

CHRONIC KIDNEY DISEASE STAGE IDENTIFICATION IN HIV INFECTED PATIENTS USING MACHINE LEARNING

¹ Dr. Y. Geetha Reddy, ² Parisa Nithya Sree, ³ Narahari Lahari, ⁴ Nampelly Ashwika

¹Professor, ^{2,3,4}Students

Department Of CSE

Malla Reddy Engineering College for Women

ABSTRACT

One of the leading causes of illness and mortality in the world's medical communities is chronic kidney disease (CKD). Patients often misdiagnose CKD since there are no symptoms in the early stages of the illness. Individuals living with HIV are more likely to develop critical care kidney disease (CKD). Early diagnosis of CKD prevents the illness from worsening and enables patients to get treatment more quickly. The application of machine learning algorithms for illness categorization and prediction in healthcare has increased due to the availability of pathology data. The categorization of CKD using machine learning models is presented in this research. For individuals with CKD, the CKD stages are also determined based on the glomerular filtration rate. The DNN model performs better, diagnosing CKD patients with HIV with 99% accuracy.

1. INTRODUCTION

Chronic kidney disease (CKD) is an irreversible kidney disease that raises the risk of several other illnesses, including heart failure, anemia, and bone damage. Kidneys are quite flexible. Kidney injury will, however, take time to manifest symptoms. Patients often do not have symptoms until the very end of the illness. The prevalent symptoms that coincide with

different diseases are shown in Figure 1. It is possible to manage some types of kidney disease by preventing symptoms. It helps patients prevent further progression of the condition by partially recovering renal function. Dialysis and kidney transplant are two main treatments for end-stage kidney disease, particularly in cases of congestive kidney disease (CKD). Only 10% of patients globally undergo dialysis or a kidney transplant due to the high expense of care [2]. Kidney failure claims the lives of almost a million people annually in 112 low-income countries [5]. Because they lack glomeruli filters, often referred to as nephrons, patients with acquired immunodeficiency syndrome (AIDS) are more likely to have complications from kidney disease. It is possible for kidney cells to get infected by the HIV treatment. Early detection, management, and control of the development of CKD are crucial. Healthcare has benefited greatly from the growing interest in automated diagnosis and the quick development of machine learning techniques. Despite the fact that several studies have classified CKD into several phases using machine learning approaches. Nonetheless, several researchers have shown a link between HIV and CKD. This study has examined machine learning approaches and conducted

The procedure of obtaining stage information for CKD by automated

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computer-aided diagnosis involves using patient data, including age, blood pressure, and blood test findings. The Support Vector Machine (SVM) method has been used by Yu et al. [2] to identify and predict people with diabetes and pre-diabetes. The results demonstrate that SVM can identify patients with common illnesses. E. Perumal et al. [6] have used the Probabilistic Neural Network (PNN) algorithm, Naïve Bayes algorithm, and decision tree algorithm to forecast the incidence of heart disease. When compared to other cardiovascular prediction systems, it yields superior results. R. Shinde and others [8] The results show that the Multilayered Perceptron (MLP) separator offers good prediction results for liver disease, especially in HBV-related patients with liver failure. The MLP separator was utilized to predict HBV-induced hepatic cirrhosis.

2. LITERATURE SURVEY

Contemporary issues and new challenges in chronic kidney disease amongst people living with HIV

Chronic kidney disease (CKD) is a significant clinically relevant comorbidity among people living with HIV (PLWHIV) and is associated with a high mortality and morbidity rate. Antiretroviral therapy (ART) is becoming more frequent, however chronic kidney disease (CKD) is still on the rise and is increasingly associated with ART toxicity and common non-infectious comorbidities (NICMs). Among PLWHIV, the prevalence of CKD is highest in Africa, indicating a substantial disparity. People with HIV/AIDS may develop kidney disease for a variety of reasons. Some of them include HIV-related disorders including immunological complex disease or classic HIV-associated

nephropathy, NICM-related renal disease, and antiretroviral toxicity-related renal disease. Once CKD has progressed to an advanced level, it may lead to ESRD and continues to worsen. It is critical to screen adequately for the early diagnosis of CKD in order to improve patient outcomes by identifying people with risk factors for the illness. Poor and irregular adherence to screening protocols is common. Research into the effects of treatment modalities on the progression of chronic kidney disease (CKD) is urgently needed; yet, there is a lack of data from studies involving PLWHIV and CKD. When used to control blood pressure in the setting of proteinuria, angiotensin-converting enzyme inhibitors and angiotensin receptor blockers likely slow the progression of chronic kidney disease (CKD) in HIV/AIDS patients. Additional challenges faced by the PLWHIV population include drug-drug interactions, strong medication reactions, and polypharmacy. As the PLWHIV group matures and their cumulative ART exposure increases, the potential nephrotoxicity of ART must be carefully considered. An increasing number of PLWHIV are diagnosed with ESRD. Dialysis and kidney transplants are forms of renal replacement therapy that should not be denied to PLWHIV just because they are HIV positive. When it comes to treating PLWHIV, kidney transplantation is an effective alternative to ongoing dialysis and is associated with a better prognosis. With the aging of the PLWHIV population comes an increase in comorbidity and the prevalence of chronic kidney disease (CKD). Therefore, treatment approaches need to change to accommodate the growing chronic healthcare needs of patients.



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A Machine Learning Methodology for Diagnosing Chronic Kidney Disease

The high mortality and morbidity rates caused by chronic kidney disease (CKD) and its potential complications make it a major global health problem. Because chronic kidney disease (CKD) often does not cause noticeable symptoms in its early stages, patients may be unaware that they have it. Early treatment of chronic kidney disease (CKD) may help patients whose condition is in its early stages by delaying the progression of the disease. Machine learning models might be useful for therapists in this regard because of how fast and precise they are at identifying targets. We propose a machine learning strategy for chronic kidney disease (CKD) diagnosis in this paper. A large portion of the CKD data set is missing; it was sourced from the machine learning repository at UCI. Using KNN imputation, which selects a small number of complete samples with very similar measurements to process the missing data from each incomplete sample, the missing values were filled in. Missing data is common in real-world medical settings because patients could forget to measure specific things for different reasons. After the missing data set was filled in, six machine learning approaches were used to generate models: naive Bayes classifier, feed forward neural network, k-nearest neighbor, random forest, and logistic regression. Among the machine learning models tested, random forest had the highest diagnosis accuracy at 99.75%. By analyzing the errors made by earlier models, we proposed an integrated model that combines perceptron with logistic regression and random forest; after 10 runs, it achieved an average accuracy of 99.83%. Hence, we postulated that this method may be valuable for

illness diagnosis using more intricate clinical data.

3. SYSTEM ANALYSIS

EXISTING SYSTEM

Researchers Corinne Isnard Bagnis, Jack Edward Heron, David M. Gracey, et al. [1] studied the relationship between chronic kidney disease and worsening outcomes. Research demonstrates that lowering blood pressure with angiotensin receptor blockers and angiotensin converting enzyme inhibitors reduces the course of chronic kidney disease (CKD) in HIV patients, especially when proteinuria is present. According to Y. Liu, J. Qin, C. Feng, L. Chen, C. Liu, and B. Chen et al. [2], sample diagnosis and data imputation are feasible with CKD. The KNN technique may be used to get enough accuracy for the integrated model that is provided in this research. The model is unable to examine the phases of chronic kidney disease since the dataset only includes two classes: Chronic Kidney Infection and Not Chronic Kidney Disease. Anwar, A. S., and E. H.

A lab dataset of 361 individuals with chronic renal illness is used by A. Rady et al. [3]. The PNN, SVM, and MLP algorithms are used to determine the duration of chronic renal disease. This analysis indicates that the most effective algorithm that physicians may use to eliminate diagnostic and therapeutic errors is the probabilistic neural organization algorithm. Using logistic regression and feed forward neural networks, M. N. Amin, A. Al Imran, and F. T. Johora et al. [4] examine model performance on actual (imbalanced) data and



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model performance on oversampled (balanced) data. The greatest performance was shown by feed forward neural networks, which had 0.99 Recall, 0.97 Precision, 0.99 F1-Score, and 0.99 AUC score for both actual and oversampled data. It was advised by K. S. Vaisla, N. Chetty, and S. D. Sudarsan et al. [5] Models for attribute evaluation and classification were applied to the CKD dataset. When the number of attributes was reduced from 25 to 6, 12, and 7, the attribute evaluator model worked better. The JRip, SMO, Naive Bayes, algorithms, and studies that show JRip produces the greatest results are used by P. Arulanthu and E. Perumal et al. [6].

The Ant Lion Optimization (ALO) approach is used by P. Manickam, K. Shankar, M. Ilayaraja, and G. Devika et al. [7] to choose the best characteristics for classification. Deep neural networks perform more accurately in classification as a consequence of this improvement. Maurya, R. Wable, R. Dakshayani, R. Jadhav, R. Shinde, S. John, and others. [8] Utilize the potassium zone, which is calculated using blood potassium levels, to halt the course of CKD and to adhere to the suggested dietary plans. The relationship between different selection and dimensionality reduction techniques and the effectiveness of chronic illness categorization and prediction is examined by R. Yadav, S. C. Jat et al. [9].

Disadvantages

Identifying CKD stages is not possible inside the system.

Although the Multilayered Perceptron (MLP) separator could not reliably predict HBV-induced hepatic cirrhosis, it does offer very good

predictions for liver illness, especially in patients with liver failure associated with HBV.

PROPOSED SYSTEM

The literature uses a variety of machine learning approaches to classify CKD. In this study, we have constructed six machine learning models—a deep neural network with KNN, SVM, random forest, decision tree, ada-boost, and xg-boost algorithms—to determine whether or not a patient has chronic kidney disease. Figure 2 shows the flow of the suggested experimental setup. Support vector machines, or SVMs, are supervised machine learning models that are based on classification and are used in binary classification scenarios. Using feature comparison, the K-nearest neighbors (KNN) method predicts a value based on how similar it is to the training dataset. Decisions on classification are represented graphically using decision trees. Often, effective classification accuracy cannot be achieved with only one decision tree. This issue is resolved by the Random Forest method, which makes use of many decision trees.

The AdaBoost algorithm, which is often referred to as adaptive boosting, is a machine learning ensemble approach for boosting. By giving each instance a new weight, it seeks to transform a group of weak classifiers into a strong one. An other boosting approach that makes use of a gradient boosting framework is called XG Boost (eXtreme Gradient Boosting). Many researchers have used feature-based deep neural networks (DNNs) in addition to machine learning to get improved classification outcomes. Since deep neural networks employ several layers of nodes to perform high-level functions from input data,



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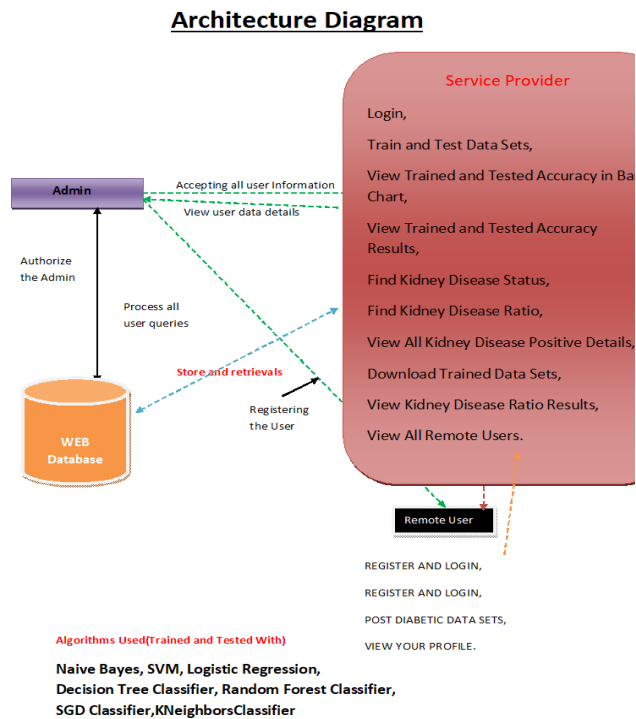
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they are able to identify important diseases. We used the feature selection approach to exclude a few characteristics before using the classification algorithm.

Advantages

A popular characteristics selection approach, RFE (Recursive Feature Elimination) prioritizes training dataset features (columns) based on their predictive power for the target variable. Data from patients, including age, blood pressure, and test results, may be used to automate the computer-assisted diagnosis of chronic kidney disease (CKD). Using the SVM method, Yu et al. [2] were able to identify and predict whether patients will develop diabetes or pre-diabetes.

SYSTEM ARCHITECTURE



4. IMPLEMENTATION

Modules

Service Provider

To access this module, the Service Provider has to provide a valid username and password. There are a number of things he can do when he signs in, such as access training and test data sets, Verify the Accuracy of Training and Testing by Looking at the Bar Chart. Check out the Results of the Accuracy Tests and Training, Learn about kidney illness, its prevalence, and all the information that points to a diagnosis, then get your hands on training data sets. Take a Look at the Kidney Disease Ratio and All Remote Users.

View and Authorize Users

All users who have registered for this module may be seen by the administrator. Users' names, email addresses, and physical addresses are viewable to the administrator, who may also authorize users.

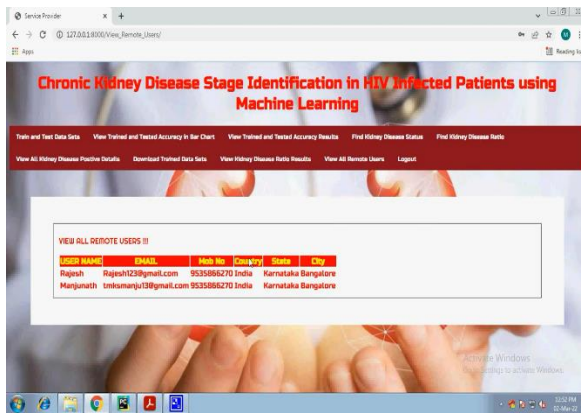
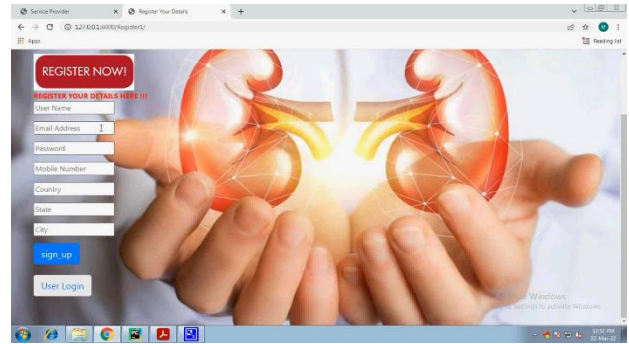
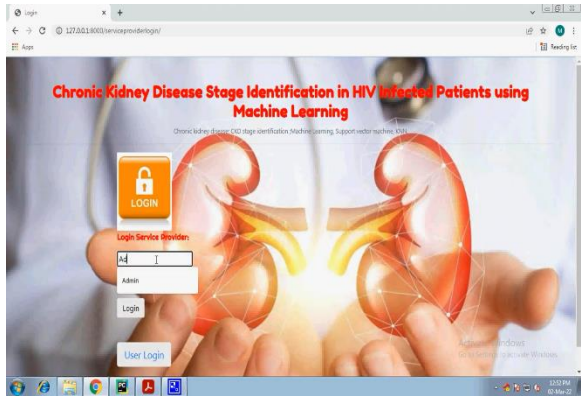
Remote User

In this module, you will find n users. The user must register before they may begin any activity. Upon registration, the user's details are stored in the database. He will be prompted to enter his approved username and password after he successfully registers. After logging in, the user will be able to access features like the "ADVANCED PAGE," "POST DIABETIC DATA SETS," and more.

5. SCREEN SHOTS

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id	age	sex	bp	cho	glu	hba1c	creatinine	gfr	hct	hematocrit	hemoglobin	hemoglobinA1c	hemoglobinA1cStandardized	potassium	totalBilirubin	totalCholesterol	totalProtein	triglycerides	uricAcid	weight
R0R0R0Y95697344	48	M	102	1	0	normal	normal	notpresent	notpresent	121	36	1.2	138	11	184	64	44	31		76
R0R0R0Y95697366	7	SO	102	4	0	normal	normal	notpresent	notpresent	230	18	0.8	117	17	113	38	66			66
R0R0R0Y95697366	62	BO	101	2	3	normal	normal	notpresent	notpresent	423	53	1.8	138	41	9.6	31	71			71
R0R0R0Y95697389	48	70	1005	4	0	normal	abnormal	present	notpresent	117	56	3.8	111	2.5	112	32	6			66
R0R0R0Y95697416	51	BO	101	2	0	abnormal	normal	notpresent	notpresent	105	26	1.6	138	17	116	35	72			72
R0R0R0Y95697477	60	SO	1015	3	0	abnormal	abnormal	notpresent	notpresent	76	25	1.1	142	5.2	122	39	71			71
R0R0R0Y95697487	58	70	101	0	0	normal	normal	notpresent	notpresent	100	54	24	104	4	124	36	75			75
R0R0R0Y95697536	24	NO	1015	2	4	normal	abnormal	notpresent	notpresent	410	31	1.1	138	31	124	44	61			61
R0R0R0Y95697535	52	100	1015	3	0	normal	abnormal	present	notpresent	138	60	1.9	138	3.9	10.8	33	91			91
R0R0R0Y95697572	53	NO	102	2	0	abnormal	abnormal	present	notpresent	70	107	72	114	3.7	9.5	29	12			12
R0R0R0Y95697586	50	SO	101	2	4	abnormal	abnormal	present	notpresent	430	55	4	138	4.5	5.4	28	77			77
R0R0R0Y95697531	63	70	101	3	0	abnormal	normal	present	notpresent	380	60	2.7	131	4.2	10.8	32	44			44
R0R0R0Y956975047	68	70	1015	3	1	abnormal	normal	present	notpresent	208	72	2.1	138	5.8	9.7	28	12			12
R0R0R0Y956975024	68	70	102	2	1	abnormal	abnormal	notpresent	notpresent	98	86	4.6	135	3.4	9.8	44	71			71
R0R0R0Y956975060	68	BO	101	3	2	normal	abnormal	present	present	157	90	4.1	130	0.6	5.6	16	111			111
R0R0R0Y956975077	40	NO	1015	3	0	normal	normal	notpresent	notpresent	78	162	9.8	141	4.9	7.8	24	31			31

```
def main():  
    # Load data  
    data = pd.read_csv('data.csv')  
    # Feature engineering  
    data['log_bun'] = np.log(data['bun'])  
    data['log_creat'] = np.log(data['creatinine'])  
    data['log_gfr'] = np.log(data['gfr'])  
    data['log_hct'] = np.log(data['hct'])  
    data['log_hemoglobin'] = np.log(data['hemoglobin'])  
    data['log_hemoglobinA1c'] = np.log(data['hemoglobinA1c'])  
    data['log_potassium'] = np.log(data['potassium'])  
    data['log_totalBilirubin'] = np.log(data['totalBilirubin'])  
    data['log_totalCholesterol'] = np.log(data['totalCholesterol'])  
    data['log_triglycerides'] = np.log(data['triglycerides'])  
    data['log_uricAcid'] = np.log(data['uricAcid'])  
    data['log_weight'] = np.log(data['weight'])  
    # Train-Test Split  
    X = data[['log_bun', 'log_creat', 'log_gfr', 'log_hct', 'log_hemoglobin', 'log_hemoglobinA1c', 'log_potassium', 'log_totalBilirubin', 'log_totalCholesterol', 'log_triglycerides', 'log_uricAcid', 'log_weight']]  
    y = data['stage']  
    X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=42)  
    # Model Training  
    model = LogisticRegression()  
    model.fit(X_train, y_train)  
    # Model Evaluation  
    y_pred = model.predict(X_test)  
    accuracy = accuracy_score(y_test, y_pred)  
    print('Accuracy: %f' % accuracy)
```

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    data['log_totalCholesterol'] = np.log(data['totalCholesterol'])  
    data['log_triglycerides'] = np.log(data['triglycerides'])  
    data['log_uricAcid'] = np.log(data['uricAcid'])  
    data['log_weight'] = np.log(data['weight'])  
    # Train-Test Split  
    X = data[['log_bun', 'log_creat', 'log_gfr', 'log_hct', 'log_hemoglobin', 'log_hemoglobinA1c', 'log_potassium', 'log_totalBilirubin', 'log_totalCholesterol', 'log_triglycerides', 'log_uricAcid', 'log_weight']]  
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```

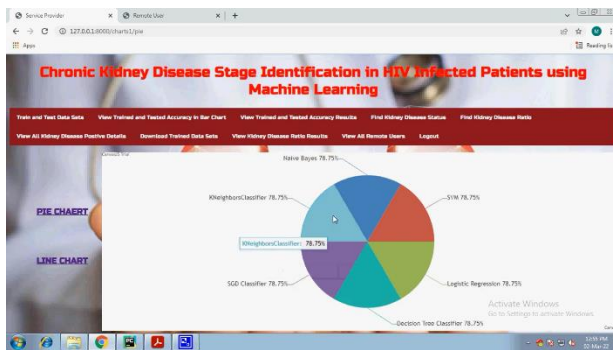
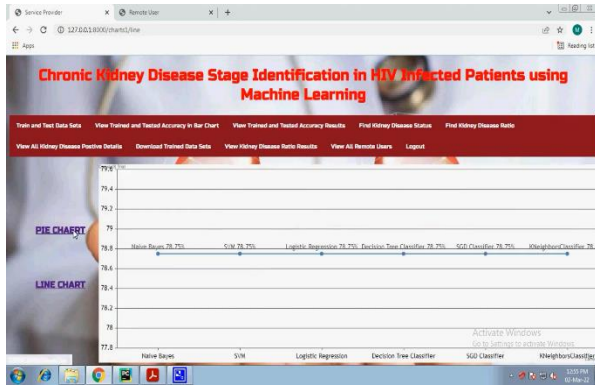


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    data['log_hct'] = np.log(data['hct'])  
    data['log_hemoglobin'] = np.log(data['hemoglobin'])  
    data['log_hemoglobinA1c'] = np.log(data['hemoglobinA1c'])  
    data['log_potassium'] = np.log(data['potassium'])  
    data['log_totalBilirubin'] = np.log(data['totalBilirubin'])  
    data['log_totalCholesterol'] = np.log(data['totalCholesterol'])  
    data['log_triglycerides'] = np.log(data['triglycerides'])  
    data['log_uricAcid'] = np.log(data['uricAcid'])  
    data['log_weight'] = np.log(data['weight'])  
    # Train-Test Split  
    X = data[['log_bun', 'log_creat', 'log_gfr', 'log_hct', 'log_hemoglobin', 'log_hemoglobinA1c', 'log_potassium', 'log_totalBilirubin', 'log_totalCholesterol', 'log_triglycerides', 'log_uricAcid', 'log_weight']]  
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    # Model Training  
    model = LogisticRegression()  
    model.fit(X_train, y_train)  
    # Model Evaluation  
    y_pred = model.predict(X_test)  
    accuracy = accuracy_score(y_test, y_pred)  
    print('Accuracy: %f' % accuracy)
```



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ID	age	sex	hemoglobin	serum creatinine	...																	
R00001950097341	48	80	1.02	1	0	normal	normal	notpresent	notpresent	121	36	1.2	130	3.1	15.4	44	7000	5.2	yes	no	good	no
R00001950097096	7	50	1.02	4	0	normal	normal	notpresent	notpresent	236	18	8.0	131	3.7	11.3	38	6000	4.4	no	no	good	no
R00001950097096	62	80	1.01	2	0	normal	normal	notpresent	notpresent	423	53	1.8	130	4.1	9.6	31	7000	4.4	no	yes	poor	no
R00001950097789	48	70	1.002	4	0	normal	abnormal	present	notpresent	117	56	3.8	111	2.9	11.2	32	6700	3.9	yes	no	poor	yes

6. CONCLUSION

Both patients and doctors may benefit greatly from the classification of chronic kidney disease stages in HIV-positive patients, as it helps them make early and appropriate clinical choices. In this work, we have examined the efficacy of the

most recent machine learning algorithms in conjunction with DNN for the categorization of CKD in HIV-positive patients. According to our research, DNN has done better in the categorization of CKD. We've also shown how to utilize the EGFR calculation to determine a disease's stage. In the future, diagnosis based on various imaging modalities may be supported by combining features-based DNN with medical image analysis.

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