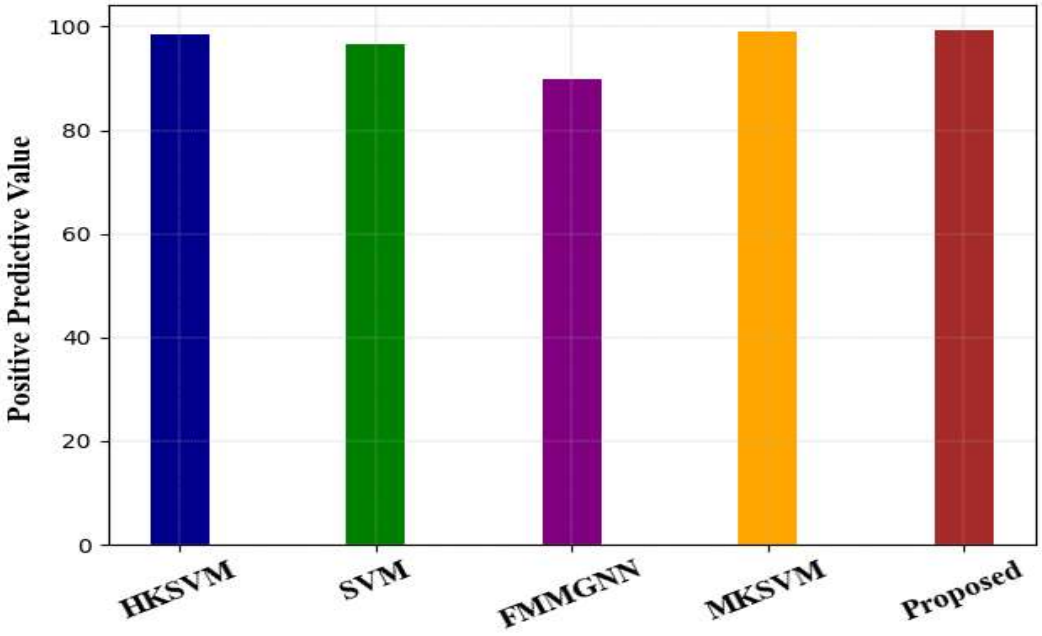


Figure 12: PPV performance

Figure 12 establishes the comparison of PPV with different methods including SVM, MKSVM, HKSVM, and FMMGNN. From the graph, it can be analysed that the proposed technique has accomplished better result when compared to the other approaches. The proposed method attains maximum PPV of 0.992 so the false detection rate is found to be very low. When comparing with the other techniques, FMMGNN has attained very low PPV of 0.89 whereas the MKSVMhas reached better value of 0.99, which is inferior than the proposed technique. Overall, it is shown that the proposed model outperformed when compared to the existing methods considerably.

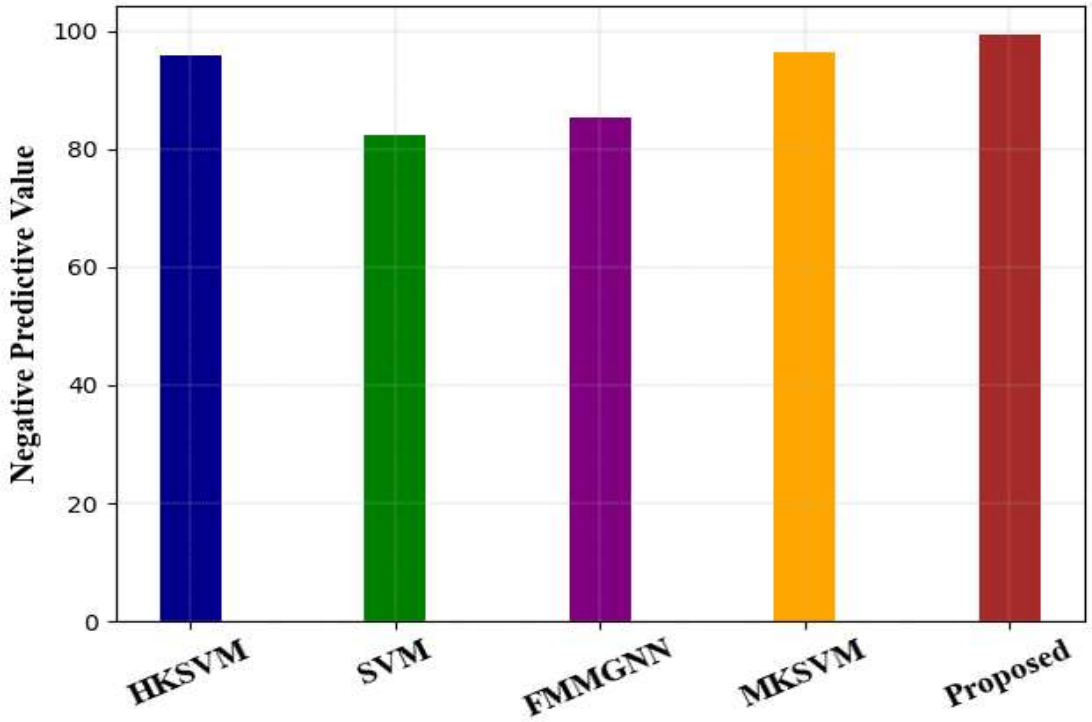


Figure 13: NPV performance

The performance evaluation of NPV in terms of proposed and existing methods are illustrated in Figure 13. The existing methods such as MKSVM, HKSVM, SVM and FMMGNN are adopted to analyse the NPV performance in comparison with the proposed model to classify CK disease. From the figure, it is perceptibly analysed that the proposed approach has attained maximum NPV than recent existing approaches. The NPV value obtained by the proposed model is99.3 whereas, the existing methods have secured95.99, 82.37, 85.49 and 96.30 for HKSVM, SVM, FMMGNN, and MKSVM considerably.

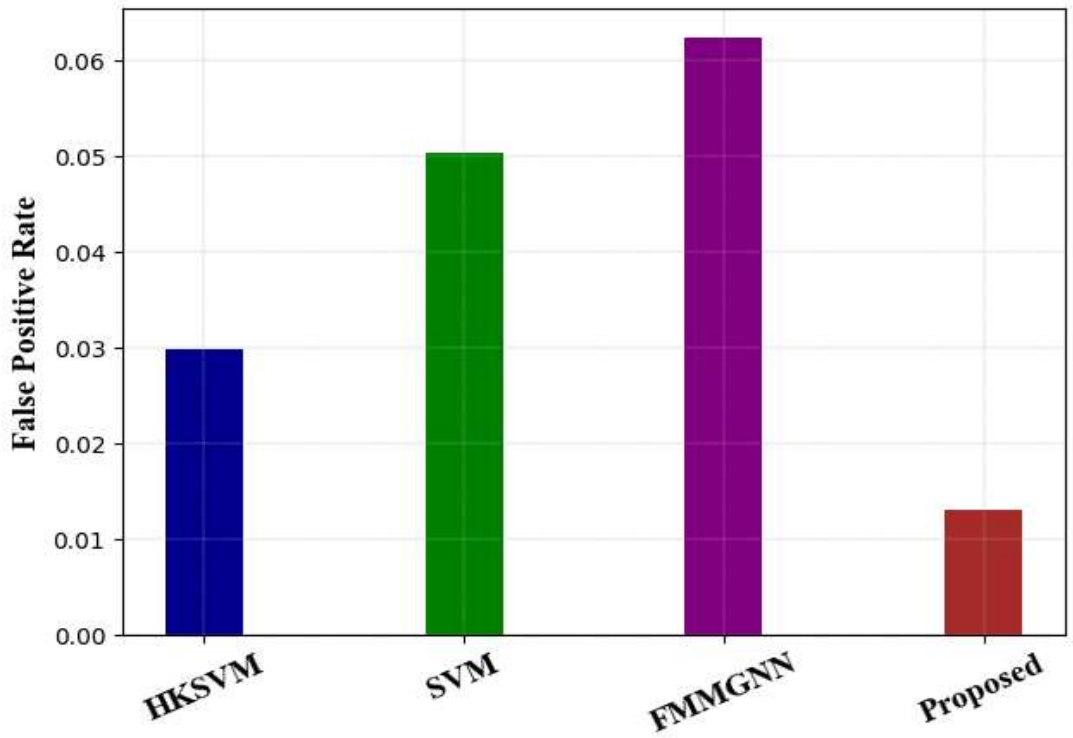


Figure 14: FPR performance

FPR of the proposed method is compared with the existing approaches and the attained outcomes are demonstrated in Figure 14. From the graph, it can be analysed that the proposed technique has accomplished less FPR than the existing techniques. This shows that the proposed method is superior in classifying the different stages of CK disease. The FPR value achieved by the proposed method is 0.011 whereas, the FPR values of the existing methods including HKSVM, SVM, FMMGNN are 0.029, 0.050 and 0.062 respectively.

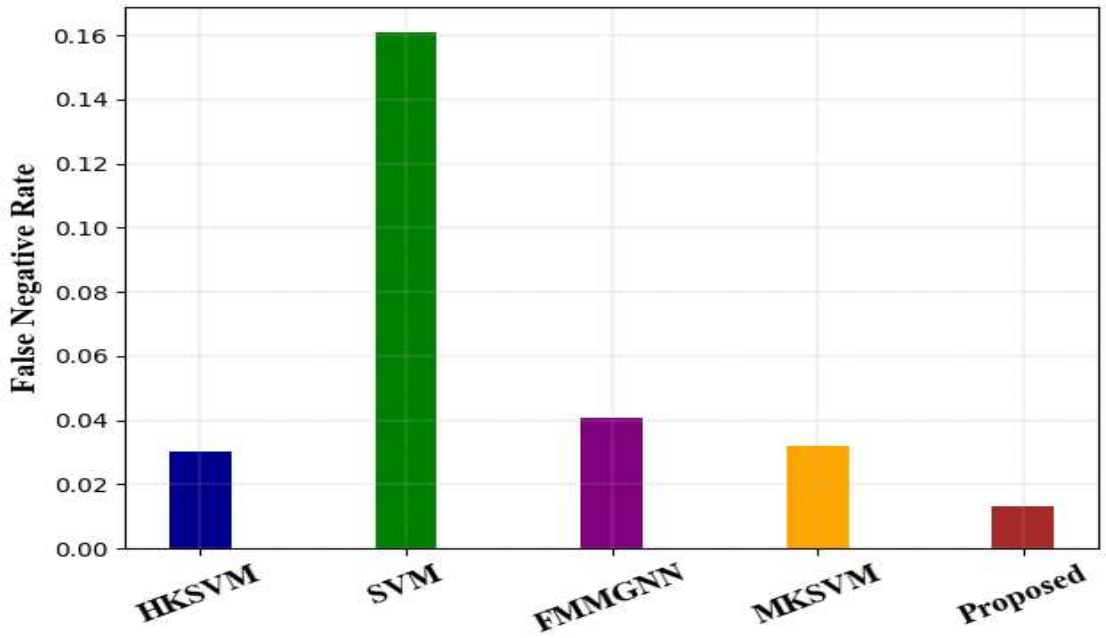


Figure 15: FNR performance

FNR of the proposed method is compared with the existing methodologies and the obtained outcomes are presented in Figure 15. For an efficient system, the FNR performance value has to be comparatively low. It is clearly observed from the figure that the proposed technique has attained less FNR than the existing techniques. This indicates that the proposed method has accomplished less false rate and appropriate for effective classification. The FNR value obtained by the proposed method is 0.013 whereas, the FNR values of the compared methods like HKSVM, SVM, FMMGNN, MKSVM are 0.030, 0.160, 0.040 and 0.032 correspondingly.

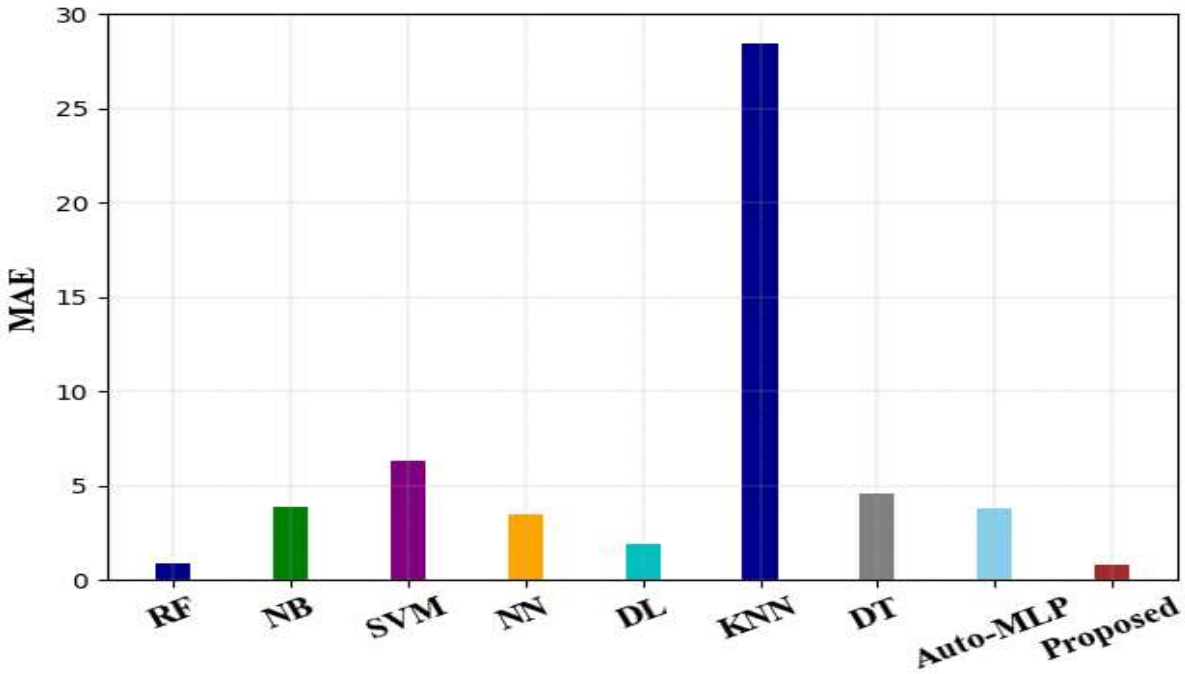


Figure 16: MAE performance

Figure 16 presents the MAE performance of the proposed modelanalysed in CK disease classification. Minimized error rates enhance the classification performance with reduced wrong predictions. The MAE performance is comparatively low for the proposed model compared to the existing approaches like RF, NB, SVM. NN, DL, KNN, DT and Auto-MLP [29].Therefore, the existing approaches are found to be inappropriate for CK disease classification process. The MAE is obtained to be 0.86 which is adversely low than the existing methods because of effective learning algorithm.

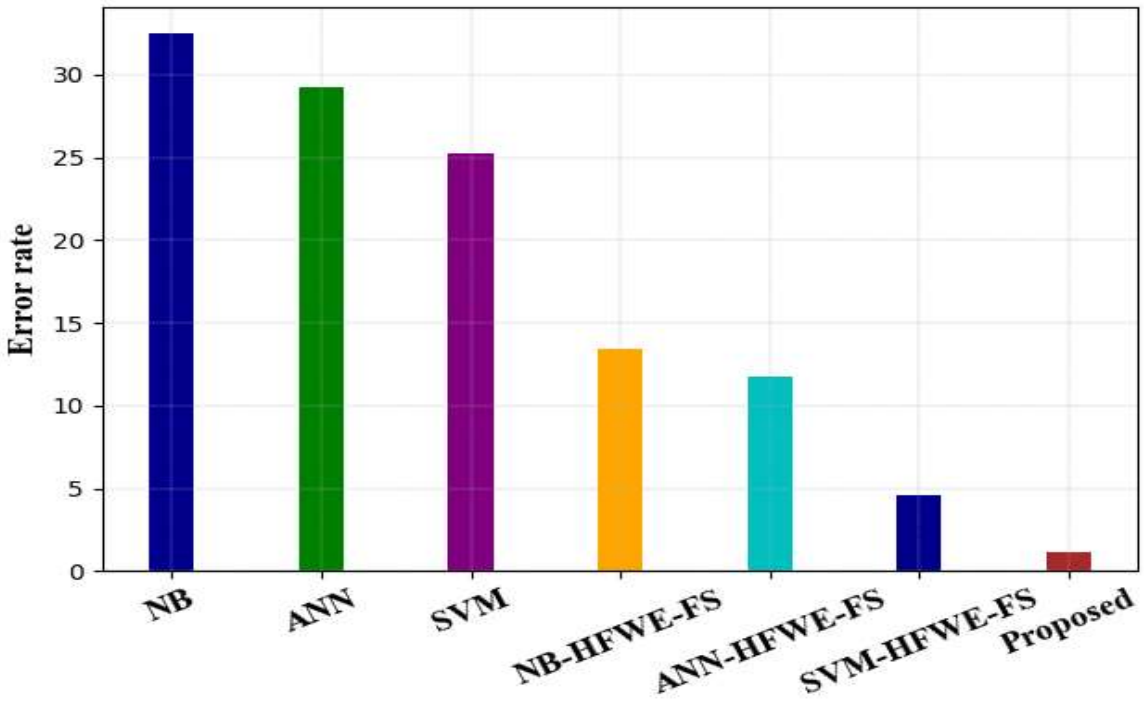
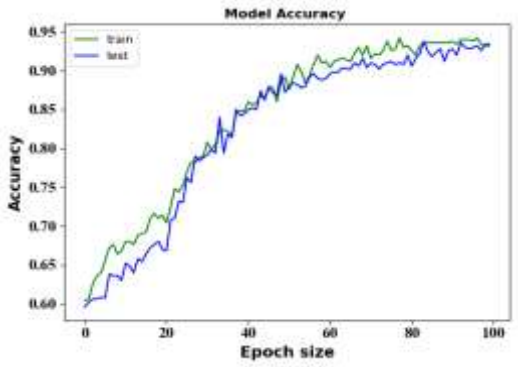


Figure 17: Performance of error rate

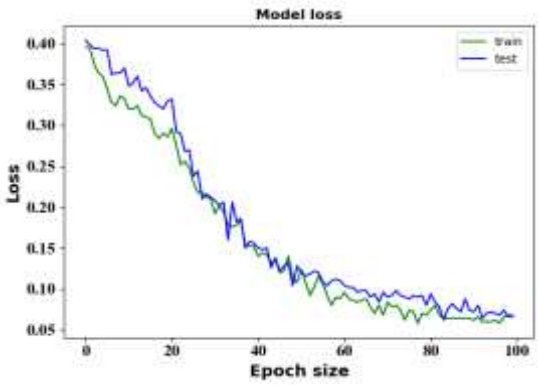
Figure 17 presents the error rate outcomes of the proposed and existing models obtained during CK disease classification. The figure shows that the error performance of the proposed modelis found to be more optimal than the other existing methods. The error rate of hybrid model is found to be 0.115 and the error rates of existing approaches like NB-HFWE-FS, ANN-HFWE-FS, SVM-HFWE-FS, NB, ANN and SVM [30] are found to be 14.77, 13.33 6.67, 33.33, 30.00 and 26.67 respectively. The classification of the proposed model isobtained to provide fruitful results than the other models.

Training and testing measures for model accuracy and loss

The loss and accuracy of the proposed approach is analysed with training and testing data. In the proposed research, 80% of data is adopted to train the model and 20% of data is adopted to test the model. The training and testing model accuracy and loss of the proposed approach is depicted in Figure 18 (a) and (b).



(a)



(b)

Figure 18: (a) Model Accuracy (b) Model loss

By varying the epoch size, all the accuracies and losses of the proposed model are evaluated. The accuracy for the two cases is similar. While observing the training and testing accuracy, only slight variations are captured with high accuracy. The increase in accuracy may occur due to the increased epoch size. If the epoch size is 40, the proposed model procures a training and testing accuracy in the range of 80 to 85% consecutively. If the epoch size is 60, the model retains accuracy in the range of 85 to 90% and if the epoch size is increased to80, the proposed model generates an accuracy in the range of 90 to 100%. And from the figure, it is obvious that the proposed approach achieves maximum accuracy and the accuracy is almost similar for training and testing data samples.

The training and testing loss is procured for the proposed model and the network has been trained for 100 epoch size. The increase in epoch size decreases the loss. If the epoch size is 40, the model attains a training and testing loss in the range between 0.15-0.20. If the epoch size is 60, the model acquires a loss in the range of 0.10 to 0.15. For epoch size 80, the value ranges between 0.10 to 0.5. The model achieved minimal error value due to optimal training through the adoption of MAO approach for optimizing.

5. Conclusion

CK disease is one of most threatening diseases in the recent years and exact diagnosis is most challenging. In the proposed research work, precise classification of five stages of CK disease like normal, mild, moderate, severe and end is attained through GNN-DQL approach. The unwanted distortions are eradication through data pre-processing which includes Handling Missing Values, Categorical Data Encoding, Data Transformation and Outlier Detection. The GFR rate is evaluated with respect to age and SC level for obtaining the enhanced result. Then, GNN-DQL technique is carried out for improving the classification accuracy. The parameters are optimized through AMO method and the five stages of CK disease are precisely classified. The classification performance is analysed with respect to accuracy, precision, recall, specificity, F1 score, confusion matrix and so on. The proposed method is implementedand the performances are analysed using PYTHON simulation tool. The classification accuracy of 99.93% is observed in the CK disease classification of five different stages. The MAE and the error rate are attained to be 0.86 and 0.115 which are comparatively less than the other existing approaches. The proposed model is tested with smaller datasets and to enhance the system performance, significant volumes of data will be gathered in the future for better results. In addition to this, valuable features will be implemented to attain a wider perception over the enlightening parameters regarding CK disease.

Abbreviations

CK:Chronic Kidney ,GNN-DQL :graph neural network based deep Q learning, IoMT: Internet of medical things, GFR: Glomerular Filtration rate ,AMO: Adaptive Mayfly Optimization, HB:High Blood, SEED: Singapore-epidemiology-eye-diseases, KNN:K-Nearest Neighbour,LR: Linear Regression, DT:Decision Tree, NB:Naive Bayes, MCC:

Mathew's correlation coefficient, BS: Balanced score, MLP: Multilayer Perceptron, GNB: Gaussian Naive Bayes, FMMGNN: Fuzzy Min-Max GSO Neural Network,;

Acknowledgements

Not applicable.

Authors' contributions

TBPR has found the proposed algorithms and obtained the datasets for the research and explored different methods discussed. and contributed to the modification of study objectives and framework. The rich experience was instrumental in improving our work. VD has done the literature survey of the paper and contributed writing the paper. All authors contributed to the editing and proofreading. All authors read and approved the final manuscript.

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Availability of data and materials

This dataset comprises of 400 instances, 76 parameters and 25 attributes. But the data may subject to noisy data and numerical missing values that has been retrieved systematically through pre-processing. For analysing the results, the dataset has been splitted into training and testing sets as 80% and 20%. The download link of the gathered dataset is https://www.kaggle.com/mansoordaku/ckdisease/activity

Declarations

Ethics approval and consent to participate

Not applicable

Consent for publication

Not applicable.

Competing interests

The authors declare that they have no Competing interests.

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