GNN-DQL-Based Chronic Kidney Disease Classification Using GFR in the Internet of Medical Things Environment

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Abstract: *Detection of Chronic Kidney (CK) disease is one of complex technique even in this modern technological era. Precise identification of CK disease is essential to provide treatment for patients with care. Several techniques were recently developed for precisely diagnosing CK diseases. However, certain forms of disadvantages still appear, including an incorrect selection of features, the need for large storage space, a requirement for an effective learning model, less accuracy, and high complexity related to time and cost. Few limitations and drawbacks are occurred and it provide less performance to detect CK disease. Therefore, the Neural Network Graph-based Deep Q-Learning (GNN-DQL) technique is proposed to classify five different states such as end, severe, moderate, mild and normal. First, real-time data will be gathered using and Bio-Medical sensors (BMs) and Internet of Medical Things (IoMT). Then, pre-process the data to improve the quality using missing value treatment, categorical data coding, transformation, and outlier detection to eradicate unwanted biases. The age and Serum Creatinine (SC) level of patient will be diagnosed using Glomerular Filtration Rate (GFR). Finally, classify the CK disease based on classes using GNN-DQL technique which provide better accuracy. The Adaptive Mayfly Optimization (AMO) algorithm is used to optimize the parameters. The simulation tools analyze the classification performance based on accuracy, precision, recall, specificity, F1-score and so on. The obtained accuracy of proposed model is 99.93% to detect the CK disease based on the five different classes from the real-time data.*

Keywords: *Deep learning, neural network, Q-learning, glomerular filtration rate, mayfly optimization, optimal features, parameter optimization, AMO.*

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1. Introduction

Chronic Kidney (CK) is a serious disease, mainly in developing countries [20]. The timely detection of chronic diseases and the tracking of risk factors slow the progression of diseases and can rule out dangerous events in everyday patient life. An unidentified CK disease leads to various problems that put patients in high-risk circumstances [6]. 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 for CK disease are heart disease, diabetes, and High Blood (HB) pressure [10]. Diabetes frequently gets referred as HB sugar that may harm human kidney blood vessels. The blood arteries in the kidneys are additionally damaged by HB pressure [5]. Kidney disease, is most serious condition which closely linked to heart disease.

Chest pain, tiredness, loss of hunger, feeling dizzy, loss of weight, muscular pain, problems with concentration, and sleep issues are symptoms of CK disease [13]. The health of a person is significantly affected by their body temperature. The patient's health can be routinely monitored to reduce the risk of their life. Therefore, Bio-Medical sensors (BMs) can able to diagnose the disease by detecting it in early stages. It identified the CK disease by comparing breath samples from patients with analysis of breath samples from healthy subjects [12]. A typical BM device consists of a small battery-operated board with memory, a microprocessor, and a radio frequency transceiver. Data Mining (DM) combines information from BM devices, stores information, and successfully sends information to patients [25].

Some common features of the DM process are flexibility, robustness, trade-off energy efficiency, etc. The simple reasoning of health identifying devices in BM readings like calculating hours of sleep or the number of processes per day at better information processing levels to provide correct patient data [11]. To enhance the well-being of individuals, medical facilities has recently cantered on higher DM activities [22]. Model data learning, extraction and identification, and information pre-processing form the DM technique [23]. Meta-data and specialized understanding belong to the features which facilitate tasks like identification, prediction, and Decision-Making (DM). Pre-processing

techniques help filter unusual input data information to remove high-frequency noise [1].

The purpose of identify the features by extracting some particular feature of data from information which categorize the CK disease. There two classified methods used in Machine Learning (ML) named unsupervised and supervised learning, also known as descriptive and predictive, respectively [4, 16]. The training information of supervised learning methods, including facial recognition via images, medical diagnosis systems and spam classifiers of patient emails, can be considered from prediction and query data [17]. Several supervised methods include Support Vector Machines (SVMs), kernel machines, Decision Trees (DTs), Logistic Regression (LR), decision forests, Bayesian classifiers and Neural Networks (NNs). ML can achieve a significant task, but it is still unable to replicate Human Intelligence (HI) [7]. These drawbacks can be rectified using Deep Learning (DL), a subcategory of ML.

NN in DL is majorly used for clustering, classification and predication which trains some amount of data to provide efficient outcome [9]. It has its roots in NN, consisting of algorithms loosely modelled on the human brain and designed primarily to find patterns. The main goal of DL models is to bring better performance outcomes based on Internet of Medical Things (IoMT) data, thereby expediting research in this field [3, 24]. BMs are used all over the world, which used to measure blood levels and help patients cope with diabetes [14, 28]. Such sensors are specifically implanted under the skin. It offers continuous monitoring and measurement of blood levels in patients. As mentioned earlier, this research proposes a new deep-learning technique to overcome ML problems.

The proposed research uses a novel methodology to accurately classify the five stages of CK disease. Few prominent contributions described the process of proposed model briefly as follows.

1. To generate the CK disease data through BMs on several people and gather the data using IoMT.
2. To pre-processing the data through handling missing values, categorical data encoding, data transformation, and outlier detection to eliminate undesired deviations.
3. To classify different stages of CK disease, Glomerular Filtration Rate (GFR) is used to diagnose based on age and Serum Creatinine (SC) level.
4. To classify the using a Graph Neural Network with a Deep Q-Learning Technique (GNN-DQL) classifier based on five classes.
5. The Adaptive Mayfly Optimization (AMO) approach optimizes the parameters for precise classification outcomes.

The remaining content of this paper is organized into several sections such as: Section 2 contains the survey over CK disease with several classification and predication techniques using DL. Section 3 includes the overall process and descriptions of proposed model with equations briefly. The overall performance and obtained values of proposed model described with graphs and discussion also includes in describe the outperformance of proposed mode; in section 4 using the Python simulation tool. Finally, overall conclusion of the paper is described with future work in section 5.

2. Related Works

Based on the classification of CK disease, most researchers have used several techniques to get precise results. Some related works were analysed and described briefly in Table 1 as follows.

Table 1. Survey over related techniques with its performance and demerits.

Author name and reference	Techniques used	Objective	Merits	Demerits	Performance (%)	Dataset used
Venkatesan *et al*. [26]	DSCNN	To classify the CK and non-CK diseases	Less computational effort	Limited number of data were used for testing	99.18% categorization accuracy	CKD dataset
Jerlin *et al*. [8]	Deep-kidney	To predict CKD possible occurrence within 6 or 12 months	Efficient performance	Higher time consumption	99.3% and 99.2% accuracy for 6 and 12-month data prediction	CKD dataset
Rezayi et al. [18]	SVM and RF	To predict the CKD by balancing the dataset	Lowest false-negative rates	Limited features were extracted to train the model	99.33% and 98.6% accuracy	UCI NL dataset repository
Parthiban *et al*. [15]	XGBoost	To predict the CKD through prior detection	Achieve best classification results	Required to fine-tune the model for efficient performance	98.00% accuracy	CKD dataset
Susan and Subashini [21]	Inductive transfer-based ensemble DNN	To predict the CKD for quality and noisy image datasets	Increase the classification accuracy	Lower learning rate	99.8% and 96.7% accuracy for quality and noisy image	KD1, KD2, and KD3 datasets

Venkatesan *et al*. [26] developed a novel Hybrid DL Network model (HDLNet) model for Chronic Kidney Disease (CKD) early detection and prediction. Here, the Deep Separable Convolutional Neural Network (DSCNN) was developed for early CKD detection and Capsule Network (CapsNet) was utilized to extract more processing attributes of features. The Aquila Optimization Algorithm (AO) was used to select optimal features to reduce computational effort. Finally, the Sooty Tern Optimization Algorithm (STOA) was

used to optimize DSCNN technique to detect the key illness as CKD or non-CKD.

Jerlin *et al*. [8] developed a three-predictive mode to predict the Diabetic Kidney Disease (DKD) within 6 or 12 months. The deep ensemble model fuse Convolutional Neural Network (CNN), deep ensemble model and Long Short-Term Memory (LSTM) were combined these three based DL classifiers using majority voting techniques. This technique attains 99.3% and 99.2% accuracy for 6 and 12-month data prediction.

Rezayi *et al*. [18] analyzed robust ML models named Support Vector Machine (SVM) and Random Forest (RF). Here, the Synthetic Minority Over-sampling TEchnique (SMOTE) algorithm and scaling of features were used to balance the dataset. Then, the least-required set of adequate and highly correlated features were extracted using the statistical technique named chi-squared test. This technique attains 99.33% and 98.6% accuracy for CKD detection of SVM and RF.

Parthiban *et al*. [15] analyzed ML techniques such as SVM, K-Nearest Neighbors (KNN), RF, Decision Tree (DT), LR and eXtreme Gradient Boosting (XGBoost) for CKD detection. By comparing to other ML techniques, the XGBoost achieves higher accuracy at 98.00%.

DL inpainting model on digital and medical images-a review by Susan and Subashini [21]. An automated detection of Computed Tomography (CT) kidney stone image. The pre-trained Deep Neural Network (DNN) models named InceptionV3, DarkNet19 and ResNet101 were used to generate three datasets for feature extraction. Then, the feature concatenation was performed using the ensemble deep feature vector. The most informative ensemble deep feature vector was selected using the Iterative ReliefF feature selection. Finally, the KNN classifier with Bayesian optimizer approach to detect kidney stones. This technique achieves 99.8% and 96.7% accuracy for quality and noisy image.

When reviewing the existing approaches to CK disease classification, certain drawbacks emerge that severely impact the overall system's performance. Due to limited available dataset, lower-performance models were obtained, require a larger amount of training data to promote an effective classification process, and quantified variations of vessels and unusual lesions degrade the output performance. In addition, high computational time and power consumption were obtained. In addition, diagnose the disease require high time to process and power. An effective deep-learning technique is proposed in this research paper to solve these issues.

3. Proposed Methodology

CK disease is found to be highly threatening as it adversely affects the working conditions of the kidney. If it is not recognized early, affected people can get into severe conditions. Most patients are left at critical stages due to improper or wrong prediction of diseases. Although many CK disease classification techniques are presented in the existing works, precise results cannot be attained [19]. Hence in the proposed research work, the GNN-DQL model adopted precise classification stages of CK disease. The overall architecture for accurate classification of CK disease with different stages is illustrated in Figure 1.

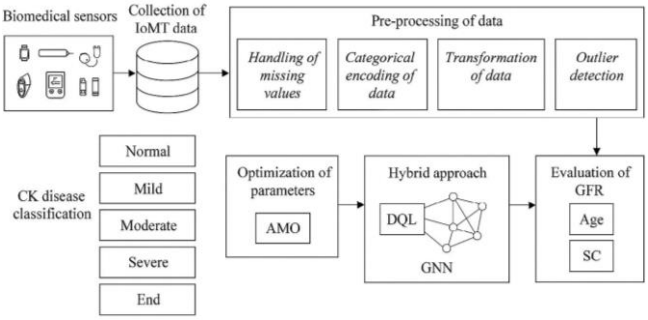


Figure 1. Overall architecture of CK disease classification.

Initially, the BMs are used to evaluate different factors of CK disease, such as SC, sugar, Red Blood Cells (RBC), White Blood Cells (WBC), potassium, etc. The data centre collects the data which gathered from BM sensor through IoMT. To improve data quality, pre-processing is the first step to eliminate the unwanted alterations present in the data. GFR is evaluated, and the GNN-DQL model is utilized to classify and predict several stages of CK disease, including normal, mild, moderate, severe and end-stage. Parameters of NN are then optimized through the AMO approach [22]. The steps processed in the proposed research work are given as follows:

3.1. Data Pre-Processing

In this stage, the evaluation of missing values and eradication of noises like outliers is performed. Also, validation and normalization of unstable data are undertaken. During the patient assessment, some of the estimations are incomplete or missing. To compensate that, several pre-processing steps are accepted out in proposed research work is described as follows:

3.1.1. SMOTE for Data Augmentation

Although some dataset categories include much fewer samples than others, which is known as class imbalance. It leads to inaccurate prediction of CKD. This issue is addressed by using the Synthetic Minority Over-sampling TEchnique (SMOTE) technique. By ensuring balanced representation, these techniques improve the model's generalization and classification precision at all stages of CKD. The SMOTE is used to reduce the issue of imbalanced datasets. This technique is used to oversample the minority class in the dataset by generating new samples for each minority class and its

nearest neighbours. The mathematical expression for each synthesized sample is described as follows.

$$A_{Sample} = A_x + R(0,1) \times |A_x - A_N| \quad (1)$$

Here, the given sample from the minority class is denoted as A_x, a randomly selected sample from K-nearest neighbours to the sample A_x is represented as A_N. The random number between 0 and 1 is denoted as *Rand*(0,1).

3.1.2. Handling of Missing Values

The modest method of working with the missing values neglects the records, but it is impossible with the smaller datasets. During the data generation process, the datasets were analysed to confirm that any attributes values are missing. The missing values for numerical structures are evaluated through the adoption of arithmetical method of mean imputation. The mode is used for lost value replacement of insignificant features [26].

3.1.3. Categorical Encoding of Data

As most DL procedures takes only input such as numeric values and category values were encoded into arithmetical values. Characteristics of categories, including yes and no, are represented by the binary values 0 and 1.

3.1.4. Transformation of Data

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

The standardization of data can be stated as,

$$s = \frac{v - \bar{v}}{\sigma} \quad (2)$$

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

3.1.5. Outlier Detection

Outliers exist to be the observation facts inaccessible from rest of data. An outlier can be created in the experiment by variability estimation or signal error. The DL algorithm is analysed, distorted and misled by outliers. The presence of outliers leads to longer training time, poorer result generation and less model accuracy. Before the data transferring to the learning algorithm, this research utilizes the Inter-Quartile Range (IQR) based method to eliminate the outliers [2].

Based on division of a dataset, IQR is evaluation of inconsistency into quartiles. Values dividing each part are termed to be first, second and third quartiles which are denoted as V_1, V_2, and V_3. The formula to calculate IQR is given as follows:

$$IQR = V_3 - V_1 \quad (3)$$

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 crucial to most characteristics, including public health, medical care and research. Clinical laboratories are essential for GFR assessment and diagnosis of CK disease. In the GFR evaluation, the recommended first step is measuring SC and the estimated GFR. From the gathered data, GFR is estimated to classify the five stages of CK disease. Here, the filtration rate is estimated based on age and SC level. The equation for estimating GFR for 18 and older can be expressed mathematically as:

$$GFR = 142 \times \min(SC/k, 1)^b \times \max(SC/k, 1)^{-1.200} \times 0.9938^{age} \times 1.012 \quad (4)$$

From the above equation, k=0.7 for women and 0.9 for men, b=-0.241 in the 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 that equation to be estimated *GFR* from the *SC* level.

Table 2. GFR estimation values.

Age	Gender	SC mg/dL	GFR
≥18	Woman	0.70 or <0.71	$=142\times(SC/0.7)^{-0.241}\times0.9938^{age}\times1.012$
		> 0.70	$=142\times(SC/0.7)^{-1.200}\times0.9938^{age}\times1.012$
≥18	Man	0.90 or <0.91	$=142\times(SC/0.9)^{-0.302}$
		> 0.90	$=142\times(SC/0.9)^{-1.200}$

3.3. Graph Neural Network with Deep Q-Learning Technique

GNSs are the framework for collecting node dependencies into graphs by passing messages between nodes. The GNN performs on the graph to describe the data from its neighborhood with random stages. It made GNN an appropriate tool for wireless networks with compound features that can't get closed form. In the proposed model, the GNN-based method is used to measure both relationships of cells and entities between the nodes.

The GNN and Deep Q-Learning (DQL) are combined in the GNN-DQL architecture to improve the classification accuracy of CKD by using reinforcement learning and structured data representations. To analyze relational data, GNNs define patient records as graph structures. Each patient is expressed as a node, and edges highlight medical commonalities based on demographics, test results, or the progress of a disease. The GNN component enhances the learning of

underlying patterns by extracting essential feature representation from this graph. CKD is classified into five phases named End, Severe, Moderate, Mild, and Normal using the DQL module, which uses these extracted features as input and a reinforcement learning-based decision-making method. To improve classification accuracy, the Q-network updates its policy to reward input. In order to achieve highly accurate, generalizable, and accessible CKD detection, this integration ensures adaptive learning, enhanced feature correlation comprehension, and effective handling of complex CKD patterns.

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 is denoted as $R_e \in \{0,1\}^{P \times Q}$. The mathematical expression can be given as,

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

$$R_e(u,v) = \begin{cases} 1 & if\ e_{f_u^{cl}, e_{f_v^{cl}}} \in \varepsilon^{e} \\ 0 & Otherwise \end{cases} \quad (6)$$

Consider an L-layer GNN computed on the graph, which are the basic node properties 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 reported network capacities and entities. The channel capacity matrix $C \in Z^{P \times Q}$ is defined with the elements $c(f_u^{cl}, f_v^e)$, and the user rate matrix $Z \in Z^{P \times Q}$ with elements $\frac{c(f_u^{cl}, f_v^e)}{C(f_u^{cl})}$ for an assumed cell-entity connectivity graph. The input features can be calculated as,

$$Y_{cl,1}^{(0)} = [R_{cl} Z 1_P \parallel Z 1_P] \in Z^{Q \times 2} \quad (7)$$

$$Y_{cl,2}^{(0)} = [R_e Z^T 1_Q \parallel C 1_P] \in Z^{Q \times 2} \quad (8)$$

$$Y_e^{(0)} = [C^T 1_Q \parallel Z^T 1_Q] \in Z^{P \times 2} \quad (9)$$

From the above equation, the vector concatenation operator is denoted as [‖]. Vector size of all nodes 1_P and 1_Q is denoted as P, Q. Every latent feature attains either the sum of nearby cells or capacity of node or channel in case of entities. Then the feature form these chosen gather relevant data to make better decisions.

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

$$H_{cl}^{(L)} = \sigma\left(Y_{cl,1}^{(L)} w_1^{(L)}\right) + \sigma\left(Y_{cl,2}^{(L)} w_2^{(L)}\right) \epsilon Z^{P \times d} \quad (10)$$

$$H_e^{(L)} = \sigma\left(Y_e^{(L)} w_3^{(L)}\right) \epsilon Z^{Q \times d} \quad (11)$$

$$Y_{cl,1}^{(L+1)} = R_{cl} H_{cl}^{(L)} \epsilon Z^{P \times d} \quad (12)$$

$$Y_e^{(L+1)} = R_e^T H_{cl}^{(L)} \epsilon Z^{Q \times d} \quad (13)$$

$$Y_{cl,2}^{(L+1)} = R_e H_e^{(L)} \epsilon Z^{P \times d} \quad (14)$$

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

In the last layer of GNN, the feature vectors are integrated to attain a scalar-valued score for G. The GNNs output layer is combined over cells, and the score estimation $H_{cl}^{(l-1)}$ invariant to nodes before transforming to the single entirely connected NN layer. The network score of graph G is expressed in below equation:

$$S(G) = \sigma\left(1_P^T H_{cl}^{(l-1)} w_4\right) w_5 \quad (15)$$

All-ones vector of size P is denoted as 1_P^T, the weight matrix of the fully connected NN is represented as $w_4 \in Z^{d \times d}$, and the vector to combine the output of a NN is represented as $w_5 \in Z^{d \times 1}$. Once the evaluations of GNN are over, the scores of G, $S(G)$ is adopted to pick best connection graph. The DQL algorithm learns the optimal weights of GNN.

The Q-function is learned through a DQL approach from the cell and entity placement instances. The major merit of the Q-function is establishing GNN accessible over various scopes could gather limited network features with a different number of cells and entities. The right Q-function has to be learned to generate the optimal selection. When Q-function is gathered renders to absorb the GNN parameters from GNN is done by sequential accumulation of new cell entity connections over a partly connected graph. The state, action and reward in DQL approach are provided as follows:

The S_T state is well-defined as present G_T graph that holds cell and linked entities at several iterations. Also, the input features of corresponding nodes $Y_{cl}^{(0)}$ and $Y_e^{(0)}$ are held. The beginning phase is assumed as a partly linked network with both linked and unlinked entities. The ending phase is attained when 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 cells. The reward $R(S_T, A_T)$ at state after choosing the action as A_T can be expressed in below equation,

$$R(S_T, A_T) = U(G_T) - U(G_{T-1}) \quad (16)$$

Reward is described as variation in network utility function when linking a new entity. The deterministic greedy policy can be expressed as $\delta(A_T \backslash S_T) = Argmax_{AT}$

$Q(S_T, A_T)$ with ε greedy examination during training process. Here $Q(S_T, A_T)$ is denoted in Equation (15) with $G_T = S_T \cup e_{f_u^{cl}, f_v^e}$

At first, the parameters are initialized in a DQL approach 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 $\delta(A_T \backslash S_T)$ where the exploration rate is denoted as ε. Number of stages T is provided by end phase S_T. The graph G_T is updated, and so the following step S_{T+1} is attained. Every time when graph is efficient, new input features are 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. The GNN with DQL parameters is optimized to enhance the classification accuracy by adopting the AMO approach.

The mayflies separated into males and females, which would randomly update the velocities. The individual velocities are updates from weighted present rates with few other weighted distance among them and global finest individuals. The weighted distance of either part can be found through the following expression,

$$J_o = K_m e^{-\lambda r_n^2}(U_n - U_m) \tag{17}$$

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 probably cannot be acceptable 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 Equation (17) can be updated to optimize the parameters of GNN-DQL as,

$$J_o = K_m e^{-\frac{\lambda}{r_n^2}}(U_n - U_m) \tag{18}$$

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. The classification accuracy can be greatly improved by implementing the proposed research. The evaluation time for conducting this research is low, and overall performance of proposed model is enhanced. The parameters of AMO algorithm are described in Table 3.

Table 3. Parameter details of AMO algorithm.

Epochs	100
Population size	50
Beta 1	0.85
Beta 2	0.999
c1, c2, w_min and w_max	1.2, 1.2, 0.4 and 0.9

4. Results and Discussions

The performance of proposed method is conferred in this section based on several metrics. The experiments are analysed by implementing with Python simulation tool. Overall performance of proposed technique is obtained. Then, compare both analysed performance of proposed and existing techniques. The performance metrics, including accuracy, F1-score, recall and precision of proposed method are analysed and compared with existing approaches like Linear Regression (LR), KNN, SVM, DT and NB. The metrics like specificity, Mathew's Correlation Coefficient (MCC), Kappa, Balanced Score (BS) and Area Under Curve (AUC) are compared with existing techniques like LR, KNN, SVM, NB, Adaboost (ADB), Stochastic Gradient Descent (SGD), Multi-Layer Perceptron (MLP) and Gaussian Naive Bayes (GNB). According to some methods such as SVM, Multi-Kernel SVM (MKSVM), Hybrid Kernel SVM (HKSVM), and Fuzzy Min-Max GSO NN (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 RF, NB, SVM, 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), Artificial Neural Network-Hybrid Filter Wrapper Embedded-Feature Selection (ANN-HFWE-FS) and Support Vector Machine-Hybrid Filter Wrapper Embedded-Feature Selection (SVM-HFWE-FS).

The proposed technique is performed in python platform which includes some libraries for prediction such as Natural Language ToolKit (NLTK), Numerical Python (NumPy), TensorFlow, Keras, SciKit-learn (Sklearn), Tweepy, etc. The system configuration and hyperparameter details of the proposed method are described in Tables 4 and 5.

Table 4. Analysis of the proposed technique's system configuration.

Processor	Intel (R) Core (TM) i5-6500 COU @ 3.20 GHz 3.19 GHz
Installed RAM	16.0 GB (15.9 GB usable)
System type	64-bit operating system, x64-based processor
Edition	Windows 10 pro
Version	22H2

Table 5. Analysis of the proposed technique's system configuration.

Parameter	**Value**
Activation	"SoftMax"
Learning rate	0.0002
Batch size	32
Epoch	300
Optimizer	AMO

4.1. Dataset Description

In this section, the gathered data for this CK disease detection technique from this CK disease dataset. This dataset comprises four hundred instances, seventy-six parameters and twenty-five attributes. But data may be subjected as noisy data and missing numerical values that have been recovered analytically through pre-processing. The dataset was categorized into training and testing sets to analyse the results as 80% and 20%. The download link for the gathered dataset is

https://www.kaggle.com/mansoordaku/ckdisease/activity. Age, anemia, germs, albumin, hunger, blood urea, heart rate, glucose levels, diabetes mellitus, heart disease, hypertension, hemoglobin, pus cell clumbs, pus cell, packed cell volume, potassium, RBC, pedal edema, SC, WBC count, specific gravity, sodium, sugar, and RBC count are additional features that are present in the dataset. The performance of proposed technique is evaluated based on various performance metrics to determine its efficiency. Here, the dataset is balanced and increased into larger dataset using the SMOTE technique. The data augmentation is performed using the SMOTE which is used to generate the synthetic samples for CKD prediction. The Synthetic samples of proposed model using SMOTE are described in Table 6.

Table 6. Synthetic samples of proposed using SMOTE.

Class of dataset	Technique without using SMOTE	Technique with using SMOTE
Normal	74	200
Mild	76	200
Moderate	98	200
Severe	102	200
End	50	200

4.2. Performance Metrics

Description of overall performance of every metric were measured individually for proposed method and its mathematical expression are explained as follows:

- **Accuracy**

The overall count of precise estimates from whole number of predictions is known as accuracy. The accuracy can be mathematically denoted as,

$$Accu = \frac{D + E}{D + E + F + G} \tag{19}$$

Where D signifies True Positive Rate (TPR), E denotes true negative rate, F defines FPR and G signifies FNR.

- **F1-Score**

Harmonic means of PPV and recall or TPR is used to evaluate F1-score and it mathematically represented as,

$$F1S = 2\frac{PPV \times TPR}{PPV + TPR} \tag{20}$$

- **Recall**

Recall is a term used for the percentage of samples with favourable outcomes against every sample w. The equation used for recall is described in below equation.

$$R = \frac{D}{D + G} \tag{21}$$

- **Precision**

Precision is represented as the availability of obtained positive outcomes form overall positive sample. The mathematical expression of precision can be denoted as,

$$P = \frac{D}{D + E} \tag{22}$$

- **Specificity**

Number of negative outcomes over entire number of truly negative samples is measure as specificity which is evaluated using the below equation,

$$S = \frac{E}{E + F} \tag{23}$$

- **MCC**

MCC is evaluated as combination of exact and predictable decisions by undertaking correlation coefficient evaluation formula, which can be expressed as in below equation,

$$MCC = \frac{(D^*E) - (F^*G)}{\sqrt{(E + G)(E + F)(D + G)(D + F)}} \tag{24}$$

- **Kappa**

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

$$K = \frac{\beta_0 - \beta_f}{1 - \beta_f} \tag{25}$$

Here, β_0 represents score agreement between predicted and actual values. Then, β_f describes the variance between actual and predicted ones.

- **Balanced Score**

The balanced score that can be explained numerically as is the mathematical average of sensitivity and the actual negative rate.

$$BS = \frac{1}{2}\left(\frac{D}{D + E} + \frac{E}{E + F}\right) \tag{26}$$

- **AUC**

The capability of the technique to differentiate between aimed classes is signified by AUC. It termed to be area below receiver operating curve. Overall performance of AUC is evaluated by mapping TPR over FPR value as graph.

- **Positive Predictive Value**

The possibility that proposes with a positive selection test showing occurrence of actual disease which analysed in PPV is described in below equation,

$$PPV = \frac{D}{D + E} \tag{27}$$

- **Negative Predictive Value**

Number of cases with negative test outcomes that truly positive is analysed in the NPV, which described in below equation:

$$NPV = \frac{E}{E + G} \tag{28}$$

- **False Positive Rate**

Analysing the ratio between numbers of negative

outcomes incorrectly considered as positive is FPR, which can be represented as,

$$FPR = \frac{F}{F+E} \tag{29}$$

- **False Negative Rate**

FNR denotes to quantity of essential tests that failed to eliminate null hypothesis while incorrect. It can be mathematically expressed as,

$$FNR = \frac{G}{D+G} \tag{30}$$

- **Mean Absolute Error**

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

$$MAE = \frac{\sum_{v=1}^{m}|x_v - y_v|}{m} \tag{31}$$

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

- **Error Rate**

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

$$Err = \left|\frac{V_a - V_e}{V_e}\right| \tag{32}$$

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

Significant performance metrics adopted to estimated and compare both proposed and remaining methods, including accuracy, F1-score, recall, precision, MCC, Kappa, BS, AUC, PPV, NPV, FPR and FNR are analysed with their explanation and graphical symbol that is explained as follows. Table 7 describes proposed outcomes in terms of several metrics.

Table 8 describes overall performance of proposed and existing methods [27] based on accuracy, F1-score, recall and precision.

Table 9 signifies overall performance results of both proposed and existing techniques [26] based on specificity, MCC, Kappa, BS and AUC.

Table 7. 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
	ER	0.115
	MAE	0.86

Table 8. Performance results of proposed and surviving 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 9. Result analysis of both proposed and existing techniques.

Techniques	Performance analysis (%)				
	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 10 demonstrates overall performance comparison of suggested and surviving techniques [8] based on PPV, NPV, FPR and FNR

Table 10. 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 ER is described in Table 11.

Table 11. Comparison of MAE and ER.

Performance	Techniques used								
	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**	
ER	13.33	14.77	6.67		33.33	30.00	26.67	**0.115**	

4.4. Confusion Matrix

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

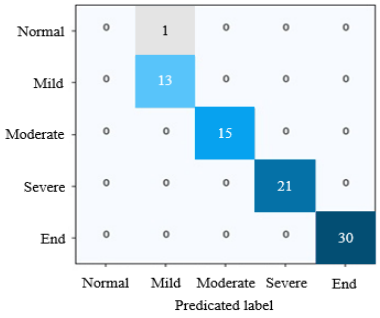


Figure 2. Confusion matrix.

Figure 2 shows proposed model accurately classifies stages of CK disease with improved accuracy, which is represented in the diagonal format. The remaining values represent the number of wrong predictions made concerning each stage. For example, 1 normal person is wrongly predicted as a mild stage. The mild, moderate, severe and end stages are precisely classified with no error, and hence overall accuracy of proposed model is widely enhanced.

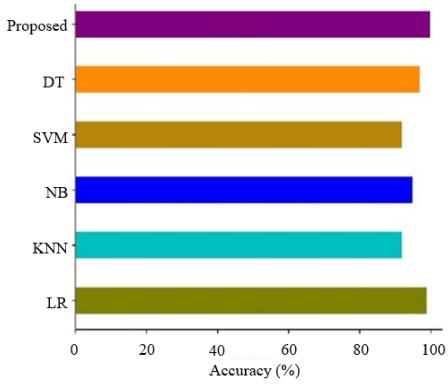


Figure 3. Accuracy comparison.

Figure 3 provides the graphical representation of the performance measures in terms of accuracy. The figure describes that proposed model's accuracy is highly accurate compared to existing models like LR, KNN, NB, SVM and DT. The overall accuracy of proposed model is attained be 99.93%. The existing models obtained lower accuracy based on larger increase of datasets, degraded system performance and increased complexities. A higher accuracy rate insists that the technique achieves better classification performance.

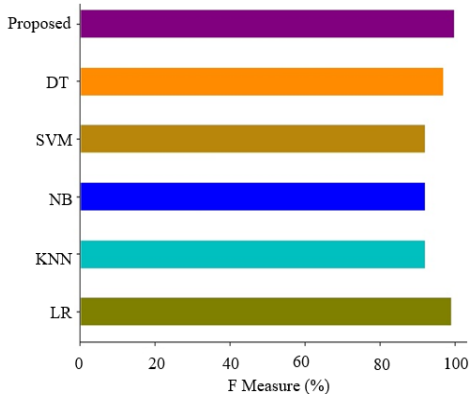


Figure 4. Performance comparison of F1-score.

Figure 4 illustrates the graphical representation of F1-score in terms of proposed and existing techniques. It is made clear that proposed method achieves more ability to categorise CK disease depending on input parameters compared to existing techniques. Value of F1 measure is attained to be 99.86% in suggested method, whereas the remaining 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 proposed method, F1 measure shows better results in classifying the different stages.

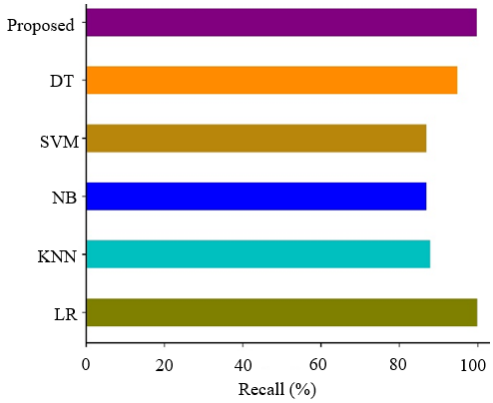


Figure 5. Performance comparison of recall.

The graphical representation of recall based on proposed and existing approaches is presented in Figure 5. 99.86% of recall is obtained while assessing the performance of proposed technique in contrast to remaining approaches. The existing learning algorithms have accomplished 100%, 88%, 92%, 87%, and 95% concerning LR, KNN, NB, SVM and DT. Due to the high complexities of time and storage, the existing approaches tends to offer lower performance other than the LR approach compared to the proposed method.

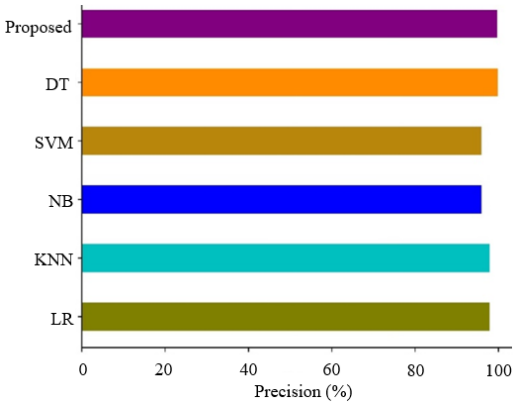


Figure 6. Precision performance.

The graphical representation of precision in terms of proposed and existing approaches is shown in Figure 6. Precision is one of prominent metrics to be measured for gathering effectiveness of outcomes. The proposed GNN-DQL method has attained 98% of precision and showed a better outcome in reducing false detection rate. While existing learning methodologies other than NB and DT have achieved lower results when compared

to the proposed approaches. Finally, the precision estimated that proposed technique outperforms existing methods due to its higher ability in the data handling process.

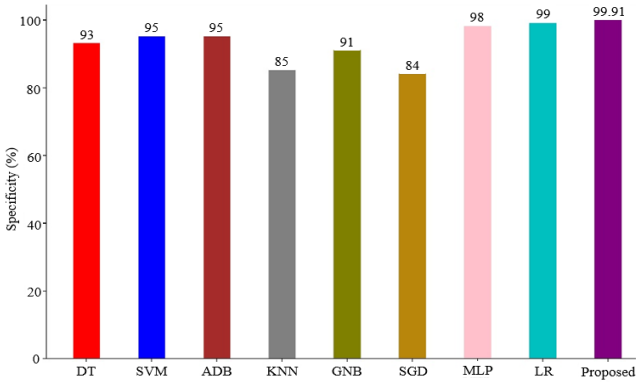


Figure 7. Specificity performance.

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

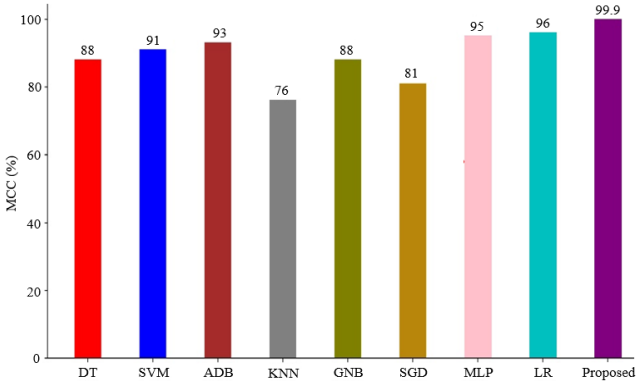


Figure 8. MCC performance.

The performance of MCC for proposed technique is analyzed with remaining methods, and achieved outcomes are showed in Figure 8. This figure shows that proposed technique has gained an improved correlation between true and predicted decisions than existing methods. This obviously exposed that suggested method has established a minimum false rate and superior to CK disease classification stages. MCC accomplished by suggested method is 99.90%, whereas existing methods like DT, SVM, ADB, KNN, GNB, SGD, MLP and LR are 88%, 91%, 93%, 76%, 88%, 81%, 95% and 96% respectively.

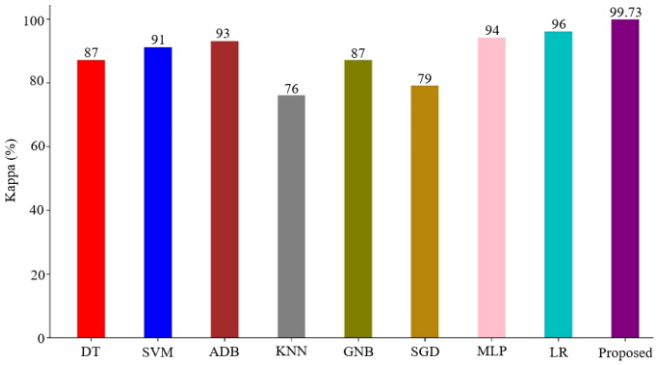


Figure 9. Kappa performance.

Figure 9 represents the graphical illustration of kappa performance in CK disease classification. High kappa values are obtained in suggested approach at 99.72%, showing better outcomes than the existing approaches. Compared to the existing 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 is low because of the larger accumulation of information from the datasets.

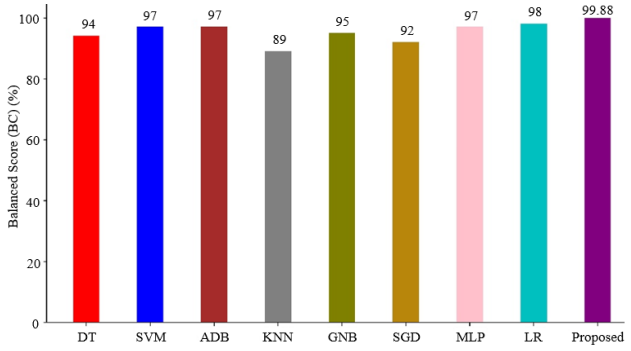


Figure 10. Performance of BS.

Figure 10 signifies the BS performance of a suggested and remaining methods. The suggested model has conquered 99.88% because of limited redundant features and false rates. Result of BS is analyzed with other standing methods like DT, SVM, ADB, KNN, GNB, SGD, MLP and LR, which have obtained 94%, 97%, 97%, 89%, 95%, 92%, 97% and 98% respectively. This performance evaluation of proposed model provides better score in CK disease classification.

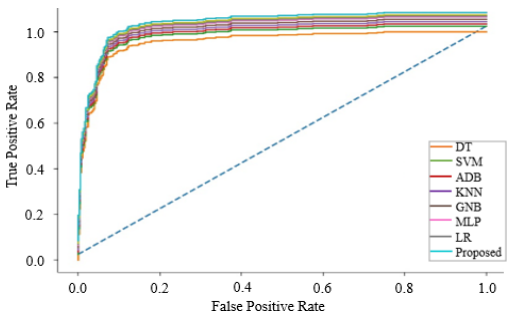


Figure 11. AUC analysis.

Figure 11 represents the AUC comparison in terms of proposed and existing methods. Proposed model retains a better capacity to separate between the objective classes. Graph has been plotted between FPR and TPR to establish AUC value. The suggested model has accomplished AUC value of 99.89%, which is greater than other state-of-art techniques since its better-quality capability in CK disease classification based on input parameters.

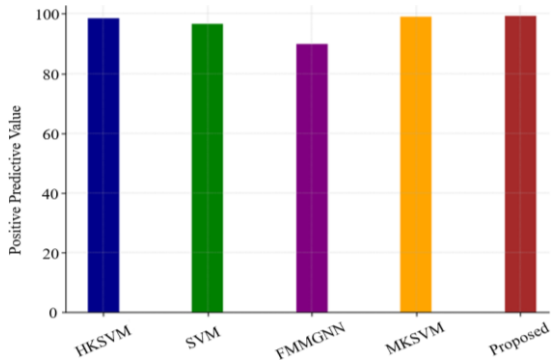


Figure 12. PPV performance.

Figure 12 compares PPV with multiple methodologies, such as SVM, MKSVM, HKSVM, and FMMGNN. The graph indicates that, in comparison to previous approaches, the prediction strategy generated better results. The suggested approach has an extremely low incorrect detection rate and an optimal PPV of 0.992. The MKSVM has a better score of 0.99, which is superior to the suggested technique, while FMMGNN has a relatively low PPV of 0.89 when compared to other techniques. Overall, it is obvious the proposed approach outperforms alternative methods expressively.

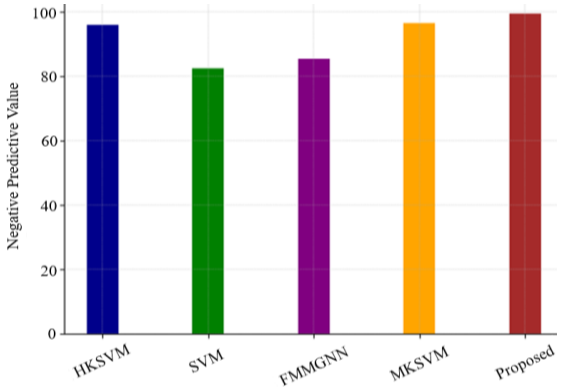


Figure 13. NPV performance.

Figure 13 illustrates how the suggested and remaining techniques compare with regard to of NPV performance evaluation. The approved techniques, including MKSVM, HKSVM, SVM, and FMMGNN, are used to evaluate NPV performance in comparison to the proposed model for classifying CK illness. Figure demonstrates that the proposed strategy has a higher NPV than more recent existing approaches. The proposed model's NPV value is 99.3, compared with other approaches' substantially greater values of 95.99, 82.37, 85.49, and 96.30 for HKSVM, SVM, FMMGNN, and MKSVM.

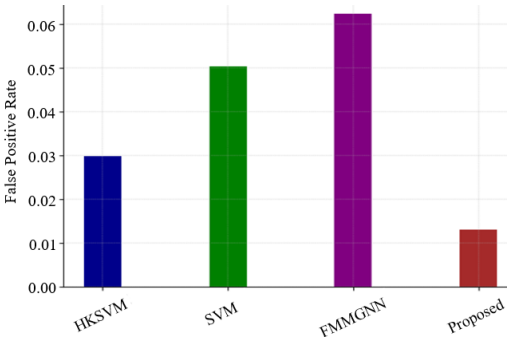


Figure 14. FPR performance.

The proposed method's FPR contrasts to the current methods, and Figure 14 illustrates the results that were obtained. The graph shows that the suggested method has achieved fewer FPR than the techniques already in use. This demonstrates that the proposed strategy is more effective at classifying all of the CK disease phases. The suggested method's FPR value is 0.011, whereas the FPR values of the presently employed methods, such as HKSVM, SVM, and FMMGNN, are 0.029, 0.050, and 0.062, respectively.

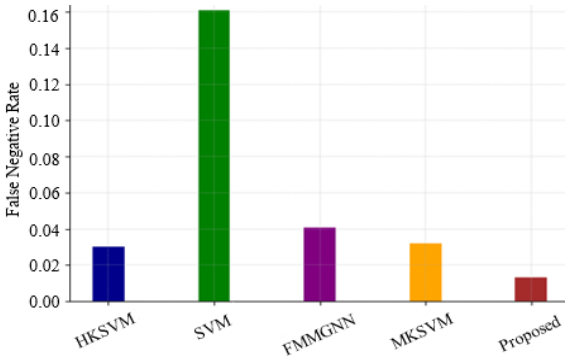


Figure 15. FNR performance.

FNR of suggested model is compared to existing methodologies, and obtained outcomes are presented in Figure 15. The FNR performance value has to be comparatively low for an efficient system. The suggested method yielded lower FNR than existing techniques, as can be seen from the graph. It indicates that the suggested approach accomplished a lower false rate and is appropriate for accurate categorization. The suggested method's FNR value is 0.013, but the corresponding FNR values of the compared methods HKSVM, SVM, FMMGNN, and MKSVM are 0.030, 0.160, 0.040, and 0.032.

The MAE accuracy of the proposed model evaluated in the classification of CK disease is displayed in Figure 16. Fewer wrong predictions enhance classification performance with low ERs. Comparatively to methods such as RF, NB, SVM, NN, DL, KNN, DT, and Auto-MLP, the suggested model's MAE performance is low [18]. As a result, the present techniques are insufficient for the process of classifying CK diseases. The efficient

learning technique yields an MAE of 0.86, a value lower than the current methods.

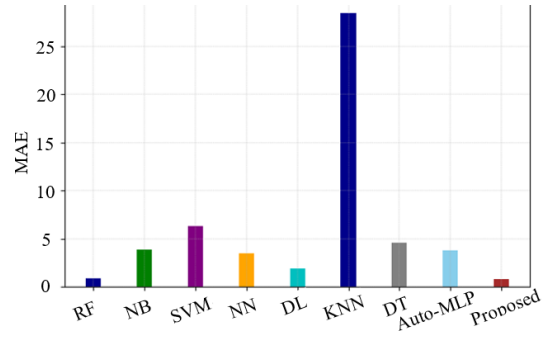


Figure 16. MAE performance.

The results of suggested and existing models' rate of error estimated during the detection of CK disease are presented in Figure 17. The figure demonstrates that the suggested model's error performance is better to that all other approaches currently in practice. A hybrid model demonstrates an C of 0.115, while existing techniques such as NB-HFWE-FS, ANN-HFWE-FS, SVM-HFWE-FS, NB, ANN, and SVM [15] have been discovered to have ERs of 14.77, 13.33, 6.67, 33.33, 30.00, and 26.67, respectively. The suggested approach is considered as yielding better outcomes than the competing methods.

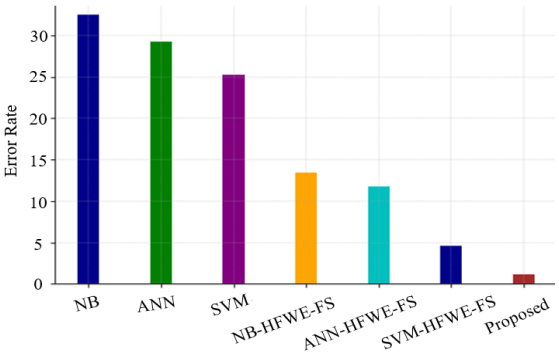
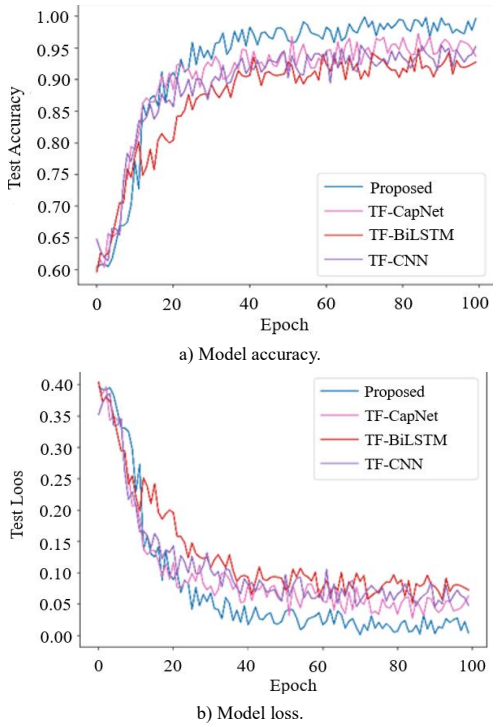


Figure 17. Performance of ER.

4.4.1. Training, Testing and Validation Measures for Model Accuracy and Loss

Employing training and testing data, the proposed approach's accuracy and loss are evaluated. In the proposed research, 70% of a data is adopted to train the model, 20% is adopted to test the model, and 10% of data used for validation process. The model accuracy, loss of training, testing and validation are represented in Figures 18-a) and (b).

By changing the time period size, all the indicated model's gains and losses are evaluated. For the two scenarios, the precision is similar. Only minor changes are accurately captured when matching training and testing accuracy. The wider period size could be a result of improved accuracy. The suggested model obtains accuracy in training and testing in a range of 80 to 85% while the epoch size is 40. The accuracy of model is between 85 and 90% if the epoch size is 60, and between 90 and 100% when its epoch size is raised to 80. Furthermore, it is obvious from Figure 18-a) that the recommended approach obtains maximum accuracy, almost identical to training and testing data samples.



a) Model accuracy.

b) Model loss.

Figure 18. Performance measures.

By changing the time period size, all the indicated model's gains and losses are evaluated. For the two scenarios, the precision is similar. Only minor changes are accurately captured when matching training and testing accuracy. The wider period size could be a result of improved accuracy. The suggested model obtains accuracy in training and testing in a range of 80 to 85% while the epoch size is 40. The accuracy of model is between 85 and 90% if the epoch size is 60, and between 90 and 100% when its epoch size is raised to 80. Furthermore, it is obvious from Figure 18-a) that the recommended approach obtains maximum accuracy, almost identical to training and testing data samples.

The NN has been trained with a 100epoch size, and the testing and training loss is obtained for the proposed model. The loss is reduced by boosting the epoch size. The model achieves a testing and training loss in a range of 0.15 to 0.20 if the epoch size is 40. The model receives a loss of 0.10 to 0.15 if the period size is 60. The value lies in the 0.10 to 0.5 range for epoch size 80. Due to perfect training and the MAO technique for efficiency, the model had a low error value.

4.5. Ablation Study

The ablation study is conducted for the proposed technique with accuracy, precision and recall, which is described in Table 12. Here, module 1 determines the proposed technique is performed with only the GNN-DQL model. Module 2 performed the proposed GNN-

DQL model with SMOTE technique. Module 3 performed the proposed technique GNN-DQL with AMO algorithm and the module 4 is performed with every technique used in the proposed methodology.

Table 12. Ablation study analysis of proposed technique.

Modules	Accuracy	Precision	F1-score
Module 1 (GNN-DQL)	92.68	93.01	92.58
Module 2 (SMOTE+GNN-DQL)	96.67	96.20	96.92
Module 3 (GNN-DQL+AMO)	97.35	97.39	97.12
Module 4 (pre-processing technique +SMOTE+GNN-DQL+AMO)	98.36	97.45	98.01

The performance of proposed technique is evaluated by using each of the techniques to determine its efficiency.

4.6. Statistical Analysis

The statistical analysis is conducted to determine the efficiency of proposed GNN-DQL model for CKD detection.

4.6.1. P-value

The P-values are evaluated using suitable statistical tests for ANOVA test to determine when the accuracy increases are statistically significant. While the alternative hypothesis implies a substantial variance between the accuracy of the proposed method and existing methods. The null hypothesis indicates that there is no significant difference. A low p-value (usually less than 0.05) indicates the accuracy gains are statistically significant since the improvements are considered to be an outcome of randomness. The proposed technique achieves 0.0236 p-value which clearly determines its efficiency.

The efficacy of the GNN-DQL model in CKD classification is statistically verified using the ANOVA test in comparison with standard models like RF, SVM, CNN, and LSTM. The ANOVA test evaluates when there are significant differences in the mean classification performance across these models. The mathematical expression for one-way ANOVA formula is described as follows.

$$S = \frac{F_{between}}{F_{within}} \tag{33}$$

Here, the variance between model performances and the variance within multiple iterations of each model are represented as $F_{between}$ and F_{within}. The null hypothesis N_0 is rejected if the obtained F-statistic provides a P-value less than 0.05, indicating that GNN-DQL performs better than other models in the classification of CKD.

4.7. Discussions

DQL updates, the AMO algorithm for parameter adjustments, and GNN calculation all modify the GNN-DQL model's computational complexity and training time. The GNN component has complexity of $E(P+D)$, number of nodes and number of edges are represented as P and D which provide efficient performance for structured data processing. The Q-network updated through experience replay of DQL component which has a complexity of $E(ab)$, where number of training samples and number of network parameters are represented as a and b. Although the AMO approach improves convergence, it includes optimization overhead. Iterative reinforcement learning makes training computationally intensive, but once trained, the model achieves rapid prediction. GNN-DQL achieves a balance between performance and computational efficiency as compared to standard ML models, ensuring accurate CKD classification with lower training times and improved scalability.

4.7.1. Limitation and Future Scope

One significant drawback of the model is the lack of methods like SHapley Additive exPlanations (SHAP) or Local Interpretable Model-agnostic Explanations (LIME), particularly when it comes to healthcare applications. Understanding the model's decision-making process is essential for establishing confidence and transparency in clinical settings, and these interpretability techniques are essential to performing the same. Being able to explain the reasoning behind forecasts is crucial in the healthcare industry since choices have an enormous impact on patient outcomes. Implementing SHAP or LIME would ensure safer and more dependable application in actual medical scenarios by providing physicians valuable insights into the model's decision-making process as well as aiding in learning and validation of the predictions. Interpretability approaches like SHAP and LIME, which are essential for comprehending model predictions in healthcare, are not included in this research. The constraint affects how transparent and reliable the proposed method's decisions. Hence, the proposed technique focusses on implementing interpretability measures in future.

The approach eliminates interpretability tools that are essential for healthcare which describe the decision-making process. Concerns over the model's generalizability and performance in comparison to other optimization strategies are caused by its excessive reliance on AMO. Applicability in resource-constrained contexts can be enhanced by assessing the model's performance on a range of IoT devices and examining runtime, resource usage, and energy efficiency. The performance of AMO can be verified and potentially improved by experimenting with other optimization techniques or hybrid approaches.

5. Conclusions

In recent years, CK disease has become one of harmful diseases, and exact diagnosis is the most challenging. In this paper, an advanced model is introduced to provide

precise classification of five stages of CK disease such as normal, mild, moderate, severe and end, which is attained through GNN-DQL approach. The annoying distortions are eliminated through data pre-processing. GFR rate is evaluated to age and SC level for obtaining the enhanced result. Then, the GNN-DQL technique is carried out to progress the accuracy. Optimize the parameters using AMO method, and stages of CK disease are classified precisely. The classification performance is analyzed for accuracy, precision, recall and so on. The suggested method is employed, and the performances are analyzed using Python simulation tool. Overall accuracy of 99.93% is observed in CK disease by classifying it based on five stages. MAE and ER are attained to be 0.86 and 0.115, which are comparatively less than the other existing approaches. Compared to the first work based on Ebola deep wavelet extreme learning machine, the proposed GNN-DQL has improved classification accuracy due to the consideration of best features and effective parameter optimization using the proposed model. Compared to the first work, a higher convergence rate and less time consumption are attained. Suggested model is verified through smaller datasets, and to enhance the system performance, significant volumes of data will be gathered in the future for better results. In addition, valuable features will be implemented to attain a wider perception of the enlightening parameters regarding CK disease.

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