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Optimized dense convolutional network with conditional autoregressive value-at-risk for chronic kidney disease detection through group-based search

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ABSTRACT

Chronic kidney disease (CKD) is the gradual decrease in renal functionality that leads to kidney failure or damage. This disease is the most severe worldwide health condition that kills numerous people every year as an outcome of hereditary factors and worse lifestyles. As CKD progresses, it becomes difficult to diagnose. Utilizing regular doctor consultation data for evaluating diverse phases of CKD can assist in earlier detection and timely inference. Furthermore, effectual detection methods are vital owing to an increased count of patients with CKD. Here, group search conditional autoregressive value-at-risk based dense convolutional network (GSCAViaR-DenseNet) is introduced for CKD detection. Firstly, chronic data is acquired from the dataset and Min-Max normalization is utilized to pre-process considered chronic kidney data. Thereafter, feature selection (FS) is performed based on Topsoe similarity. Lastly, CKD detection is executed by dense convolutional network (DenseNet) and group search conditional autoregressive value-at-risk (GSCAViaR) is employed to train DenseNet. However, GSCAViaR is designed by incorporating a group search optimizer (GSO) with a conditional autoregressive value-at-risk (CAViaR) model. Additionally, GSCAViaR-DenseNet acquired a maximal accuracy of about 91.5%, sensitivity of about 92.8% and specificity of about 90.7%.

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1. INTRODUCTION

The problem of chronic kidney disease (CKD) detection is a significant challenge in the medical field. CKD is a term that defines to the state, whereupon kidneys can no longer filter blood more efficiently [1]. Previous research has highlighted various methodologies for early detection, but limitations remain. This research addresses these limitations by introducing a novel approach that leverages the optimized dense convolutional network (DenseNet) with conditional autoregressive value-at-risk (CAViaR) for CKD detection through group-based search. This approach not only improves detection accuracy but also provides a more detailed analysis of risk factors.

Moreover, CKD is categorized by a gradual decrease in kidney functioning that damages renal organ functions. Owing to the lack of obvious symptoms in earlier stages, the beginning of renal failures may

firstly not have been identified [2]. It is clear that CKD affects any person and some of people are more vulnerable to this disease than others particularly, patients having heart problems, diabetes, and abnormal potassium or calcium levels. As CKD increases, body may collect too much quantity of fluid, waste products and electrolytes [1]. CKD is an increasingly serious condition in the current ageing community. The aged population and related high hypertension enhance the occurrence of hyperglycemia and hyperlipidemia, thereby increasing CKD incidence [3]. In addition, CKD is a common category of kidney disease that can be only cured effortlessly when it is detected at earlier stages [4]. However, this disease has no symptoms in its earlier stage; testing is an only mode to identify whether patient is affected with kidney disease or not [5].

Earlier detection of CKD in its beginning phases can assist the patients in getting effectual treatments and then, prevent the development of end-stage renal disease (ESRD) that needs a kidney transplant or dialysis to enhance the patient's life [5]. Hence, certain blood and urine tests are taken for detecting CKD. However, detecting CKD at the starting stages is not simple without accurate examinations [6]. Additionally, CKD has higher mortality and morbidity, with a comprehensive impact on the human body. CKD diagnosis is crucial and may be capable of obtaining timely treatments as it is an irreversible and progressive pathologic syndrome [7]. Accurate management of CKD is pivotal for protecting the functionality of kidneys, decreasing disease development and enhancing patient results [8]. The existing researchers have revealed that machine learning (ML) and deep learning (DL) methods can be employed for the accurate diagnosis of CKD [9]. Employing DL's skill discovery abilities like classification and data mining approaches [10], it is presently probable to manage valuable and huge data for enhancing clinical prognosis and diagnosis in decision-making [11], [12]. When healthcare providers integrate this data with other information sources, they can develop newer solutions with an assistance of predictive analysis for earlier CKD detection, related health threats and even prescriptive analysis for the precision medicines [13].

The vital aim is to introduce GSCAViaR-DenseNet for CKD detection. CKD is progressively acknowledged as a worldwide health issue and an important determinant of worse health results. In this research, chronic kidney data is taken from a specific dataset. Then, pre-processing is conducted utilizing Min-Max normalization. After pre-processing of data, FS is accomplished based on Topsoe similarity. Finally, CKD is detected utilizing DenseNet and GSCAViaR does its training. However, GSCAViaR is designed by joining GSO with CAViaR. Proposed GSCAViaR-DenseNet for CKD detection: Nowadays, earlier detection of CKD and its complexities seem to be very crucial for enhancing a patient's life. Here, the detection of CKD is conducted by DenseNet. However, DenseNet is trained utilizing GSCAViaR which is modelled by combining GSO with CAViaR.

CKD is also termed as chronic renal disease, wherein kidneys fail to function gradually. For reducing the chances of CKD that lead to kidney transplantation or dialysis, earlier CKD detection is crucial. This motivated, To design a method to detect CKD by reviewing current approaches developed for CKD detection. The reviewed techniques along with their advantages and challenges are interpreted in this part.

Saif *et al.* [14] designed a deep ensemble model for CKD prediction. It enhanced complicated feature depictions and performed better in classification tasks. Nevertheless, this method failed to investigate the robustness of this model. Rao *et al.* [15] presented a fusion DL model for the prediction of CKD. This approach was ideal for medical applications, which employ data in different formats. However, size of dataset was not expanded, and it did not assess its generalizability to diverse populations. Introduced the novel weight convolution neural network (NWCNN) for diagnosing CKD [16]. This technique efficiently handled missing data imputations, even though it failed to identify the severity level of CKD while improving generalization performance.

Ismail [1] developed a snake-optimized framework termed CKD-SO for earlier identification of CKD. This approach provided early interferences that decreased high trouble of CKD-associated diseases as well as mortality, but still, it faced storage and computational challenges:

A few demerits of existing CKD detection methods collected for review are explained below.

- The technique developed in [1] was only suitable for population study and it did not assist clinical experts with each patient. Moreover, it required much memory storage and lengthy training time.
- Fusion DL model [15] had better flexibility and durability, even though it failed to enhance illness predictions, treatment and prevention, thereby improving patient care and results.
- CKD detection in its early phases can prevent serious health problems. However, accuracy of traditional approaches for detecting CKD is decreased frequently owing to their dependence on a limited number of biological features.

This study introduces a hybrid model that combines the GSCAViaR model with DenseNet for detecting CKD. By merging statistical modelling with deep learning, this novel approach significantly boosts prediction accuracy and robustness, even with diverse patient data. The research not only achieves superior performance compared to existing methods but also provides a thorough methodological framework that other researchers can use and expand upon, advancing the field of CKD detection.

The structure of the paper is as follows: section 2 details the proposed GSCAViaR-DenseNet methodology, and section 3 presents the results alongside the experimental setup, dataset description, evaluation metrics, and a comparative analysis with existing approaches. Finally, section 4 concludes with a discussion of the findings and their implications, offering a thorough overview of the research outcomes.

2. METHOD

To detect CKD, specific blood and urine tests must be taken and therefore, CKD detection at its earlier phase is not simple without appropriate tests. Here, GSCAViaR-DenseNet is presented for detecting CKD. Initially, chronic kidney data is obtained from a particular dataset. The data is pre-processed by Min-Max normalization. Then, features are selected based on Topsoe similarity. Lastly, CKD is detected by employing DenseNet and it is trained by GSCAViaR. Moreover, GSCAViaR is devised by integrating GSO with CAViaR. Figure 1 exhibits a pictorial illustration of GSCAViaR-DenseNet for CKD detection.

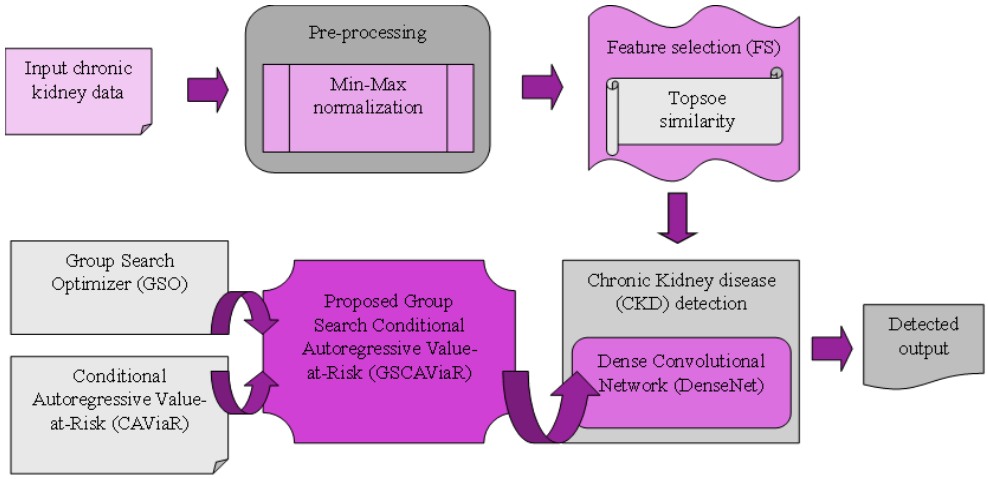

Figure 1. A pictorial illustration of GSCAViaR-DenseNet for CKD detection

2.1. Acquisition of chronic kidney data

The chronic kidney data is acquired from the dataset [16] to carry out CKD detection and it is given by,

$$R = \{R_1, R_2, \ldots, R_h, \ldots, R_i\} \quad (1)$$

here, R_h represents h^{th} input chronic kidney data whereas total data in the dataset R is implied as R_i.

2.2. Pre-processing utilizing Min-Max normalization

Data pre-processing is carried out to impute missing data and recognize the variables, which must be considered in prediction systems. Here, Min-Max normalization is employed for data pre-processing by considering R_h with dimension $k \times x$ as input. Min-max normalization [17] is the easiest method, wherein this technique is capable of fitting data in a pre-defined boundary with the pre-defined boundary. It can be formulated as follows,

$$M_h = \frac{H - H_{min}}{Hmin_{max} * (I - N) + N} \quad (2)$$

where, $[I, N]$ mentions pre-defined boundary, H denotes a range of actual data and M_h specifies pre-processed data with dimension $k \times x$.

2.3. FS based on topsoe similarity

An intention of FS is to detect most informative and significant subset of the features in certain databases. Moreover, it discards the features that are redundant or not appropriate. Here, features are selected based on Topsoe similarity by taking $M_h$with dimension $k \times x$ as input. Topsoe similarity [18] computes the distance between two probability distributions and it can be calculated by,

$$d_T = \sum_{r=1}^{j} \left(U_r \, ln \left(\frac{2U_r}{U_r + Y_r} \right) + Y_r \, ln \left(\frac{2Y_r}{U_r + Y_r} \right) \right) \quad (3)$$

Here, U_r indicates candidate features and Y_r notes target. After computing Topsoe similarity for individual features, top v features with higher values are selected. The outcome after FS is symbolized as T_h with dimension $k \times z$, where $x > z$.

2.4. CKD detection utilizing DenseNet

Early diagnosis and detection of CKD is more critical for stopping the development to kidney failures. Here, Densenet is employed to detect CKD by obtaining T_h with dimension $k \times z$ as input and Densenet is trained by GSCAViaR. Furthermore, GSCAViaR is designed by merging GSO with CAViaR.

2.4.1 Architecture of DenseNet

DenseNet [19] links individual layers to all other layers in a feed-forward (FF) manner. Consider an image T_h, which is given to a convolutional (conv) network. It contains *P* layers, each one implements the non-linearity transformation $A_p(.)$, wherein p indexes a layer. $A_p(.)$ refers to composite functioning of operations like batch normalization (BN), conv, rectified linear unit (ReLU) or pooling. An output of p^{th} layer is denoted as m_p.

(a) ResNets

ResNets include skip-connections that bypass a non-linearity transformation with the identity operation and it is modeled by,

$$m_p = A_p(m_{p-1}) + m_{p-1} \quad (4)$$

A benefit of ResNets is that a gradient can directly flow by means of identity operation from the later layers to the earliest layers. Nevertheless, identity operation and the outcome of A_l reintegrated by a summation that may delay information flow in a network.

(b) Dense connectivity

For enhancing information flow amongst layers, diverse connectivity pattern is developed and direct associations from any layer to every succeeding layer. Accordingly, p^{th} layer accepts feature maps of every previous layer, $T_h, \ldots, m_{p-1}$ as an input.

$$m_p = A_p([T_h, m_1, \ldots, m_{p-1}]) \quad (5)$$

here, $[T_h, m_1, \ldots, m_{p-1}]$ indicates concatenation of feature maps generated in the layers $0, \ldots, p-1$. Due to its dense connectivity, this network is specified as DenseNet.

(c) Composite operation

$A_p(.)$ is defined as a composite operation of the three following functions such as BN, followed by ReLU and 3×3 conv.

(d) Pooling layers

An important segment of conv networks is the down-sampling layers, which vary in feature map dimensions. For facilitating down-sampling in this structure, network is divided into numerous densely associated dense blocks. The layers amid blocks are referred as transition layers that perform pooling and conv.

(e) Growth rate

If an individual operation A_p generates t feature maps, it pursues that p^{th} layer has

$t_0 + t \times (p-1)$ input feature maps, wherein t_0 represents the count of channels in an input layer. A hyperparameter t is specified as the growth rate of the network.

(f) Bottleneck layers

Even though individual layer only generates t output feature maps, it generally has several inputs. The 1×1 conv is presented as the bottleneck layer, before an individual 3×3 conv reduces the count of an input feature map and therefore, to decrease computational effectiveness.

(g) Compression

For enhancing system compactness, the count of feature maps at the transition layers is reduced. If the dense block comprises v feature maps, pursuing transition layer is permitted to generate $[\theta_v]$ output feature maps, wherein $0 < \theta \leq 1$ is mentioned as a compression factor. The CKD-detected output from DenseNet is implied as D_h and DenseNet model is shown in Figure 2.

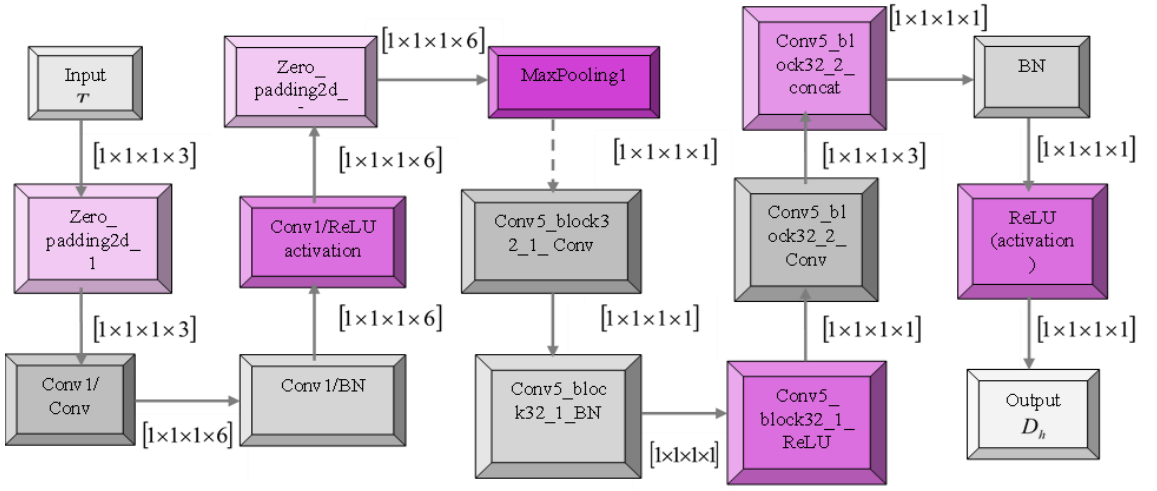

Figure 2. DenseNet model

2.4.2. Training of DenseNet utilizing GSCAViaR

GSO [20] is the nature-enthused optimization approach that can resolve various diverse optimization troubles. GSO is inspired by the searching attributes of animals in usual life. This algorithm is employed for discovering excellent outcome over the group of candidate solutions to resolve any optimization issues by identifying minimal or maximal objective functions for particular problems. CAViaR [21] specifies an evolution of quantile over time utilizing a remarkable kind of autoregressive procedure. CAViaR model is capable to adapt newer threat environments. Here, GSO is combined with CAViaR to design GSCAViaR that is more suitable for training DenseNet for detecting CKD.

– Group search position encoding

The learning parameter of DenseNet μ is continuously tuned in β search space for acquiring superior outcomes, in such a manner that $\beta = [1 \times \mu]$.

– Fitness function

The fitness function is evaluated by identifying variation amongst target and DenseNet outcomes that can be specified as,

$$F = \frac{1}{i}\sum_{h=1}^{i}[G_h - D_h]^2 \quad (6)$$

here, G_h indicates targeted output, D_h mentions DenseNet output whereas $i$specifies total data.
GSCAViaR performs the following steps to attain the best outcome.

Step 1: Initializing of solution

Firstly, a group of candidate agents that is termed as group and individual agents specified as members are randomly initialized. It can be formulated by,

$$B = \{B_1, B_2, \ldots, B_s, \ldots, B_n\} \quad (7)$$

where, $B_s$implies s^{th}candidate solution, $B_n$denotes total variables in a population B.

Step 2: Computing objective function

It is determined by taking the difference amongst DenseNet and targeted outputs, which is calculated utilizing (6).

Step 3: Producing stage

An apex is the existing location of the producer. In GSO, a producer performs at k^{th} iteration as mentioned below.

A producer investigates at zero and there after examine besides using stochastic testing of three positions in the validation place. The first criterion at a zero rate can be illustrated by,

$$B_v = B_y^l + \Re_1 \alpha_{max} J_y^l(\vartheta^l)_{max} \quad (8)$$

A point in the right-hand side hypercube can be given by,

$$B_{\Re} = B_y^l + \Re_1 \alpha_{max} J(\vartheta^l + \Re_2 \theta_{max}/2) \quad (9)$$

A point in the left-hand side hypercube is modelled as,

$$B_a = B_y^l + \Re_1 \alpha_{max} J_y^l(\vartheta^l - \Re_2 \theta_{max}/2) \quad (10)$$

Here,$\Re_1 \in \not{R}^1$ that specifies to normally distributed stochastic value having mean=0 and the standard deviation (SD) as 1. $\Re_2 \in \not{R}^{w-1}$ implies to stochastic values that are distributed uniformly in a range 0 and 1.

If a better region has superior fitness value than its existing location, then it moves to this region. Or else, it stays in its present location and changes its head to a newer angle as:

$$\vartheta^{l+1} = \vartheta^l + \Re_2 \rho_{max} \quad (11)$$

Here, $\rho_{max} \in \not{R}^1$ enotes maximal adjusting location.

If a producer is not capable of acquiring superior search space after ρ out of iterations, it employs the leader back to 0°.

$$\vartheta_{l+\rho} = \vartheta_l \quad (12)$$

Here, $\rho \in \not{R}^1$ indicates constant value.

Step 4: Scrounging stage

At an individual iteration, various grouping agents are selected as scroungers. At l^{th} redundancy, space copying attribute of s^{th} scrounger is implied as stochastic walking nearer a producer.

$$B_s^{l+1} = B_s^l + \Re_3 \circ \left(B_y^l - B_s^l\right) \quad (13)$$

$$B_s^{l+1} = B_s^l(1 - \Re_3) + \Re_3 \circ B_y^l \quad (14)$$

From CAViaR, the expression can be given as,

$$B_s^l = \chi_0 + \sum_{d=1}^{u} \chi_d \, B_s^{l-d} + \sum_{c=1}^{b} \chi_d \, f(B_s^{l-c}) \quad (15)$$

Consider, $u = b = 2$, therefore above equation becomes,

$$B_s^l = \chi_0 + \chi_1 B_s^{l-1} + \chi_0 B_s^{l-2} + \chi_1 f B_s^{l-1} + \chi_2 f f(B_s^{l-2}) \quad (16)$$

Substitute (16) in (14) and thus, the equation becomes,

$$B_s^{l+1} = \left(\chi_0 + \chi_1 B_s^{l-1} + \chi_0 B_s^{l-2} + \chi_1 f B_s^{l-1} + \chi_2 f f(B_s^{l-2})\right)(1 - \Re_3) + \Re_3 \circ B_y^l \quad (17)$$

The above expression is an updated equation of GSCAViaR, wherein $\Re_3$ notes uniform stochastic sequence values ranging between 0 and 1, B_y^l refers to a producer at l^{th}iteration whereas ∘ indicates product that computes a product of two vectors.

Step 5: Dispersion stage

In GSO, it makes classification if l^{th} The offers agent is dispersed. At l^{th}search, it develops scholastic front location and then, it obtains random distance that can be mentioned by,

$$a_s = \rho . \Re_1 a_{max} \quad (18)$$

Then, newer locations can be formulated as,

$$B_s^{l+1} = B_s^l + a_s J_s^l(\vartheta^{l+1}) \quad (19)$$

Step 6: Termination
GSCAViaR is terminated after obtaining the best solution by continuous execution of the above steps.

3. RESULTS AND DISCUSSION

The outcomes achieved by GSCAViaR-DenseNet that is designed for CKD detection are elucidated in this part. GSCAViaR-DenseNet outperformed existing methods, achieving 91.5% accuracy, 92.8% sensitivity, and 90.7% specificity with 90% training data. In comparison, the Deep ensemble model, Fusion DL model, NWCNN, and CKD-SO had lower metrics across the board.

3.1. Experiment setup

The GSCAViaR-DenseNet model for CKD detection was implemented using the PYTHON tool. The implementation involved the use of various libraries, including TensorFlow, Keras, and scikit-learn, to build and train the DenseNet architecture integrated with the CAViaR model. The experiments were conducted on a high-performance computing environment to ensure the efficient training of the model on the CKD dataset.

3.2. Dataset description

The study utilizes the CKD dataset, which comprises 400 patient records collected. The dataset includes key features such as age, gender, blood pressure, serum creatinine, and glomerular filtration rate (GFR) [16].

3.3. Evaluation metrics

Accuracy, specificity, and sensitivity are considered for evaluating the GSCAViaR-DenseNet model. Accuracy measures overall correctness, specificity assesses the identification of negative cases, and sensitivity evaluates the detection of positive cases. Together, these metrics provide a comprehensive view of the model's performance [22], [23].

3.3.1. Accuracy

Accuracy implies a percentage of exactly detected cases as positive and negative CKD by the system out of overall cases estimated that can be computed by,

$$\alpha = \frac{V+N}{V+N+I+X} \tag{20}$$

Here,V indicates true positive (TP),N represents true negative (TN), I specifies false positive (FP) and X notes false negative (FN).

3.3.2 Specificity

Specificity computes a proportion of TN instances that are accurately detected by a model and it is evaluated as,

$$\eta = \frac{N}{N+I} \tag{21}$$

3.3.3 Sensitivity

Sensitivity evaluates a proportion of TP instances that are perfectly detected by a system, which is given by,

$$\kappa = \frac{V}{V+X} \tag{22}$$

3.4. Comparative techniques

The Deep Ensemble model [8], Fusion DL model [15], Novel Weight Convolutional Neural Network (NWCNN) [9], and Snake-efficient Feature Selection-based Framework (CKD-SO) [1] are considered comparative methods to demonstrate the effectiveness of GSCAViaR-DenseNet [24], [25].

3.5. Comparative assessment

The estimation of GSCAViaR-DenseNet is performed by assessing key metrics while varying the training data and utilizing K-fold cross-validation. This approach ensures that the model's performance is robust and consistent across different subsets of the data, helping to minimize bias and variance [26], [27].

3.5.1. Analysis of training data

Figure 3 represents the analysis of GSCAViaR-DenseNet concerning evaluation measures by changing training data. In this section, values attained by GSCAViaR-DenseNet and conventional methods while training data=90% are explained. Figure 3(a) interprets the assessment of GSCAViaR-DenseNet with regard to accuracy. GSCAViaR-DenseNet attained an accuracy of 0.915 whereas the Deep ensemble model, Fusion DL model, NWCNN and CKD-SO acquired 0.749, 0.784, 0.819 and 0.854 implies enhancement in performance about 18.157%, 14.308%, 10.487% and 6.655%. Evaluation of GSCAViaR-DenseNet in terms of sensitivity is shown in Figure 3(b). The sensitivity obtained by GSCAViaR-DenseNet is 0.928 while the value achieved by the Deep ensemble model is 0.739, the Fusion DL model is 0.784, NWCNN is 0.805 and CKD-SO is 0.854. It explicates improvement in performance about 20.452%, 15.585%, 13.316% and 8.045%. Figure 3(c) mentions the estimation of GSCAViaR-DenseNet regarding specificity. Deep ensemble model, Fusion DL model, NWCNN and CKD-SO obtained specificity of 0.734, 0.785, 0.806 and 0.854 whereas GSCAViaR-DenseNet acquired 0.907. This describes enhancing in performance about 19.132%, 13.453%, 11.194% and 5.900%.

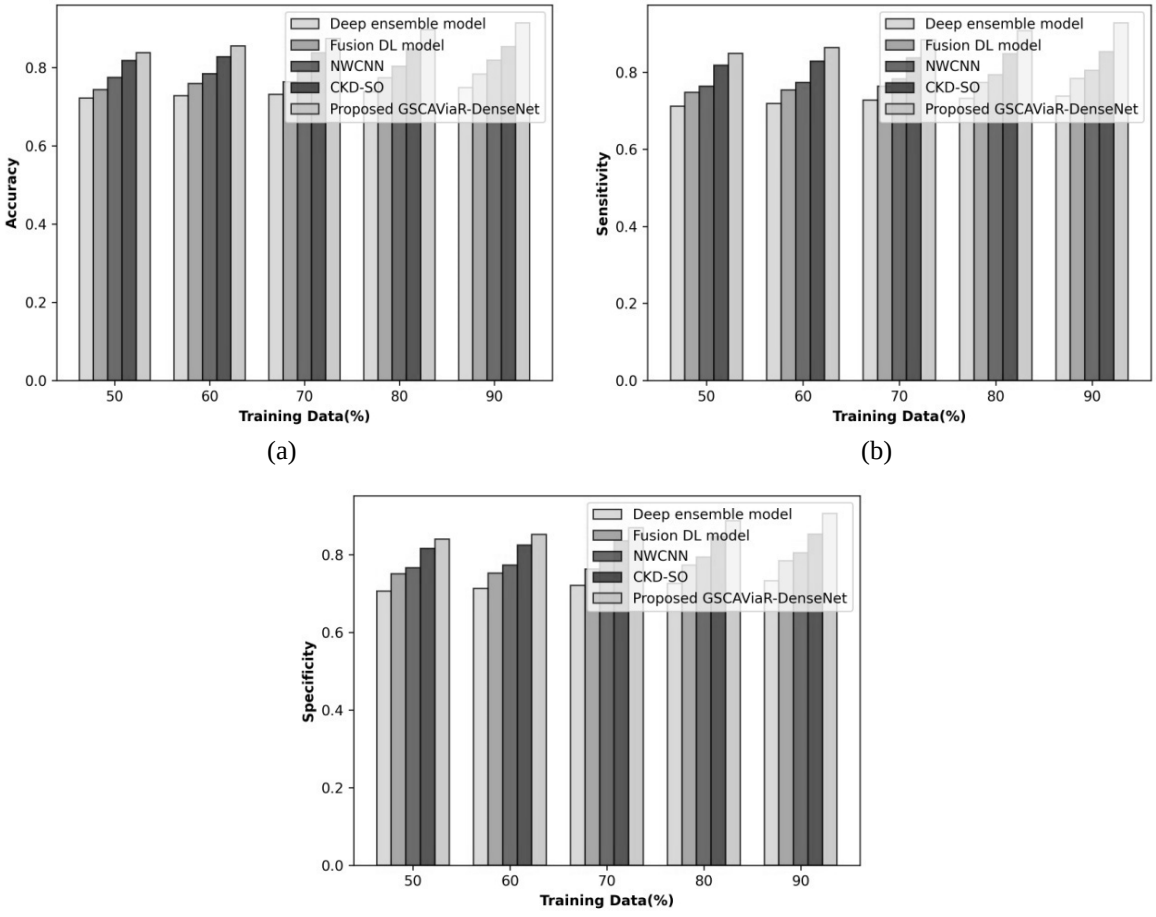

Figure 3. Comparative analysis based on training data: (a) accuracy, (b) sensitivity, and (c) specificity

3.5.2. Analysis regarding K-fold

Assessment of GSCAViaR-DenseNet regarding evaluation measures by varying K-fold is demonstrated in Figure 4. The values obtained by considered techniques while K-fold=9 are illustrated in this part. Evaluation of GSCAViaR-DenseNet in respective to accuracy is specified in Figure 4(a). The accuracy acquired by GSCAViaR-DenseNet is 0.928 whereas the value attained by the Deep Ensemble model is 0.739, the Fusion DL model is 0.786, NWCNN is 0.806 and CKD-SO is 0.853. It elucidates enhancement in performance about 17.830%, 11.313%, 9.068% and 3.755%. Figure 4(b) presents an estimation of GSCAViaR-DenseNet with relation to sensitivity. Deep ensemble model, Fusion DL model, NWCNN and

CKD-SO attained sensitivity of 0.732, 0.785, 0.805 and 0.854 whereas GSCAViaR-DenseNet achieved 0.898. This indicates improvement in performance about 18.475%, 12.640%, 10.407% and 4.896%. Analysis of GSCAViaR-DenseNet considering specificity is delineated in Figure 4(c). GSCAViaR-DenseNet obtained a specificity of 0.910 whereas the Deep ensemble model, Fusion DL model, NWCNN and CKD-SO attained 0.737, 0.786, 0.804 and 0.853 signifies performance enhancement of about 18.953%, 13.584%, 11.581% and 6.222%.

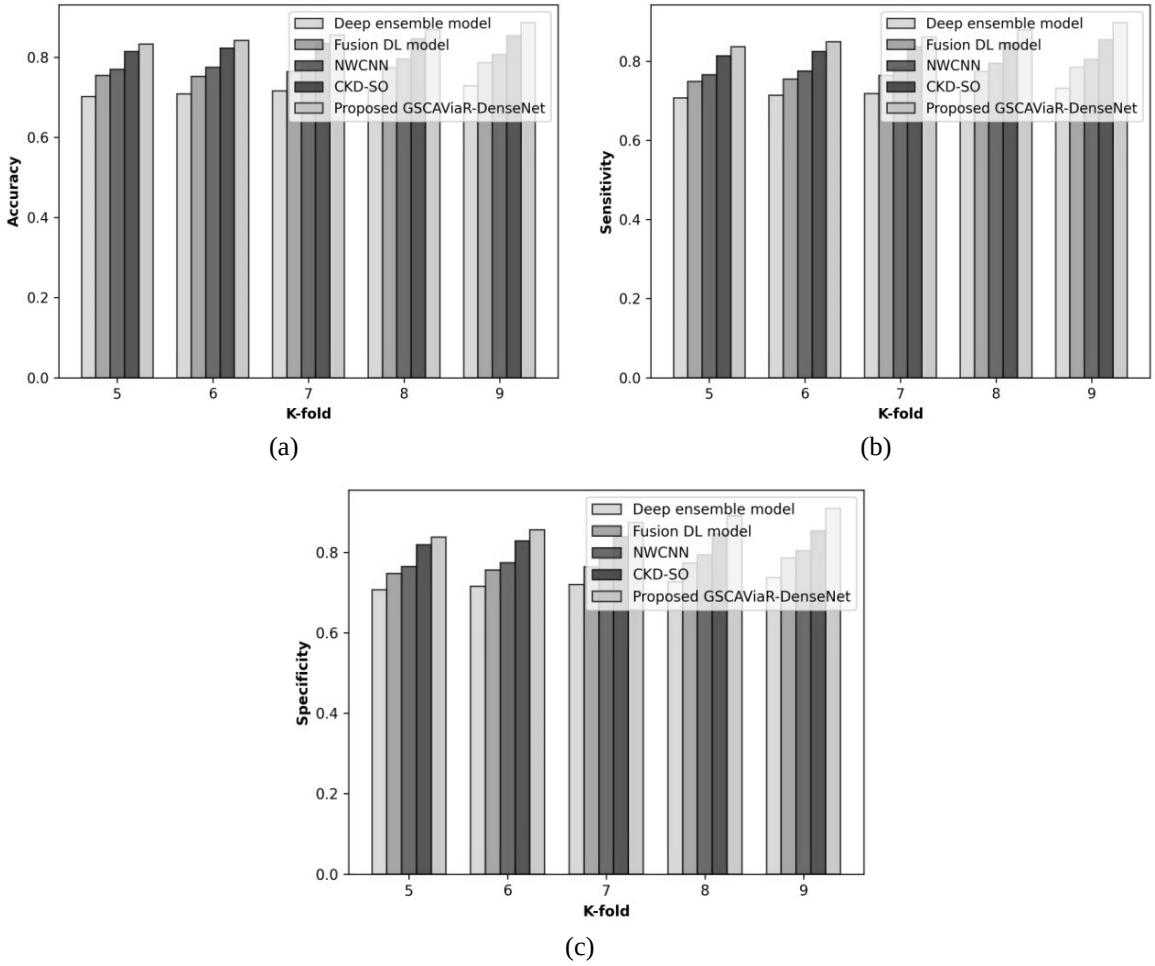

Figure 4. Comparative analysis based on K-fold: (a) accuracy, (b) sensitivity, and (c) specificity

3.6. Comparative discussion

GSCAViaR-DenseNet acquired superior results while comparing with existing schemes like the Deep ensemble model, Fusion DL model, NWCNN and CKD-SO. The discussion table of assessments performed is illustrated in Table 1. When training data=90%, GSCAViaR-DenseNet achieved 91.5% of accuracy whereas the Deep ensemble model, Fusion DL model, NWCNN and CKD-SO obtained 74.9%, 78.4%, 81.9% and 85.4%. This describes that GSCAViaR-DenseNet is capable of detecting possible symptoms of CKD. Sensitivity acquired by the Deep ensemble model is 73.9%, Fusion DL model is 78.4%, NWCNN is 80.5% and CKD-SO is 85.4% while sensitivity attained by GSCAViaR-DenseNet is 92.8% while training data is 90%. It elucidates that GSCAViaR-DenseNet detected each person at risk for CKD. Deep ensemble model, Fusion DL model, NWCNN and CKD-SO achieved a specificity of 73.4%, 78.5%, 80.6% and 85.4% whereas GSCAViaR-DenseNet acquired a specificity of about 90.7%. This indicates that GSCAViaR-DenseNet perfectly identified individuals who have CKD. From the assessments conducted, it can be concluded that GSCAViaR-DenseNet is the better approach for CKD detection as it achieved 91.5% accuracy, 92.8% sensitivity and 90.7% specificity for 90% of training data.

Table 1. Comparative discussion of GSCAViaR-DenseNet

Setups	Metrics/Methods	Deep ensemble model	Fusion DL model	NWCNN	CKD-SO	Proposed GSCAViaR-DenseNet
Training data=90%	Accuracy	74.9%	78.4%	81.9%	85.4%	91.5%
	Sensitivity	73.9%	78.4%	80.5%	85.4%	92.8%
	Specificity	73.4%	78.5%	80.6%	85.4%	90.7%
K-fold=9	Accuracy	72.9%	78.6%	80.6%	85.3%	88.7%
	Sensitivity	73.2%	78.5%	80.5%	85.4%	89.8%
	Specificity	73.7%	78.6%	80.4%	85.3%	91%

4. CONCLUSION

CKD specifies an impairment of the kidneys that gets worse over time. It is a deteriorating issue that causes worldwide trouble as the existing remedial choices are not effective. Effectual treatment and earlier diagnosing are significant to avoid CKD progression. Furthermore, earlier detection of CKD is vital to save numerous people. As an outcome, various researchers are presently concentrated on developing proficient techniques to detect CKD. However, most of the approaches are time-consuming to identify CKD. In this research, GSCAViaR-DenseNet is newly designed for CKD detection. At first, chronic kidney data is taken from a specific dataset. Then, pre-processing of considered data is accomplished by Min-Max normalization. After that, FS is carried out for selecting appropriate features for detection process. The features are selected based on Topsoe similarity. At last, CKD is detected utilizing DenseNet and the training of DenseNet is done by GSCAViaR. Moreover, GSCAViaR is presented by joining GSO with CAViaR. In addition, GSCAViaR-DenseNet attained maximum accuracy, sensitivity and specificity of about 91.5%, 92.8% and 90.7% while considered training data is 90%. GSCAViaR-DenseNet demonstrated superior performance in CKD detection, highlighting its potential for early diagnosis. Future work may explore optimizing the model for broader datasets to enhance generalizability.

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