Journal of Neonatal Surgery
ISSN(Online): 2226-0439
Vol. 14, Issue 10s (2025)
https://www.jneonatalsurg.com

OPEN ACCESS

An Accurate Ckd Prediction Model With Using Integrated Layered Network With Optimizer

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Cite this paper as: Suhaila.K K, Dr. Elamparithi.M, Dr. Anuratha.V, (2025) An Accurate Ckd Prediction Model With Using Integrated Layered Network With Optimizer. *Journal of Neonatal Surgery*, 14 (10s), 855-866.

ABSTRACT

Predictive modeling course of CKD and ensuring early diagnosis is essential for individualized treatment that may enhance patients' quality of life and prolong survival time. Using readily available clinical and laboratory data from patients with mental health conditions CKD, this thesis investigates the interpretability of statistical learning and computer vision models for predicting end-stage renal disease. Machine-learning models were used with clinical, comorbid, and demographic data to ascertain whether a patient with CKD would experience end-stage renal disease. The most significant markers were discovered using the proposed Lightweight Layered Network (LLNet) with Stochastic Gradient Descent (SGD). Researchers also added sophisticated attribution techniques to improve the intelligibility of the neural network architecture. The neural network architecture had a much higher AUC-ROC of 99% than the baseline models. While the existing interpretation was inconsistent, the interpretation produced by Lightweight Layered Network (LLNet) with Stochastic Gradient Descent (SGD) with attribution techniques aligned with clinical expertise. There were negative connections between eGFR and urine creatinine with the progression of CKD, although positive relationships were seen with urine albumin to creatinine ratio, potassium, hematuria, and proteinuria. In conclusion, attribution algorithms combined with deep learning can detect comprehensible aspects of the development of CKD. Our model found several essential but underreported characteristics that could be new indicators of the advancement of CKD. This study gives doctors a strong, empirically supported basis for using predictive analytics in the healthcare management and therapy of CKD.

Keywords: *CKD, deep learning, layered network, optimization, prediction*

1. INTRODUCTION

One of the deadliest is kidney cancer, which is also, sadly, hard to find early using standard clinical methods [1]. Renal cancer is one of the top ten cancers that kill people. However, there is currently little research on it. The prevalence of several cancer kinds in the medical community has caused a delay in the adoption of contemporary detection and treatment techniques. For decades, patients with kidney cancer have had few alternatives for treatment, and their life expectancy is typically less than a year. For this reason, automatic diagnostic tools will make it easier and faster for a doctor to diagnose a patient's illness and help them live [2]. It is challenging to detect kidney disease early on. Therefore, categorization techniques are frequently utilized in numerous medical diagnostic systems incorporating image processing [3]. Using the tool can lower the testing pressure, and CKD affects the structure and function of the kidneys. Complications from a prolonged condition can include weakened bones, high blood pressure, anemia, nerve damage, problems with the heart or blood vessels, etc. [4]. Various stages of the disease are caused by the glomerular filtration rate (GFR). In addition to having a high risk of cardiovascular and end-stage kidney illnesses, both of which can be avoided by identifying and treating those who are at risk early, the incidence of CKD has increased dramatically. The disease can now be effectively assessed in the first step using predictive analytics techniques [5]. The most widely used method for detecting renal illness these days is machine prediction analysis. It is a health risk for developing and rising nations in their early phases. This means that some of the adverse effects

of CKD could not show up until crucial kidney function is impaired. CKD treatment focuses on controlling the primary cause of the illness in its early stages to reduce the progression of kidney danger.

The start of CKD and numerous other clinical characteristics are associated with epidemiology. To ascertain whether CKD is used, nephrologists typically use blood and urine tests [6]. Age, diabetes, obesity, and genetics can all have an impact on CKD. The kidneys filter creatinine, a waste product of normal muscle breakdown, from the blood. However, the pee test will reveal that the urine still contains protein. Specifically, the kidney filter typically does not transport blood components like albumin, a kind of protein, into the urine [7]. Albumin in the urine test indicates kidney filter impairment, which may be a sign of CKD. The IoMT portal prototype for the wireless embedded health monitoring framework is described in this study. This research offers several analytics methods for early prediction of renal disease. These models might be integrated into a suggested architectural monitoring system to solve the deficiency of health analytics within the system of observation that is in place now [8]. Monitoring or evaluating a patient's health status is generally possible considering different physiological indicators. For challenging chronic conditions like diabetes and kidney disease, this means depending on the disease's physiological parameters, which are insufficient to identify or forecast its emergence [9] – [10].

The Lightweight Layered Network (LLNet) with Stochastic Gradient Descent (SGD) has been suggested in this research to classify and diagnose CKD. As the vector machine developed and kidney mitosis was seen, the proposed model retrieved the network properties fed into the machine. By removing characteristics from CT scans, a pre-trained LLNet was extensively trained to detect kidney cancer. The appropriate information set samples are displayed alongside a discussion of LLnet-based automatic technique. Additional analysis of the LLNet with the SGD model's local and global contextual variables revealed that the system could detect kidney cancer more quickly by employing LLNet inside the lightweight layer. Initial training of the LLnet model and SGD training were done using patches. Finally, the system and the samples were directly calibrated. It combines a sophisticated LLNet model training strategy with patches of neighboring samples in a single pass. The random field has removed false positives following the LLNet with SGD modalities. This research's primary findings are:

- ✓ The Lightweight Layered Network (LLNet) with Stochastic Gradient Descent (SGD) was suggested to identify and forecast chronic kidney illness.
- ✓ The ability to predict CKD using blood or urine tests and evaluate their accuracy and relevance. When using predictive analytics techniques to predict CKD early, choose the most significant and representative parameters.
- ✓ The study determined the CKD-associated risks that can stop the illness from progressing to its final stage of development.
- ✓ The statistical evaluations were conducted to evaluate the result's accuracy further.

This was how the rest of the paper looked: Background information and current approaches for predicting chronic renal disease were reviewed in Sections 1 and 2. The adaptive hybridized deep convolutional neural network was suggested in section 3 to diagnose and detect CKD early. Section 4 displays the experiment's findings. The recommended article is finally concluded in part 5.

2. RELATED WORKS

Researchers and medical professionals have paid close attention to forecasting CKD. In this section, researchers comprehensively analyzed pertinent literature that looked at predictive analytics techniques to evaluate the risk of CKD [11]. The studies included here help us better grasp the state of the art, current practices, and developments in this crucial field of medicine. By examining earlier research, we can detect weaknesses and shortcomings in the existing methods and determine how we may enhance and expand upon them. First, the authors took advantage of studies using data from 551 CKD patients that Apollo Hospitals, India, gave [12]. RPART, SVM, LOGR, and MLP [13] – [16] were the four predictive analytics algorithms evaluated. Several performance indicators, including sensitivity, specificity, accuracy, and AUC, are used in the study to determine the models. These criteria thoroughly assess the models' power to discriminate between people with CKD and normal people. The MLP model achieved the highest classification rate TPR (0.9897) and AUC (0.995), whereas the LOGR model obtained the highest ACC (0.981) [17]. A study involving 551 individuals with pathologically verified CKD was carried out by [18]. Their information was gathered from the Shanghai Huadong Hospital's Department of Nephrology, affiliated with Fudan University [19]. They have created an online application that uses five demographic factors and thirteen blood markers to assess patients' proteinuria progression. Of the nine models they used to develop web applications, Elastic Net, Lasso, Ridge, and LR were among the linear models that demonstrated the strongest predictive power, 79% F1 scores, and approximately 82% accuracy [19].

The UCI predictive analytics collection provided the information set that Ekanayake and Herath examined [20]. Conventional neural networks, DT, RF, XGBoost, extra trees, and AdaBoost were among the eleven classification models considered for training. The decision tree (100%), random forest (100%), XGB (100%), additional trees (100%), AdaBoost (100%), and conventional neural network (97.5%) classifiers [21] – [25] were chosen according to the highest test accuracy possible for each of the three information sets. However, according to feature importance analysis, the classifier with the most additional

trees demonstrated the least amount of distortion towards particular characteristics. Bhattacharya et al. thoroughly explained improving disease categorization in medical image analysis through GAN-based data augmentation [26]. A 60.3% test accuracy is the only characteristic of the convolutional neural network (CNN) model, whereas their GAN-augmented CNN approach achieved 65.3% by tackling the issues of data imbalance and over-fitting [27]. A comprehensive analysis of predictive analytics algorithms' applications, particularly LR, DT, and KNN, to the prediction of chronic renal disease was conducted by [28]. With 96.25% and 97% accuracy, respectively, their models indicated that logistic regression and the decision tree technique might be applied to optimize the prediction of prolonged health effects of renal illness.

The author investigated various predictive analytics tools to forecast the probability of CKD [29]. They highlighted the importance of resolving data imbalance to develop reliable predictive models by looking at class balancing strategies, including the SMOTE, Stacking the LMT, Rotation Forest, Decision Tree, Random Forest, Random Tree, AdaBoostM1, SGD, Naive Bayes, SVM, LR, ANN, KNN, J48, and the Bayesian networks (BayesNet), as well as the classification techniques were among the predictive analytics models used for their purpose [30]. Their findings demonstrated that, with an AUC of 100%, the Rotation Forest outperformed the other models and achieved the maximum accuracy. In summary, there are four primary issues to be aware of while working with medical information sets. Missing values or incomplete cases are the first. Approximately 45% of the UCI online machine-learning information set libraries have incomplete records. Furthermore, most of the previously listed literature frequently has issues with data class imbalance and insufficient data record volume. The accuracy of popular predictive analytics models described in the literature above is compiled [30].

3. METHODOLOGY

Accurately predicting patient survival in CKD and the existence of the disease is the goal of the suggested architecture, which is depicted in Fig 1. Predictive modeling, automated hyper-parameter tuning, feature selection using a provided approach with ANOVA and chi-squared testing, pre-processing, and data collecting from four distinct information sets are all included. Six distinct performance assessments round out the process, ultimately determining whether cardiovascular disease exists.

3.1. Data set

The UCI repository is utilized in the proposed model. The medical information of 400 patients, 250 of whom have CKD and 150 of whom do not, is represented by 25 attributes (1 class, 11 numeric, and 14 nominal attributes). The features used in this study are age, bp, sg, al, su, sbc, pc, pcc, ba, bgr, bu, su, sod, pot, hemo, pcv, wbcc, rbcc, htn, dm, cad, appet, pc, anr, and class.

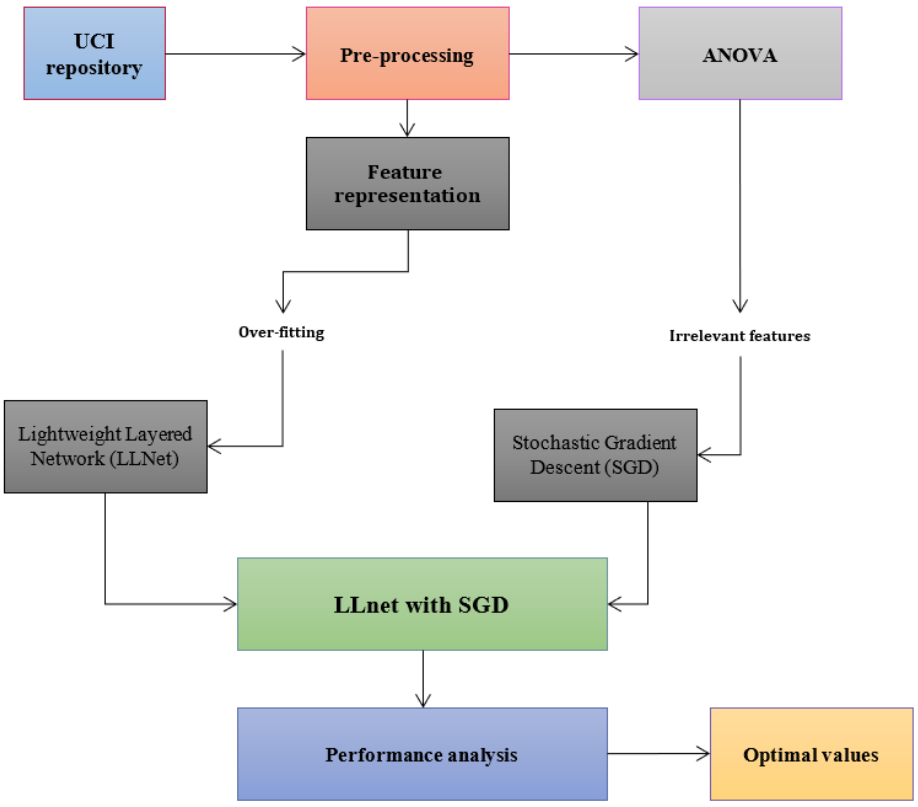


Fig 1: Block diagram of the proposed model

3.2. Pre-processing

Before analysis or modeling, pre-processing is essential to guarantee the reliability and correctness of the data. Through the detection and management of mistakes, outliers, and missing variables, it improves prediction performance and lowers computing costs. Finding the most pertinent data for model training is the goal of feature selection, which enhances prediction performance and lowers computing complexity. To improve prediction accuracy and generalization, model prediction and hyper-parameter tuning require crucial processes such as optimizing model parameters, choosing the optimal algorithm, and assessing performance metrics.

3.3. Feature selection

The curse of dimensionality must be addressed via feature selection to avoid sparsity and computational inefficiency. It improves model generalization and reduces overfitting by eliminating superfluous or irrelevant features. Focusing on the most informative features enhances the model's performance and interpretability. Faster training and inference are also made possible, maximizing computer resources. In this case, we use a layered feature selection procedure.

3.4. Prediction model

To find out if two or more groups differ statistically significantly, a statistical technique called an analysis of variance, or ANOVA for short, examines their averages. It is employed to carry out the preliminary feature selection. During the evaluation of relevant attributes for modeling, the F-value is the ratio of intra-group variation to inter-group variance and is computed to assess each feature's significance to the target variable. Higher F-values indicate that a feature is more pertinent to the target variable. The F-value for every feature in the information set is determined in the first tier. Higher F-value features are kept for additional examination in the second tier. To assess the significance of mean differences between two or more groups in an information set, ANOVA uses two statistical metrics: the F-statistic and the p-value. The two variances that comprise the F-statistic are the variance between groups and the variance within groups. It calculates the degree to which the group means differ from one another and from within the groups. The F-statistic is more prominent when group means have more significant differences. The probability that the observed F-statistic (or one more extreme) would be obtained under the null hypothesis is evaluated based on the p-value linked to the F-statistic, which assumes that the group means are equal. The null hypothesis is rejected when the observed differences between group averages are unlikely to result from random chance, as demonstrated by a small p-value, often below a chosen significance level, like 0.05.

3.5. Layered Network model

With additional refinement, the second layer is operated by X^2, a statistical metric used to ascertain the link or independence between two category variables. It measures how different the observed and expected frequencies of the variables are from each other under the assumption of independence. The chosen features from Layer 1 are subjected to the X^2 technique in the second layer. The difference between the observed and anticipated frequencies under the independence null hypothesis is calculated. The test statistic has a chi-squared distribution; the higher the chi-squared value, the less probable the association is the product of chance. The dual-tier feature selection method combines the benefits of X^2 and ANOVA. Combining these two methods results in a more thorough evaluation of feature relevance. ANOVA is good at finding important continuous features, whereas X^2 emphasizes how important categorical features are. A more trustworthy and consistent feature selection procedure can be developed by combining the two approaches to handle information sets with various feature types better. Algorithm 1, which uses a dual-tier hybrid two-filter feature selection method, thoroughly explains how our model functions internally during the feature selection process. Because our classification goal was binary and the information set was linearly separable, a tree-based classifier was the best option for our approach.

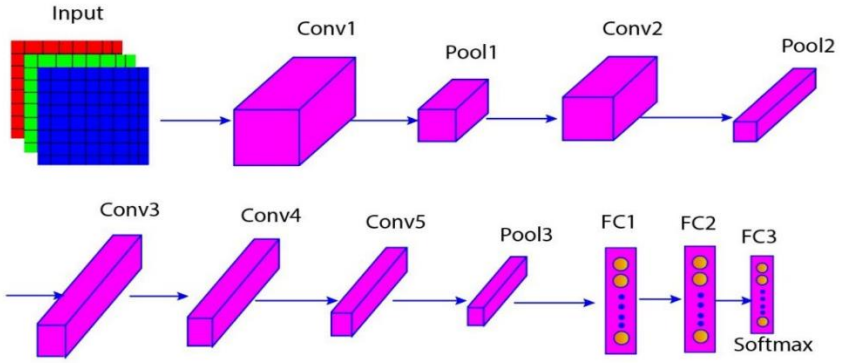


Fig 2. LLNet architecture

3.5. Lightweight Layered Network (LLNet)

Microsoft created the Light weight model, a robust gradient boosting system well-known for its remarkable speed and accuracy. Designed to facilitate the efficient training of large information sets, the boosting with layered network has unique features, including Radiant Boosting, which ensures a strong ensemble for prediction tasks by correcting faults from previous trees. Its leaf-wise technique increases training efficiency, which ranks splits according to maximum reward. Interestingly, LLNet provides smooth support for categorical features, removing the requirement for pre-processing—a benefit for information sets such as our CKD sample. LLnet is widely used in classification, regression, and ranking problems and is well known for its exceptional performance, scalability, and efficiency. For a single instance i, the LLNet prediction by Eq. 1 is $\hat{y}_i$, which is the predicted value for the i^{th} instance, $f_k(x_i)$, which is the forecast made by the k^th tree for the feature selection i^{th} instance x_i, and K, which is the total number of trees.

$$\hat{y}_i = \sum_{k=1}^{k} f_k(x_i) \quad (1)$$

3.3. Hyper-parameter tuning

Stochastic Gradient Descent (SGD) has received much praise for its user-friendly interface, flexible features, and leading-edge optimization methods in the predictive analytics world. SGD is an open-source library for maximum accuracy in NLP tasks, optimizing predictive analytics and deep learning hyper-parameters. SGD's versatile and efficient interface can automate the search for optimal hyper-parameters or the variables that control the training process of predictive analytics and neural network architectures, including, but not limited to, learning rate and number of layers, and dropout rate. Utilizing a range of optimization algorithms, such as Bayesian and evolutionary algorithms, SGD efficiently searches the hyper-parameter space to determine the collection of hyper-parameters that maximizes or minimizes a specific objective function. Without requiring human trial and error, users can quickly and efficiently adjust their models for better performance.

4. NUMERICAL RESULTS AND STATISTICAL ANALYSIS

ANOVA is beneficial when evaluating the statistical significance of numerical aspects in connection to categorical goal variables, like the diagnosis or absence of CKD. On the other hand, the Chi-Square test is perfect for assessing how independent categorical features are. Combined, these two feature selection techniques guarantee that the model contains only the most pertinent features. ANOVA is beneficial when determining the statistical significance of numerical data concerning categorical goal variables, like the existence or absence of CKD. The Chi-Square test, on the other hand, works well for determining if category features are independent. Combining these two feature selection techniques guarantees that the model contains only the most pertinent features. With its histogram-based method, LLNet, a gradient-boosting framework renowned for its effectiveness, performs exceptionally well when processing numerical and categorical data. Unlike the level-wise growth method employed by algorithms, LLNet novel leaf-wise growth strategy, which concentrates on developing the leaf with the highest delta loss, enables it to attain more precision with fewer repetitions. The histogram-based algorithm and leaf-wise growth method of LLNet significantly increase its speed and efficiency. By modifying important parameters like learning rate, number of leaves, and feature percentage, SGD's hyper-parameter tuning improves LLNet's performance even more. This fine-tuning is necessary and computationally efficient to increase the model's accuracy and produce accurate CKD disease predictions. For healthcare applications necessitating quick and precise predictive capabilities. crucial, sophisticated boosting algorithms, optimized hyper-parameters, and efficient feature selection guarantee the model's accuracy and efficiency (See Fig 3 to Fig 12).

Table 1: Proposed LLNets with existing approaches

Approaches	Accuracy	F1-score	Recall	Precision	Execution time (s)
CNN	73	72	74	69	84
Temporal model	74	68	93	52	205
DNN	80	86	80	80	85
LSTM	81	80	81	79	26
PNets	98	97	97.5	98.2	13
LLNet	**99.1**	**98**	**98.1**	**98.4**	**10**

Table 2: Proposed LLNets with SGD

Approaches	Accuracy	F1-score	Recall	Precision	Execution time (s)
CNN	73	72	74	69	84
Temporal model	74	68	93	52	205
DNN	80	86	80	80	85
LSTM	81	80	81	79	26
PNets	98	97	97.5	98.2	13
LLNet	**99.5**	**98.1**	**98.3**	**98.5**	**9**

Table 3: Proposed LLNets with epochs 5

Approaches	Epochs	Accuracy	F1-score	Recall	Precision	Execution time (s)
CNN	5	85	85	84	86	125
Temporal model		78	79	82	76	153
DNN		94	95	91	92	72
LSTM		90	91	92	91	83
PNets		98.3	97.6	97.5	98.5	12
LLNets		**98.4**	**97.9**	**97.8**	**98.9**	**9**

Table 4: Proposed LLNets with epochs 10

Approaches	Epochs	Accuracy	F1-score	Recall	Precision	Execution time (s)
CNN	10	86	86	87	86	37
Temporal model		88	88	89	87	49
DNN		84	93	95	92	71
LSTM		93	94	96	93	55
PNets		99.1	98.6	99.5	99.4	13
LLNets		**99.2**	**98.7**	**99.6**	**99.5**	**9**

Table 5: Proposed LLNets with epochs 20

Approaches	Epochs	Accuracy	F1-score	Recall	Precision	Execution time (s)
CNN		90	91	90	90	83
Temporal		89	89	87	87	72

model	20					
DNN		94	94	95	84	84
LSTM		95	96	93	95	89
PNets		99.5	99.6	99.5	99	15
LLNets		**99.6**	**99.6**	**99.6**	**99.1**	**10**

Table 6: CV analysis

Folds	**Accuracy**
1	97
2	97.9
3	98.5
4	98.8
5	99
6	99.5
7	99.5
8	99.5
9	99.6
10	99.7

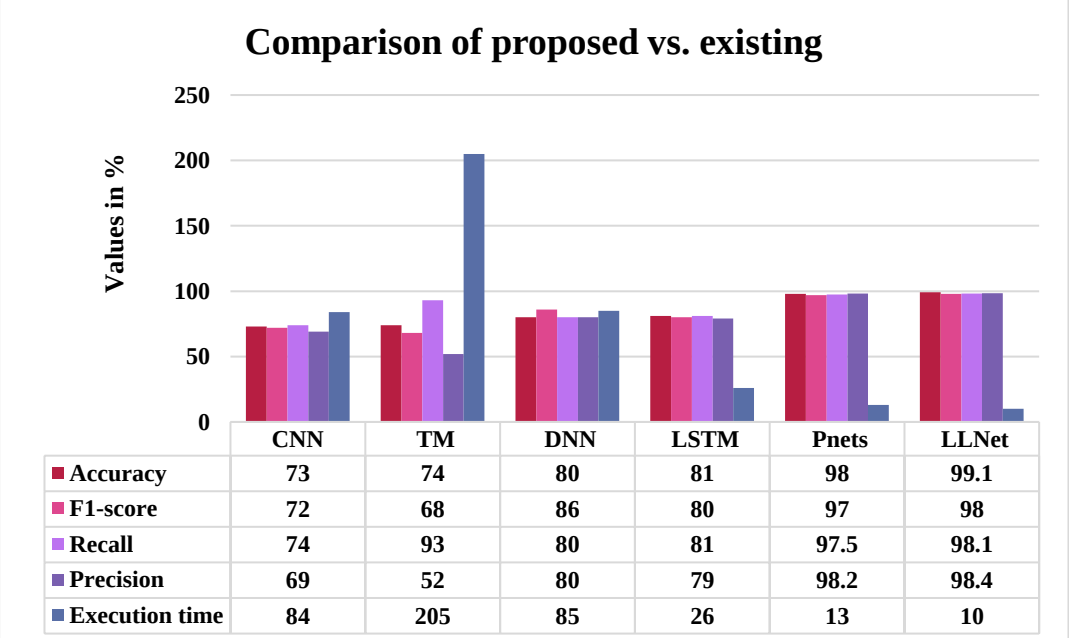
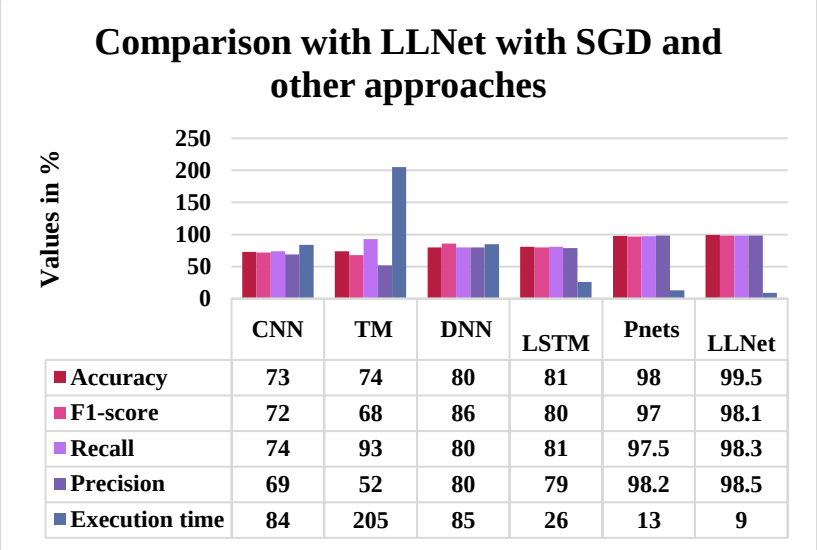
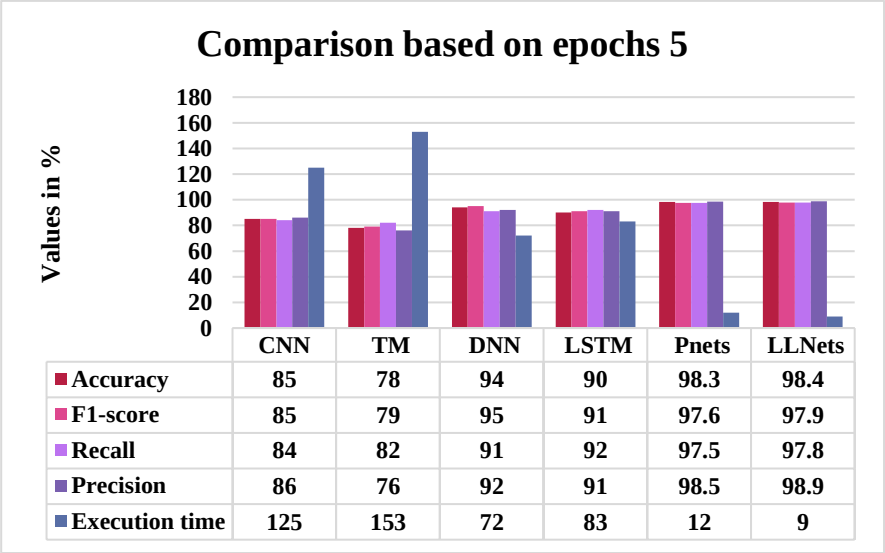


Fig 3: Comparison of proposed vs. Existing



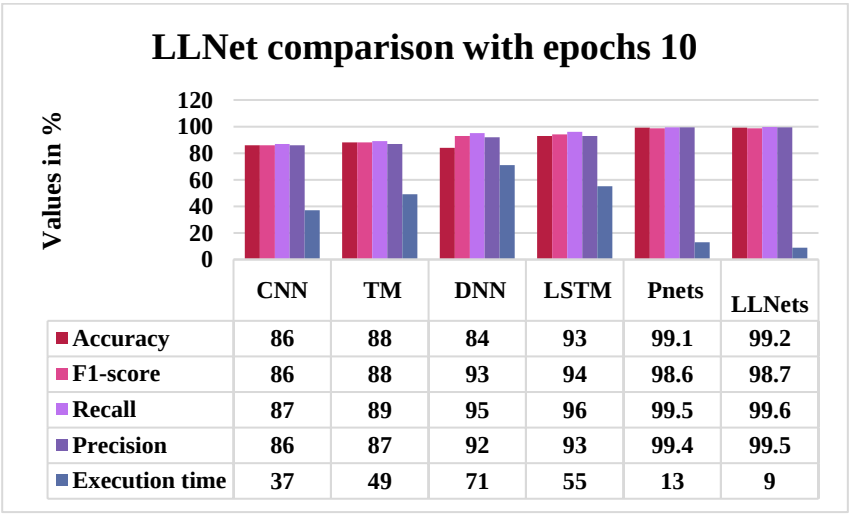
	CNN	TM	DNN	LSTM	Pnets	LLNet
Accuracy	73	74	80	81	98	99.5
F1-score	72	68	86	80	97	98.1
Recall	74	93	80	81	97.5	98.3
Precision	69	52	80	79	98.2	98.5
Execution time	84	205	85	26	13	9

Fig 4: Comparison of LLNet with SGD



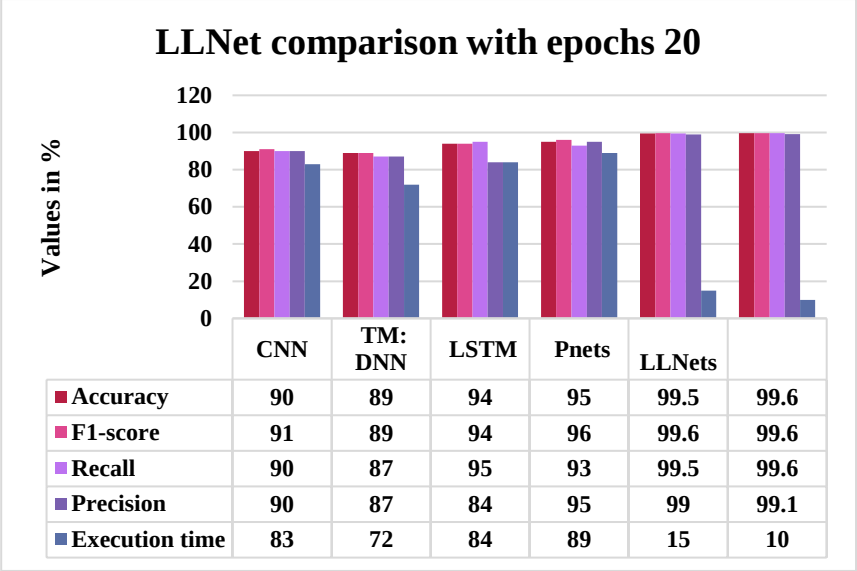
	CNN	TM	DNN	LSTM	Pnets	LLNets
Accuracy	85	78	94	90	98.3	98.4
F1-score	85	79	95	91	97.6	97.9
Recall	84	82	91	92	97.5	97.8
Precision	86	76	92	91	98.5	98.9
Execution time	125	153	72	83	12	9

Fig 5: Comparison of LLNet based on epochs 5



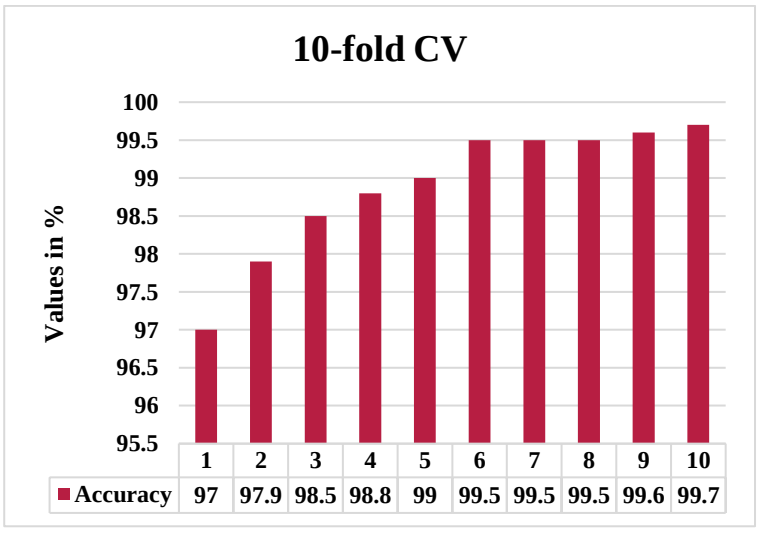
	CNN	TM	DNN	LSTM	Pnets	LLNets
Accuracy	86	88	84	93	99.1	99.2
F1-score	86	88	93	94	98.6	98.7
Recall	87	89	95	96	99.5	99.6
Precision	86	87	92	93	99.4	99.5
Execution time	37	49	71	55	13	9

Fig 6: Comparison of LLNet based on epochs 10



	CNN	TM: DNN	LSTM	Pnets	LLNets	
Accuracy	90	89	94	95	99.5	99.6
F1-score	91	89	94	96	99.6	99.6
Recall	90	87	95	93	99.5	99.6
Precision	90	87	84	95	99	99.1
Execution time	83	72	84	89	15	10

Fig 7: Comparison of LLNet based on epochs 20



	1	2	3	4	5	6	7	8	9	10
Accuracy	97	97.9	98.5	98.8	99	99.5	99.5	99.5	99.6	99.7

Fig 8: 10-fold CV comparison

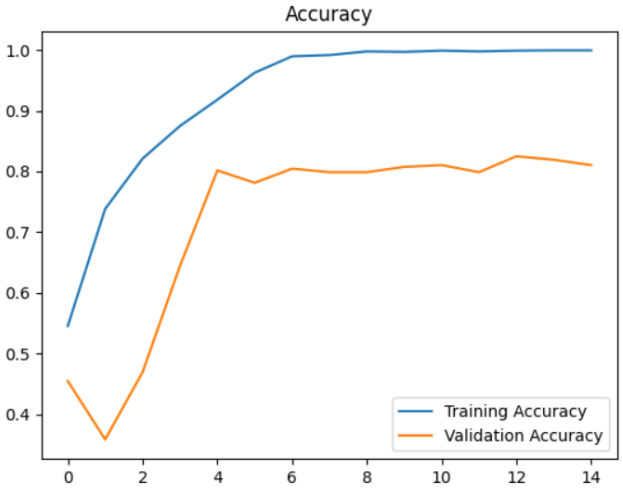


Fig 9. Accuracy comparison

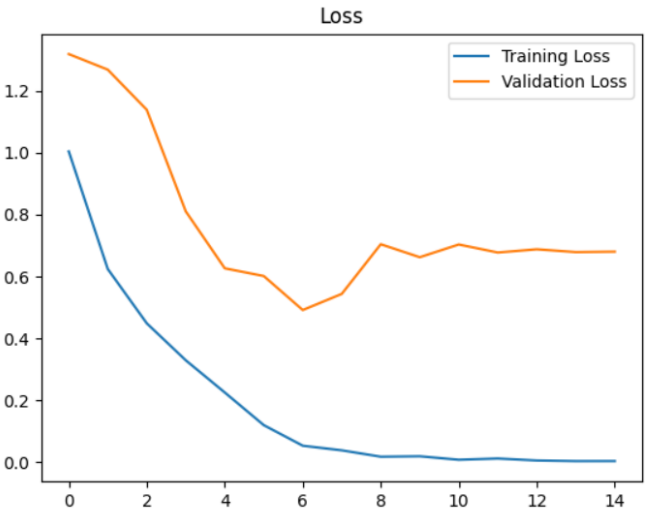


Fig 10. Loss comparison

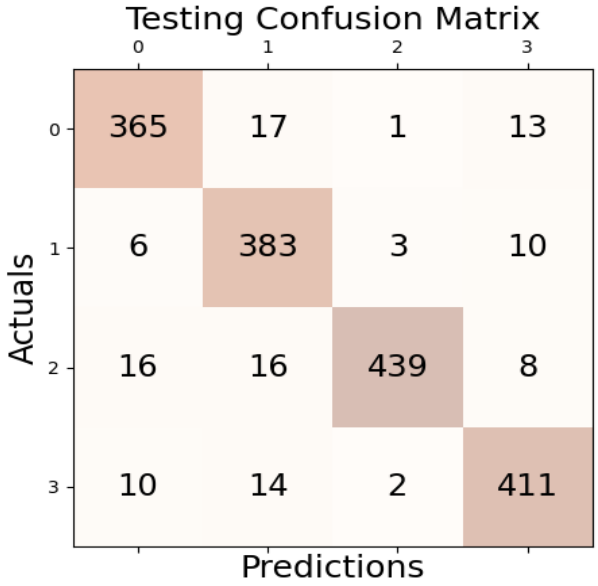


Fig 11. Confusion matrix

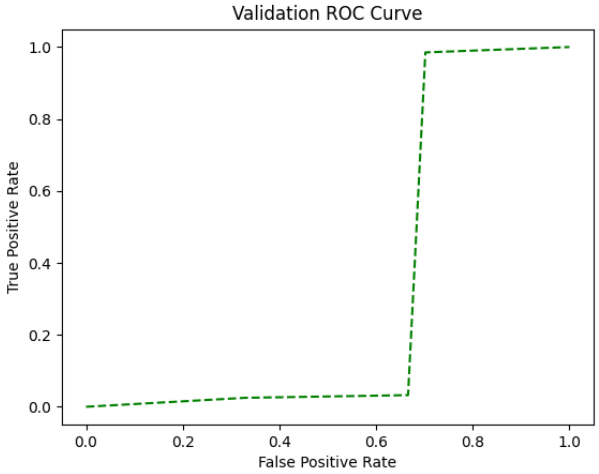


Fig 12. ROC comparison

4.1. Computation Time

The computation time represents the average processing time needed to train a deep learning or predictive analytics model to identify the optimal hyper-parameters for every technique. The testing time is the average time required to complete each information set's cross-validation test sets. The computation time for each of the suggested models is displayed in Table 2 to Table 6. Even though the testing duration was comparable to the conventional algorithms examined in the studies, the results demonstrate that deep learning algorithms typically require significantly more extended training. Deep learning methods are not worth adopting for tiny information sets like the one examined in this paper because the performance metrics (accuracy, recall, etc.) are so close. Most tests take about the same time to execute, although LTSM and Simple DNN take longer. This suggests no discernible difference between the conventional ML algorithms once the model has been trained.

5. CONCLUSION

Combining predictive analytics and computer vision algorithms enhances the predictive modeling for chronic renal disease. Lightweight Layered Network (LLNet) with Stochastic Gradient Descent (SGD) were among the existing predictive analytics algorithms used in the thorough analysis, in addition to sophisticated deep learning algorithms. After carefully applying a CKD information set from the UCI data collection, the models showed remarkable F1-score, accuracy, recall, and precision. Because of the small quantity of the information set, it is crucial to decrease the randomization of the train-test splits. The findings were validated using a 10-fold cross-validation. Finally, the proposed Lightweight Layered Network (LLNet) with Stochastic Gradient Descent (SGD) would be the best options considering the variety of algorithms available to contemporary practitioners since they combine high-quality metrics with reasonably priced training and test runtimes. However, in the future, the work is hybridization of deep learning approaches with optimization approach to attain global prediction outcomes.

REFERENCES

[1] Fadem, Introduction to Kidney Disease, Staying Healthy With Kidney Disease: A Complete Guide for Patients. Cham, Switzerland: Springer, 2022.

[2] Zisser and D. Aran, ‘‘Transformer-based time-to-event prediction for CKD deterioration,’’ J. Amer. Med. Inform. Assoc., vol. 31, no. 4, pp. 980–990, Apr. 2024.

[3] Ammirati, ‘‘CKD,’’ Revista da Associadica Brasileira, vol. 66, no. 1, pp. s03–s09, Jan. 2020.

[4] Aljaaf, D. Al-Jumeily, H. M. Haglan, M. Alloghani, T. Baker, A. J. Hussain, and J. Mustafina, ‘‘Early prediction of CKD using machinelearningsupportedbypredictiveanalytics,’’ in Proc. IEEE Congr. Evol. Comput. (CEC), Jul. 2018, pp. 1–9.

[5] Ekanayake and D. Herath, ‘‘CKD prediction using predictive analytics methods,’’ in Proc. Moratuwa Eng. Res. Conf. (MERCon), Jul. 28, 2020, pp. 260–265.

[6] Ifraz, M. H. Rashid, T. Tazin, S. Bourouis, and M. M. Khan, ‘‘Comparative analysis for prediction of kidney disease using intelligent predictive analytics methods,’’ Comput. Math. Methods Med., vol. 2021, pp. 1–10, Dec. 2021.

[7] Ahmed, M. A. Ali, N. Ahmed, and T. Bhuiyan, ‘‘Computational intelligence approaches for prediction of CKD,’’ in Advances in Distributed Computing and Predictive analytics. Cham, Switzerland: Springer, 2021.

[8] A. N, and K. S. K, ‘‘Decision tree-based explainable AI for diagnosis of CKD,’’ in Proc. 5th Int. Conf. Inventive Res. Comput. Appl. (ICIRCA), Aug. 2023, pp. 947–952.

[9] Tran, M. Zhang, P. Andreae, B. Xue, and L. T. Bui, ‘‘Multiple imputation and ensemble learning for classification with incomplete data,’’ in Proc. 20th Asia Pacific Symp., Nov. 2016, pp. 401–415.

[10] Sarkar, and M. Ahmed, ‘‘Comprehensive performance assessment of neural network architectures in early prediction and risk identification of CKD,’’ IEEE Access, vol. 9, pp. 165184–165206, 2021.

[11] Karita, N. Chen, T. Hayashi, T. Hori, H. Inaguma, Z. Jiang, M. Someki, N. E. Y. Soplin, R. Yamamoto, X. Wang, S. Watanabe, T. Yoshimura, and W. Zhang, ‘‘A comparative study on transformer vs RNN in speech applications,’’ in Proc. IEEE Autom. Speech Recognit. Understand. Workshop (ASRU), Dec. 2019, pp. 449–456.

[12] Song and Y. Lu, ‘‘Decision tree methods: Applications for classification and prediction,’’ Shanghai Arch. Psychiatry, vol. 27, no. 2, p. 130, Apr. 2015.

[13] Amlashi, P. Alidoust, M. Pazhouhi, K. P. Niavol, S. Khabiri, and A. R. Ghanizadeh, ‘‘AI-based formulation for mechanical and workability properties of eco-friendly concrete made by waste foundry sand,’’ J. Mater. Civil Eng., vol. 33, no. 4, Apr. 2021, Art. no. 04021038.

[14] Rubini, P. Soundarapandian, and P. Eswaran, ‘‘CKD,’’ UCI Mach. Learn. Repository, 2015. [Online].

Available: https://doi.org/10.24432/C5G020

[15] Elreedy and A. F. Atiya, ‘‘A comprehensive analysis of synthetic minority oversamplingtechnique(SMOTE)forhandlingclassimbalance,’’ Inf. Sci., vol. 505, pp. 32–64, Dec. 2019.

[16] Beretta andA.Santaniello, ‘‘Nearest neighbor imputation algorithms: A critical evaluation,’’ BMC Med. Informat. Decis. Making, vol. 16, no. S3, pp. 197–208, Jul. 2016.

[17] Aljaaf, D. Al-Jumeily, A. J. Hussain, T. Dawson, P. Fergus, and M.Al-Jumaily, ‘‘Predicting the likelihood of heart failure with a multi level risk assessment using decision tree,’’ in Proc. 3rd Int. Conf. Technol. Adv. Electr., Electron. Comput. Eng. (TAEECE), Apr. 2015, pp. 101–106.

[18] Saqlain, M. Sher, F. A. Shah, I. Khan, M. U. Ashraf, M. Awais, and A. Ghani, ‘‘Fisher score and Matthews correlation coefficient-based feature subset selection for heart disease diagnosis using support vector machines,’’ Knowl. Inf. Syst., vol. 58, no. 1, pp. 139–167, Jan. 2019

[19] Javeed, S. Zhou, L. Yongjian, I. Qasim, A. Noor, and R. Nour, ‘‘An intelligent learning system based on random search algorithm and optimized random forest model for improved heart disease detection,’’ IEEE Access, vol. 7, pp. 180235–180243, 2019.

[20] Ambrish, B. Ganesh, A. Ganesh, C. Srinivas, and K. Mensinkal, ‘‘Logistic regression technique for prediction of cardiovascular disease,’’ Global Transitions Proc., vol. 3, no. 1, pp. 127–130, Jun. 2022.

[21] Abdellatif, H. Abdellatef, J. Kanesan, C.-O. Chow, J. H. Chuah, and H. M.Gheni,‘‘Improving the heart disease detection and patients’ survival using supervised infinite feature selection and improved weighted random forest,’’ IEEE Access, vol. 10, pp. 67363–67372, 2022.

[22] Khan and F. Algarni, ‘‘A healthcare monitoring system for the diagnosis of heart disease in the IoMT cloud environment using MSSO ANFIS,’’ IEEE Access, vol. 8, pp. 122259–122269, 2020.

[23] Barfungpa, H. K. Deva Sarma, and L. Samantaray, ‘‘An intelligent heart disease prediction system using hybrid deep dense Aquila network,’’ Biomed. Signal Process. Control, vol. 84, Jul. 2023, Art. no. 104742.

[24] Akella and S. Akella, ‘‘Predictive analytics algorithms for predicting coronary artery disease: Efforts toward an open source solution,’’ Future Sci. OA, vol. 7, no. 6, Jul. 2021, Art. no. FSO698

[25] Srinivas and R. Katarya, ‘‘HyOPTXg: OPTUNA hyper-parameter optimization framework for predicting cardiovascular disease using XGBoost,’’ Biomed. Signal Process. Control, vol. 73, Mar. 2022, Art. no. 103456.

[26] Mohan, C. Thirumalai, and G. Srivastava, ‘‘Effective heart disease prediction using hybridmachinelearningtechniques,’’IEEEAccess,vol.7, pp. 81542–81554, 2019.

[27] Ali, A. Niamat, J. A. Khan, N. A. Golilarz, X. Xingzhong, A. Noor, R. Nour, and S. A. C. Bukhari, ‘‘An optimized stacked support vector machines based expert system for the effective prediction of heart failure,’’ IEEE Access, vol. 7, pp. 54007–54014, 2019.

[28] Almazroi, E. A. Aldhahri, S. Bashir, and S. Ashfaq, ‘‘A clinical decision support system for heart disease prediction using deep learning,’’ IEEE Access, vol. 11, pp. 61646–61659, 2023.

[29] Subramani, N. Varshney, M. V. Anand, M. E. M. Soudagar, L. A. Al-keridis, T. K. Upadhyay, N. Alshammari, M. Saeed, K. Subramanian, K. Anbarasu, and K. Rohini, ‘‘Cardiovascular diseases prediction by predictive analytics incorporation with deep learning,’’ Frontiers Med., vol. 10, Apr. 2023

[30] Polat, H. Danaei Mehr, and A. Cetin, ‘‘Diagnosis of CKD based on support vector machine by feature selection methods,’’ J. Med. Syst., vol. 41, no. 4, p. 55, Apr. 2017.