Chronic Kidney Disease Diagnostic Approaches using Efficient Artificial Intelligence methods

Avulapati Swetha [1], M. Sri Lakshmi [2], M. Rudra Kumar [*3]

Abstract: Many people worldwide are afflicted with kidney illnesses today. Thus, the primary purpose of this research is to employ several computational-based methods to categorize and diagnose Chronic Kidney Disease. Our analysis relied on data on a chronic renal disease made available to the general population. Chronic renal disease was divided into two categories with the help of eight classifiers (patient or not). For this, we employed RapidMiner Studio 9.8, which ran on the operating system Windows 10. Some performance metrics were produced to evaluate the strategies; the confusion matrix gives us the TP, FP, FN, and TN values. The evaluation of the data mining techniques showed that the accuracy rates of 99.09%, 98.04%, and 96.52% were achieved by Random Forest, Deep Learning network, and Neural Network, respectively. It is worth noting, however, that the AUC for the Deep Learning network, Support Vector Machine, and Random Forest are all equalled. Among the most effective data analysis methods is data mining, which has proven particularly valuable in medicine. These categorization strategies help doctors make more accurate diagnoses by revealing hidden patterns in the data.

Keywords: Machine Learning, Data Mining, Supervised Technique, Chronic Kidney Disease.

1. Introduction

Chronic Kidney Disease (CKD) can cause renal failure, dialysis, transplantation, cardiovascular disease, and early mortality. This disease's incidence and death are rising. Following the Global Burden of Disease (GBD) study, from 1990 to 2016, CKD prevalence rose 87%, and death rose 98% to 1,186,561. Disability-adjusted-life-years (DALYs) rose 62% to 35,032,384 in low- and middle-income nations. Chronic disease management is difficult; CKD patients face several issues. They must follow treatment plans, learn dialysis methods, and adapt to complications and therapies. These patients will encounter psychological issues, affecting their life quality. Untreated CKD will advance.

End-Stage-Renal-Disease (ESRD) has problems including dialysis and transplantation. Nephrology and kidney transplant have complications at this phase of the disease, increasing mortality [15]. Early identification of kidney illness allows for preventative strategies and treatments. Data mining can aid with early kidney disease diagnosis.

Data mining extracts patterns from vast datasets [4]. Health and medical data can yield significant insights. Healthcare is a data-rich industry. Health records and administration reports generate enormous data daily in healthcare organizations. This rich data is rarely utilized, and doctors rely on their expertise. Disease diagnosis and prognosis can use medical data patterns and knowledge. Many researchers have used data mining to diagnose diseases, define disease stages, propose therapeutic alternatives, and anticipate disease prevalence and death. Health data can be transformed into information using data mining techniques. Data mining can help doctors diagnose kidney illness by revealing hidden patterns in patient data. Rady and Anwar used PNN, MLP, SVM, and RBF to predict renal disease stages. This study included 361 Indian CKD patients and 25 factors. The PNN algorithm has 96.7% accuracy, according to the evaluation. The MLP algorithm has the lowest accuracy (51.5%). Nave Bayes and SVM were used to predict kidney illness in one study. This study used 584 kidney function test (KFT) samples and six characteristics. SVM predicted kidney illness more accurately than Nave Bayes [24]. These two algorithms successfully diagnosed 70% of cases.

Decision Tree is a disease-diagnosis method. The Decision Tree algorithm was invented. This study used the UCI Repository dataset, which includes 400 samples, 24 attributes, and one class. Eleven features were numerical, while 14 were nominal. The "Haemoglobin" property was

[1]*M.Tech Student, Department of Computer Science and Engineering, G. Pullaiah College of Engineering and Technology, (Autonomous), Kurnool Email: avulapatiswetha15@gmail.com.*

[2] *M. Sri Lakshmi, Sr. Assistant professor, Department of Computer Science and Engineering, G. Pullaiah College of Engineering and Technology, Kurnool. Email: srilakshmicse@gpcet.ac.in*

[3] *M. Rudra Kumar, Professor, Department of CSE, GPCET, Kurnool. Email: mrudrakumar@gmail.com*

* Corresponding Author Email: mrudrakumar@gmail.com

key in diagnosing the condition. Chronic renal disease's rising prevalence harms people's quality of life. It reduces life expectancy and harms health. Due to the increasing prevalence of chronic kidney disease, this study aims to diagnose the ailment using data mining methods. This study classifies Chronic Kidney Disease patients and applies data mining techniques to a public dataset. Eight categorization methods were established. We employed eight common and complicated algorithms to categorize people as healthy or sick. This study calculated and compared most classifier performance indicators.

2. Materials and Methods

Figure 1 depicts data mining. First, data was prepared for the model. Next, the data were split into training and testing. In training, input determines output for the dataset. Testing examines model performance and defines instance labels [5].
Data processing steps are shown in Fig 1. Explained about the raw level data process to the model building and evaluation process
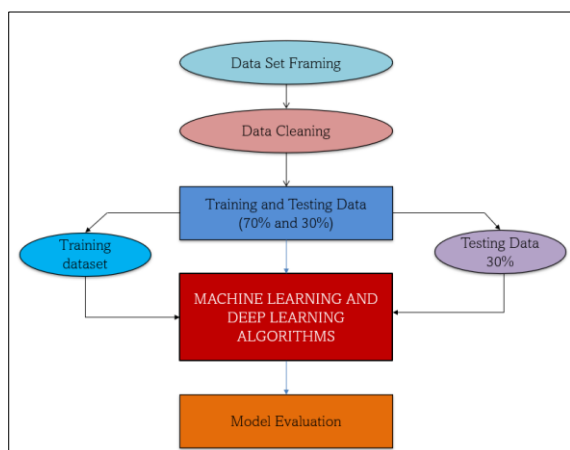

Figure 1- Data Modeling

2.1. Dataset

This research used publicly available CRD data from Kaggle. This dataset contains 250 patients and 150 healthy records; there are 24 attributes, 120 numeric, and ten nominals, and the selection is a class label. We replaced missing numbers in this dataset with the average. The model was used to substitute missing nominal data. Table 1 lists data features.

2.2. Machine learning algorithms

In this research, we used eight different algorithms to categorize patients with chronic kidney disease into two groups: Random Forest, SVM, KNN, Deep learning, Auto-MLP, Naive Bayes, Neural Net, and Decision Tree (patient or not) [3][13]. The following methods were applied to the dataset we selected: Using the criteria of gain ratio, the

maximum depth of the tree is 20, the minimum depth is 0.02, and the confidence level is 0.2. Random Forest (Gini index as a criterion, maximum depth of 20 nodes, and 200 trees total). In this case, we'll use Auto-MPL with a training cycle of 20 iterations. With a Deep Learning Net (Activation=rectifier, epochs=20, five hidden layers, and 80 neurons), the network can quickly learn very complex data structures. Neural Network (200 training cycles, 0.04% training rate, 0.9% momentum, and a hidden layer of 1). Ignorant Bayes. The Support Vector Machine and the K-Nearest Neighbors algorithm (k=5, Measure types=Mixed Measures, kernel cache=400, and maximum iteration=400000) were used. We conducted our analyses on a PC running Windows 10, and we used RapidMiner Studio 9.8.[1]

2.3. A Measurement of the Model's Effectiveness

The primary focus of our work was a comparison of the various performance indicators for each method. Algorithm performance can be measured in several ways, including accuracy, precision, sensitivity, specificity, mean absolute error (MAE), and Area under the ROC-Curve (AUC). The values for TP, FP, FN, and TN can be found in the confusion matrix. The following are the equations for the indicators: (y_i = estimate x_i = actual value n = total number of observations) True positive (TP), true negative (TN), false positive (FP), and false negative (FN).

Our analysis in RapidMiner began with 10-fold cross-validation of the data set. After that, we learned how we had fared in our assessments [14]. Dataset selection criteria were data split into a training set and a test set; the training set was used to inform the test set to construct multiple classifiers. Finally, a test set was used to verify their accuracy. We did the training and the testing. split-step cross-validation procedures (70% training, 30% testing). The result is equivalent to a 0.7:1 sample ratio and was achieved through stratified sampling. In other words, it's a data sample.
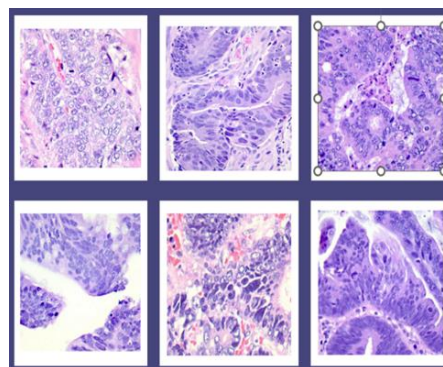
3. Results

Figure 2- Colon_ACA categorized Cancer Images

Before the analysis, part visualized the various cancer images using OpenCV methods and models. She has shown in Fig 2 and 3.
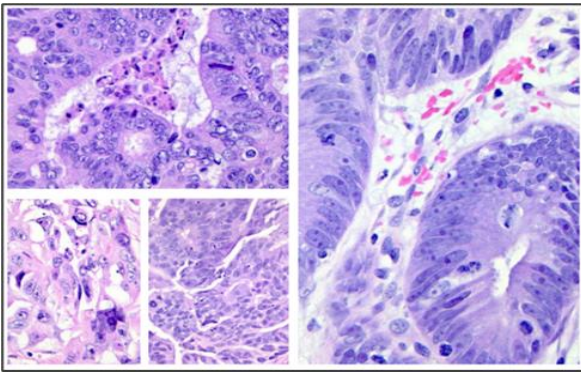

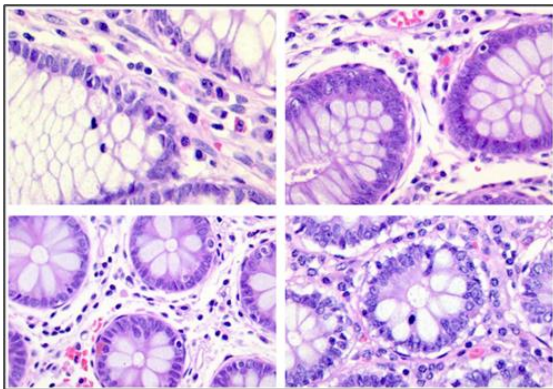**Figure 3-** Colon_ACA categorized Cancer Images

Figure 4- Lung SCC_ Cancer Images

Figure 4 shows the much-elaborated images of cancer images.

Machine Learning and Deep Learning based Algorithms based Analytics and Performance measures

The steps involved in this research are:

- Data gathering
- Data Analysis - Visualization
- Pre – Processing
- Insights extraction / Feature Extraction
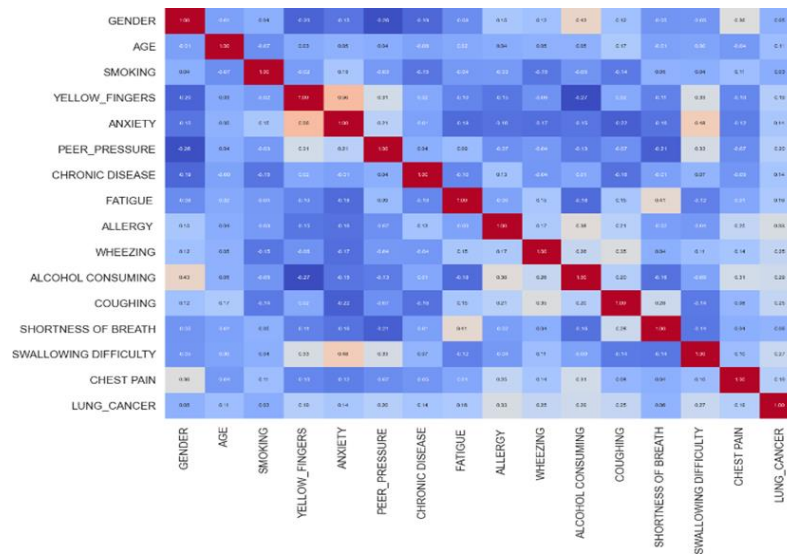- Model Building
- Results Analysis

Figure 5- Correlation between the features

4. Discussion

The enormous increase in the prevalence of chronic kidney disease, as well as its consequences, complications, and the huge expenses it imposes on society, have prompted medical professionals to seek out programs for further research, prevention, early identification, and effective treatment [21]. Knowledge gained through data mining and discovery can be utilized to enhance the care offered by medical facility administrators and help doctors predict how their kidney patients will behave in the future [6]. The most important uses of data mining and information retrieval in the kidney patients' system are making predictions based on a given history, making diagnoses based on various traits and symptoms, and assessing risk factors [10]. This research aimed to categorize CKD patients and make timely diagnoses using different potent machine learning techniques [2]. This paper uses the CKD-related dataset hosted in the Kaggle repository. Our study

stands out from the crowd because we use eight computationally robust methods to fill in the blanks, including RF, NB, ANN, DNN, SVM, AutoML, K-NN, and DT, which get excellent and impressive results. Interesting in this research is the employment of eight robust algorithms for data mining to divide the population into healthy and ill categories. Researchers did a study in which they used SVM technology combined with feature selection strategies to detect chronic kidney disease by reducing the inputs' dimensionality [7].
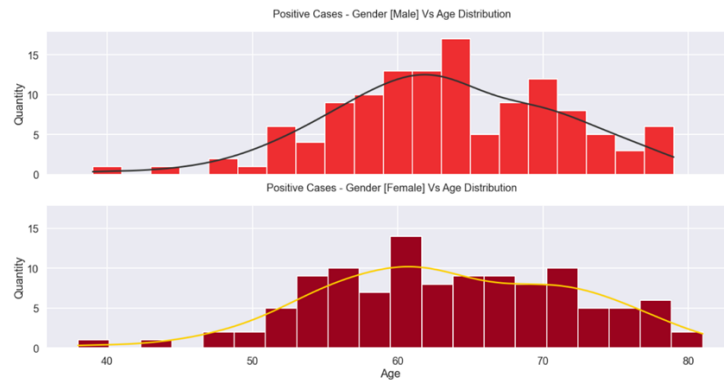

Figure 6- Age and Gender base Lung Cancer Effectiveness
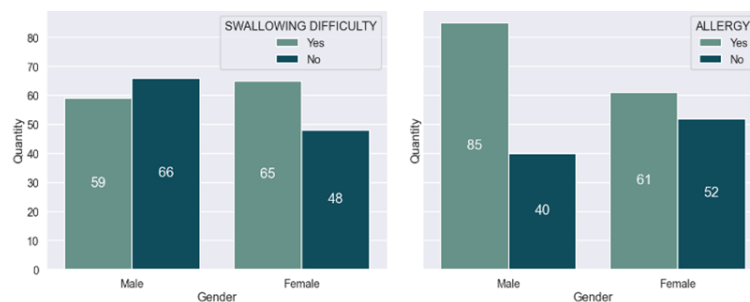

Figure 7- Gender with Swallowing and Allergy based Lung Cancer Effectiveness measuring

After feature selection via wrapping and filtering, SVM achieved 0.96, 0.1, 0.96, and 0.98 in terms of TP, FP, Precision, and AUC; the prediction accuracy of SVM by 13 attributes was maximum value (95.5%). SVM, like our work, showed promising results in classifying CKD patients than in healthy individuals and predicting which patients would develop the disease [11]. Manages non-linear classification rules while mapping data into high feature space, which improves generalization capability. Our approach differs significantly from that described in this paper since we employ feature selection techniques.

Advantages of using feature selection include lowering learning time, eliminating noise and duplicating data, and discarding irrelevant data. There may be costs associated with utilizing this strategy, such as an increased risk of over-fitting and increased computational complexity. In our research, we favored utilizing all characteristics for classification to ensure that no information was lost and that the feature space was not constrained. Notably, the dataset utilized in this study was identical to the one we used in our own, the only difference between our study and the one in question was that ours made use of feature selection. Accurate CKD diagnosis was accomplished using five different classifiers (MLP, SVM, K-NN, C4.5,

and RF). Our research made use of the CKD dataset. C4.5 and Random Forest Classifier were run using their default settings for this research [8]. With K-NN, we used a value of k = 1; with ANN, we used a value of 0.3 for the learning rate and 0.2 for the momentum, and we used a hidden layer size of ten nodes; and with SVM, we used C = 100 and L = 0.001 with a poly kernel. According to the outcomes, RF has the highest values for performance indicators, with all computed measures reaching 100%. Highest accuracy, recall, precision, and Area under the curve (AUC) are all maximized using random forest in our work. Compared to other methods, RF requires little time to train and test and has a lower susceptibility to overfitting. This means that its computation is significantly more involved than that of other methods for machine learning [20]. High-accuracy and cost-effective methods for distinguishing between ill and healthy individuals, such as support vector machines (SVMs), artificial neural networks (ANNs), and decision trees (DTs)[17], have been created. Comparable work has been done using RapidMiner and 400 clinical records obtained from the Kaggle public repository. We analyzed the data using eight different classification methods, though. As we found, the accuracy of Nave Bayes, ANN, and DNN improved after RF, whereas that of K-NN and SVM decreased [18]. Our findings suggest that K-subpar NN's performance can be explained by its inability to

handle high-dimensional datasets, as well as by the fact that it necessitates a feature scaling or normalization operation before it can be applied. Furthermore, in our study, we evaluate the performance measures of SVM classifier to provide reliable ratings. With a performance overall of 93.69%, our experimental findings demonstrated that SVM can be successfully applied, matching the performance achievement for SVM in the aforementioned work (94.60%). The findings of the survey indicate that this classifier has the potential to perform better in high-dimensional spaces, such as our preferred dataset, while still being relatively memory efficient. In, a support vector machine (SVM) predictor was applied to the CKD dataset with the primary goal of evaluating its performance in terms of accuracy, precision, and runtime [22]. The SVM assessment measure was reported to be 94.6. Both experiments employed the same dataset, and the claimed accuracy for SVM was nearly identical across the two. This classifier cannot be further compared without knowing the parameters that were utilized. The CKD datasets from the UCI repository for machine learning was used for this analysis; it has 400 samples and 24 characteristics [20]. Both the accuracy and the time required by an algorithm can be affected by the specifics of the dataset being used [23]. The following are some of the features of the information that have an impact on the algorithm's efficiency: The sample size of 400 used in this analysis is considered to be enough, since it prevents a drop in classifier efficiency and a rise in classification error. The efficiency of a given approach may change depending on whether the classes in question are binary, many, or categorical. In this analysis, we simplified the model by splitting the output class into two categories: patients and healthy people. Class without labels: in the current investigation, there was no such thing as an unlabeled class, which can be useful for improving the classifiers' accuracy. It is important to handle missing values during the preprocessing phase, as they can hinder the efficiency of the
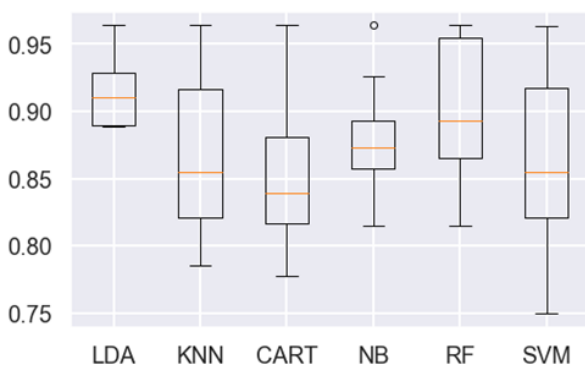
of classes: the more classes there are, the more complicated the model may become. This study uses 24 characteristics, which can be lowered in future research with dimensionality reduction tools like principal component analysis or Fuzzy Toolkit. Important and effective classification methods for disease diagnosis were created and compared in this study utilizing a set of carefully chosen markers [19]. Among the many approaches tested, the results indicated that Random Forest, Deep Learning Network, Artificial Neural Net, and Naive Bayes methods had the highest potential for distinguishing healthy individuals from those with disease [9]. Missing data in the dataset were identified as a potential weakness of our work, and researchers chose to replace them in with plausible estimates. To increase the work's impact and credibility, as well as to facilitate comparisons with existing work, researchers hope to make use of a local dataset in future directions.
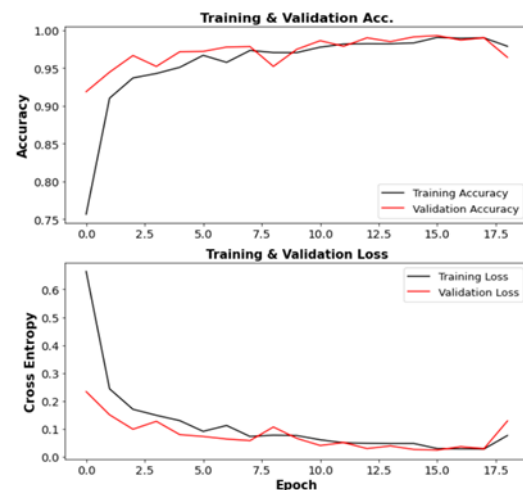

Figure 9- Deep Learning Neural networks training and validation result.

Performance parameters accuracy report

Figure 10- Accuracy report of the Deep learning based neural network algorithm.

4.1. Key Understandings from the research

Lung cancer, a subtype of cancer, begins in the lungs and, if it is not treated, can spread to other parts of the respiratory system. Lung cancer is the most common form of cancer in the United States. Whenever you take a breath

Figure 8- Algorithms results comparative chart

algorithms being used. The preprocessing phase of this study accounted for missing data [16]. The dimensionality

in, oxygen enters your respiratory system and is transported all the way to your lungs from there. On the other hand, carbon dioxide is released from the body during the process of exhalation. That which we refer to as our lungs are a pair of sponge-like organs that are housed in our chest cavities and go by the name of lungs. Lung cancer accounts for the deaths of the vast majority of people who have been diagnosed with the disease, and this statistic holds true no matter where you go in the world.

People who have never smoked but still have a chance of developing lung cancer have a lower risk of developing the disease compared to people who have never smoked but still have a chance of developing lung cancer. People who have never smoked but still have a chance of developing lung cancer have a lower risk of developing the disease. Despite this fact, people who have never smoked still run the risk of developing lung cancer in their lifetimes. A greater number of cigarettes smoked over the course of time as well as the length of time that a person has smoked cigarettes are both factors that contribute to an increased risk of developing lung cancer in a person. Similarly, the length of time that a person has smoked cigarettes also contributes to an increased risk of developing lung cancer. Quitting smoking at any point in time, regardless of how long you've been a smoker or how many packs of cigarettes you've smoked per day, can result in a significant reduction in the likelihood that you'll develop lung cancer. This is true even if you've been smoking for a long time or how many packs of cigarettes you've smoked per day. Most cases of lung cancer can be attributed to cigarette smoking.

Initial Symptoms

There are almost never any obvious signs or symptoms produced by lung cancer when it is in its earliest stages. Clinical symptoms of lung cancer don't appear until the disease has already advanced to a significant degree.

- There is a possibility that some of the following signs and symptoms are associated with lung cancer:
- Recent onset of a hacking cough that just won't quit.
- Even spitting up a very small amount of blood can put you in danger.
- A sensation that it is difficult to breathe
- Chest pain
- A reduction in weight that occurs naturally and unintentionally, hoarseness is.
- Bone pain
- Headache

When would be the most convenient time to make an appointment to speak with a qualified medical professional?

You should make an appointment with your primary care physician as soon as you are able to if you are experiencing any signs or symptoms that do not go away, especially if they are causing you concern, and you should do so as soon as you are able to after you are able to do so. Seek medical attention if you are experiencing any signs or symptoms that do not go away, especially if they are causing you concern. This is especially important if the signs or symptoms worry you [25],[26].

If you have tried to quit smoking more than once but have been unsuccessful in doing so, it is in your best interest to schedule an appointment with your primary care physician as soon as possible. If you keep smoking, there is a chance that you could damage your health. Your primary care physician may suggest that you participate in counselling, take certain medications, or use products that contain nicotine replacement therapy in order to help you kick the habit of smoking. Alternatively, he or she may suggest using products containing nicotine replacement therapy [27],[28].

Determinants of risk

The risk that you will develop lung cancer depends on a variety of factors, some of which you have no control over. Quitting smoking is one example of a risk factor that can be managed by taking preventative action. Other examples include eating a healthy diet and exercising regularly. For instance, you do not have any influence over the history of your family. This is not something you can change.

The following is a list of some of the risk factors that are associated with lung cancer:

Smoking. The length of time you have been a smoker, in combination with the number of cigarettes you smoke on a daily basis, is the single most important factor in determining your risk of developing lung cancer. Quitting smoking at any point in your life can make a significant difference in lowering the risk that you will develop lung cancer.

Inhalation of secondhand smoke on a continuous basis. Even if you don't smoke yourself, your risk of developing lung cancer will be higher if you are exposed to secondhand smoke because of other people's smoking.

Radiation therapy administered at a previous time. If you have previously been treated for another type of cancer with radiation therapy to the chest, there is a possibility that your risk of developing lung cancer is increased. This is the case if you have a history of smoking.

Exposure to Radon gas. Radon is produced when uranium breaks down naturally in rocks, soil, and water. Radon eventually becomes a component of the air that people breathe and can be harmful to their health. Any structure, including homes, has the potential to accumulate dangerous levels of radon over time. This includes private residences.

Because asbestos and other cancer-causing substances are found in the natural environment. It is possible that your risk of developing lung cancer will increase if you are a smoker and if you are exposed to asbestos and other substances that are known to cause cancer, such as arsenic, chromium, and nickel. This is especially important to keep in mind if you have a job that puts you in contact with asbestos.

A previous diagnosis of lung cancer in family members. People who have a parent, sibling, or child who has been diagnosed with lung cancer have a greater chance of developing the disease themselves. This increased risk is especially true for people who have smoked cigarettes throughout their lives.

5. Conclusion

In Using one of the many methods that are available for data mining, the individuals who took part in this investigation were assigned to one of two categories: healthy or ill. The findings of the evaluation of the methods that had been previously established demonstrated that the methods that were produced have an excellent accuracy in identifying CKD. These techniques, which make use of the vast amounts of data produced in the healthcare industry, can make a contribution to the accurate diagnosis of kidney disease in a number of different ways. In an ever-growing data pool, the application of such methods may help in the discovery of previously undetected patterns, which may ultimately lead to a reduction in the level of perplexity experienced by physicians. If the symptoms are recognized and treated in a timely manner, it is possible to completely reverse the effects of this disease. The diagnosis of CKD, which requires taking into account a great many different factors, can also benefit from the utilization of these techniques by primary care providers [12]. This is because the diagnosis of CKD requires considering a great many different factors.

References

[1]. T. N. Lakshmi, S. Jyothi, and M. R. Kumar, "Image Encryption Algorithms Using Machine Learning and Deep Learning Techniques—A Survey," in Modern Approaches in Machine Learning and Cognitive Science: A Walkthrough, Springer, 2021, pp. 507–515.

[2]. D. J. Reddy and M. R. Kumar, "Crop yield prediction using machine learning algorithm," in 2021 5th International Conference on Intelligent Computing and Control Systems (ICICCS), 2021, pp. 1466–1470.

[3]. S. Vijayarani, S. Dhayanand, and M. Phil, "Kidney disease prediction using SVM and ANN algorithms," Int. J. Comput. Bus. Res., vol. 6, no. 2, pp. 1–12, 2015.

[4]. F. Ma, T. Sun, L. Liu, and H. Jing, "Detection and diagnosis of chronic kidney disease using deep learning-based heterogeneous modified artificial neural network," Futur. Gener. Comput. Syst., vol. 111, pp. 17–26, 2020.

[5]. S. Rezayi, K. Maghooli, and S. Saeedi, "Applying Data Mining Approaches for Chronic Kidney Disease Diagnosis," Int. J. Intell. Syst. Appl. Eng., vol. 9, no. 4, pp. 198–204, 2021.

[6]. V. Kunwar, K. Chandel, A. S. Sabitha, and A. Bansal, "Chronic Kidney Disease analysis using data mining classification techniques," in 2016 6th International Conference-Cloud System and Big Data Engineering (Confluence), 2016, pp. 300–305.

[7]. P. Chittora et al., "Prediction of chronic kidney disease-a machine learning perspective," IEEE Access, vol. 9, pp. 17312–17334, 2021.

[8]. A. Subasi, E. Alickovic, and J. Kevric, "Diagnosis of chronic kidney disease by using random forest," in CMBEBIH 2017, Springer, 2017, pp. 589–594.

[9]. C. Kuruba, N. Pushpalatha, G. Ramu, I. Suneetha, M. R. Kumar, and P. Harish, "Data mining and deep learning-based hybrid health care application," Appl. Nanosci., pp. 1–7, 2022.

[10]. K. U. K. Reddy, S. Shabbiha, and M. R. Kumar, "Design of high security smart health care monitoring system using IoT," Int. J, vol. 8, 2020.

[11]. Y. Amirgaliyev, S. Shamiluulu, and A. Serek, "Analysis of chronic kidney disease dataset by applying machine learning methods," in 2018 IEEE 12th International Conference on Application of Information and Communication Technologies (AICT), 2018, pp. 1–4.

[12]. J. Qin, L. Chen, Y. Liu, C. Liu, C. Feng, and B. Chen, "A machine learning methodology for diagnosing chronic kidney disease," IEEE Access, vol. 8, pp. 20991–21002, 2019.

[13]. S. Sharma, V. Sharma, and A. Sharma, "Performance based evaluation of various machine learning classification techniques for chronic kidney disease diagnosis," arXiv Prepr. arXiv1606.09581, 2016.

[14]. A. Sobrinho, A. C. M. D. S. Queiroz, L. D. Da Silva, E. D. B. Costa, M. E. Pinheiro, and A. Perkusich, "Computer-aided diagnosis of chronic kidney disease in developing countries: A comparative analysis of machine learning techniques," IEEE Access, vol. 8, pp. 25407–25419, 2020.

[15]. N. Bhaskar and S. Manikandan, "A deep-learning-based system for automated sensing of chronic kidney disease," IEEE Sensors Lett., vol. 3, no. 10, pp. 1–4, 2019.

[16]. A. Al Imran, M. N. Amin, and F. T. Johora, "Classification of chronic kidney disease using logistic regression, feedforward neural network and wide \& deep learning," in 2018 International Conference on Innovation in Engineering and Technology (ICIET), 2018, pp. 1–6.

[17]. V. Chaurasia, S. Pal, and B. B. Tiwari, "Chronic kidney disease: a predictive model using decision tree," Int. J. Eng. Res. Technol., 2018.

[18]. H. Polat, H. Danaei Mehr, and A. Cetin, "Diagnosis of chronic kidney disease based on support vector machine by feature selection methods," J. Med. Syst., vol. 41, no. 4, pp. 1–11, 2017.

[19]. Krishnaveni, S. ., A. . Lakkireddy, S. . Vasavi, and A. . Gokhale. "Multi-Objective Virtual Machine Placement Using Order Exchange and Migration Ant Colony System Algorithm". International Journal on Recent and Innovation Trends in Computing and Communication, vol. 10, no. 6, June 2022, pp. 01-09, doi:10.17762/ijritcc.v10i6.5618.

[20]. G. Seeja, O. Reddy, K. V. R. Kumar, S. Mounika, and Others, "Internet of Things and Robotic Applications in the Industrial Automation Process," in Innov. Ind. Internet Things Smart Fact., IGI Global, 2021, pp. 50–64.

[21]. Agarwal, D. A. . (2022). Advancing Privacy and Security of Internet of Things to Find Integrated Solutions. International Journal on Future Revolution in Computer Science &Amp; Communication Engineering, 8(2), 05–08. https://doi.org/10.17762/ijfrcsce.v8i2.2067

[22]. S. D. Bhogaraju, K. V. R. Kumar, P. Anjaiah, J. H. Shaik, and Others, "Advanced Predictive Analytics for Control of Industrial Automation Process," in Innov. Ind. Internet Things Smart Fact., IGI Global, 2021, pp. 33–49.

[23]. M. K. Satheesh and K. V. R. Kumar, "Addressing the Utilization of Popular Regression Models in Business Applications," in Machine Learning for Business Analytics, Productivity Press, pp. 29–43.

[24]. André Sanches Fonseca Sobrinho. (2020). An Embedded Systems Remote Course. Journal of Online Engineering Education, 11(2), 01–07. Retrieved from http://onlineengineeringeducation.com/index.php/joee/article/view/39

[25]. K. Hemachandran et al., "Artificial Intelligence: A Universal Virtual Tool to Augment Tutoring in Higher Education," Comput. Intell. Neurosci., vol. 2022, 2022.

[26]. K. V. R. Kumar, A. A. Zachariah, and S. Elias, "Quantitative Analysis of Athlete Performance in Artistic Skating using IMU, and Machine Learning Algorithms.," DesignEngineering, no. 9, pp. 11236–11252, 2021, [Online]. Available: http://thedesignengineering.com/index.php/DE/article/view/8244.

[27]. Baes, A. M. M. ., Adoptante, A. J. M. ., Catilo, J. C. A. ., Lucero, P. K. L. ., Peralta, J. F. P., & de Ocampo, A. L. P. (2022). A Novel Screening Tool System for Depressive Disorders using Social Media and Artificial Neural Network. International Journal of Intelligent Systems and Applications in Engineering, 10(1), 116–121. https://doi.org/10.18201/ijisae.2022.274

[28]. E. M. K. Reddy, A. Gurrala, V. B. Hasitha, and K. V. R. Kumar, "Introduction to Naive Bayes and a Review on Its Subtypes with Applications," Bayesian Reason. Gaussian Process. Mach. Learn. Appl., pp. 1–14, 2022.

[29]. Madapuri, Rudra Kumar, and P. C. Mahesh. "HBS-CRA: scaling the impact of change request towards fault proneness: defining a heuristic and biases scale (HBS) of change request artefacts (CRA)." Cluster Computing 22.5 (2019): 11591-11599

[30]. Al Rubaiei, M. H., Jassim, H. S., & Sharef, B. T. (2022). Performance analysis of black hole and worm hole attacks in MANETs. International Journal of Communication Networks and Information Security (IJCNIS), 14(1). https://doi.org/10.17762/ijcnis.v14i1.5078

[31]. Rudra Kumar, M., Rashmi Pathak, and Vinit Kumar Gunjan. "Machine Learning-Based Project Resource Allocation Fitment Analysis System (ML-PRAFS)." *Computational Intelligence in Machine Learning*. Springer, Singapore, 2022. 1-14

[32]. Kumar, M. Rudra, Rashmi Pathak, and Vinit Kumar Gunjan. "Diagnosis and Medicine Prediction for COVID-19 Using Machine Learning Approach." *Computational Intelligence in Machine Learning: Select Proceedings of ICCIML 2021* 834 (2022): 123

[33]. Satish, A. B. ., & Rechanna, D. (2022). An Empirical Study on the Impact of HRD Practices on NPOs in Utilizing Foreign Contributions Received. International Journal of New Practices in Management and Engineering, 11(01), 01–14. https://doi.org/10.17762/ijnpme.v11i01.143

[34]. Suneel, Chenna Venkata, K. Prasanna, and M. Rudra Kumar. "Frequent data partitioning using parallel mining item sets and MapReduce." International Journal of Scientific Research in Computer Science, Engineering and Information Technology 2.4 (2017)