Diagnosis of Chronic Kidney Disease
Using Machine Learning Algorithm

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Abstract:

A large percentage of people globally suffer from chronic kidney disease (CKD), a serious health concern. Effective diagnosis, treatment, and referral of CKD depend heavily on early identification and prediction of the disease. However, it is difficult to evaluate and derive significant insights from health data due to its vast and complicated nature. Engineers and medical researchers are using data mining techniques and machine learning algorithms to create predictive models for chronic kidney disease (CKD) in an effort to address this issue. The goal of this research is to create and validate predictive models for chronic kidney disease (CKD) based on a variety of clinical factors, including albuminuria, age, diet, eGFR, and pre-existing medical problems. The objective is to estimate the likelihood of renal failure, which may necessitate kidney dialysis or a transplant, and to evaluate the degree of kidney disease. With the use of this knowledge, patients and healthcare providers should be able to make well-informed decisions about diagnosis, treatment, and lifestyle changes. Patterns in the gathered data can be found, and future incidence of CKD or other related diseases can be predicted, by utilising MLT such as ANN and data mining techniques. Finding novel characteristics linked to the onset of renal disease and adding more trustworthy data from CKD patients. The best algorithm to categorise the data as CKD or NOT_CKD is chosen throughout the design process, and the data is then classified according to this differentiation. Estimated glomerular filtration rate (eGFR), which offers important details about the patient's current kidney function, is used to classify cases of chronic kidney disease. By combining complete patient data with machine learning algorithms, this research advances the diagnosis of chronic kidney disease (CKD) and improves patient outcomes.

Keywords: *Chronic Kidney Disease (CKD), Feature identification, Glomerular filtration rate (eGFR), Prediction accuracy, Machine learning.*

Introduction

Chronic kidney disease (CKD) is a prevalent and serious health condition worldwide, often caused by underlying conditions such as diabetes and hypertension. Early Detection and Accurate prediction of CKD are crucial for implementing appropriate interventions and improving patient outcomes. Traditional approaches for diagnosing and monitoring CKD, such as estimated glomerular filtration rate (eGFR) and clinical markers, have limitations in capturing subtle changes in kidney function and providing comprehensive risk assessment. The goal of this research is to create and evaluate predictive models for chronic kidney disease (CKD), primarily focusing on assessing the likelihood of renal failure and the need for dialysis or kidney transplantation. These models inform medical providers about the severity of the disease, teach patients how to live a healthy lifestyle, and direct future treatment strategies. Through the application of artificial neural networks (ANN), data mining techniques, and pattern analysis of the gathered data, it is possible to forecast the probability of future occurrences of specific diseases, allowing for early intervention.

The suggested model seeks to forecast, from a person's lifestyle choices, the likelihood that they would develop chronic kidney disease. This data can assist determine whether an eGFR diagnosis of renal disease is necessary, which aids medical professionals in treating patients appropriately. When evaluating kidney function and the degree of chronic renal disease, the eGFR is an essential tool. Since blood filtration is the kidneys' main job, kidney illness frequently advances silently without causing any symptoms to become apparent. Considering the significant impact chronic kidney disease has on the world's health, it is critical to address the issue of those who cannot afford treatment not having access to it. The development of a serious sickness can be stopped by early diagnosis of the condition using reliable prediction models.

In this study, we use ML algorithms, DM strategies, and extensive patient data to overcome the shortcomings of conventional methods for CKD diagnosis and prediction. The discipline of managing renal illness could undergo a revolution with the creation of precise predictive models, which would allow for prompt interventions and enhance patient outcomes.

Methods

This study's researchers analysed a dataset pertaining to chronic kidney disorders using three distinct machine learning classifiers: logistic regression, decision trees, and support vector machines.
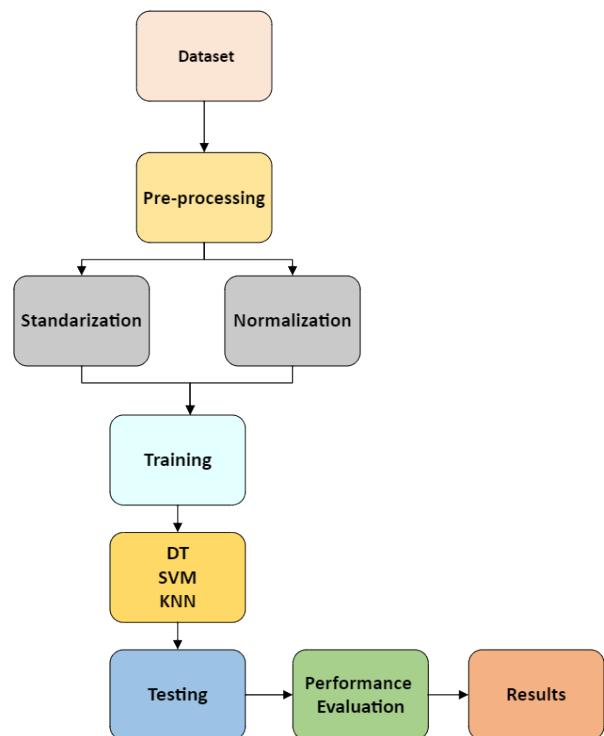

Figure 1. Block Diagram of Proposed Model
Source: visio.com

1.   **CKD datasets:** It provides an overview of the chronic kidney disease (CKD) dataset that the study employed. It offers details about the dataset's original source, the UCI machine learning repository. They might contain information on features, the quantity of occurrences, and any particular dataset attributes that are pertinent to the investigation.

2. **Data preprocessing**: They go over how the CKD dataset was preprocessed before the machine learning classifiers were used. Typically, it entails resolving any inconsistencies or inaccuracies in the data as well as handling missing values and outliers. Data preparation is done to make sure the dataset is clean.

3. **Standardization:** They concentrate on the CKD dataset's feature standardization method. The process of standardization entails converting the data to have a unit variance and zero mean. Scale discrepancies between features are reduced, which isbeneficial for some machine learning techniques.

4. **Normalization:** It describes the CKD dataset's normalization procedure. Scaling the features to a particular range—typically between 0 and 1—is known as normalization. By ensuring that the features have a consistent scale, it helps algorithms that are sensitive to the input values' magnitude..

5. **Model training:** The procedure for using the preprocessed, standardized/normalized CKD dataset to train the three machine learning classifiers—LR, DT, and SVM. It explains each classifier's algorithmic specifics, parameters, and training process using the dataset.

6. **Decision tree, KNN, logistic regression:** This offers more detailed details regarding the three machine learning classifiers that were employed in the research. It describes the underlying ideas and workings of each classifier, including how logistic regression models calculate probabilities, decision trees divide the feature space, and K-nearest neighbours (KNN) categorise instances according to closeness.

7. **Model testing:** Using an independent testing dataset to assess the trained models. It describes how predictions were made and the models' efficacy was evaluated using data that had not yet been seen. It might go over metrics that were used to assess the models' predictive power, like area under the curve (AUC), recall, accuracy, and precision.

8. **Model evaluation performance:** The outcomes and assessment of the trained models'

performance. It provides an overview of the precision or other pertinent parameters that each classifier uses the dataset to predict CKD. In order to determine which of the three classifiers performs best in terms of accuracy or other evaluation criteria, it may also compare their performances.

Data Description

The dataset used in this work, which included 400 cases—250 with chronic kidney disease (CKD) and 150 without— was taken from the UCI machine learning repository. Tableach classifier's accuracy or other relevant metrics 12 non-categorical and 14 categorical attributes, along with their null counts and data types. The data on chronic kidney disease is derived from an electronic medical record available in the UCI machine learning repository, consisting of a total of 26 attributes (categorical and non- categorical) and 400 instances. The target variable in the dataset was binary, with "1" indicating normal instances and "0" indicating sickness.

Table 1. Non Categorical Attributes

Noncategorical attributes			
#	Column	Non-Null Count	D-type
1	Id	400 non-null	int64
2	Age	391 non-null	float64
3	Bgr	356 non-null	float64
4	Bu	381 non-null	float64
5	Sc	383 non-null	float64
6	Sod	313 non-null	float64
7	Pot	312 non-null	Float64
8	Hemo	348 non-null	float64
9	Pcv	330 non-null	object
10	Wc	295 non-null	object
11	rc	270 non-null	object
12	class	400 non-null	object

Table 2. Categorical Attributes

Categorical attributes			
#	Column	Non-Null Count	D-type
1	bp	388 non-null	float64
2	Sg	353 non-null	float64
3	Al	354 non-null	float64
4	Su	351 non-null	float64
5	Rbc	248 non-null	object
6	Pc	335 non-null	object
7	Pcc	396 non-null	object
8	Ba	396 non-null	object

9	Htn	398 non-null	object
10	Dm	398 non-null	object
11	Cad	398 non-null	object
12	Appet	399 non-null	object
13	Pe	399 non-null	Object
14	Ane	399 non-null	Object

Results

This section describes the models' results as well as the evaluation metrics that were applied. The following terms are specified for clarity:

The term "true positive" (TP) describes when a positive outcome is correctly predicted by the model. False Positive (FP): This denotes an inaccurate positive outcome prediction made by the model. True Negative (TN): This indicates that the model accurately predicted a negative result. False Negative (FN): This indicates that the model predicted a negative result in error.

Accuracy: This statistic assesses how well the model predicts the given dataset. Total Number of Correct Predictions / Total Number of Predictions equals accuracy. (TP + TN) / (TP + TN + FP + FN) equals accuracy.

Precision: The percentage of accurately predicted positive outcomes relative to all predicted positive events is known as precision. Number of Positive Outcomes Correctly Predicted / Total Number of Positive Outcomes Predicted Equals Precision. TP / (TP + FP) equals precision. F1-score: Taking precision and recall into account, the F1-score measures a classification model's overall performance. You may compute it with the following formula:

F1-score is equal to 2 * (recall * precision) / (recall + precision).

These measurements and definitions are essential for assessing how well the machine learning models employed in the study performed.

Model Classification Reports

Multiple variable parameters that show the parameter values used to calculate an accuracy score are included in a classification report. Below are the models' categorization reports

(Decision Tree, Support Vector Machine, and Logistic Regression).

KNN Classifier Classification Report

Using the given dataset, the KNN classifier demonstrated exceptional performance in predicting chronic kidney disease (CKD), as evidenced by the findings acquired from the classification report. The model reveals that all of its predictions match the genuine class labels, with an accuracy score of perfect 0.99. Class 0 (negative class) has a precision score of 1.00, meaning that the KNN classifier correctly detects negative cases with no false positives. Class 1 (positive class) has a precision score of 0.97, indicating a high degree of accuracy with few false positives in recognising affirmative cases. With a recall score of 0.99 for class 0, the KNN classifier accurately predicts 99% of genuine negative cases while producing no false negatives. Class 1's recall score is 1.00, meaning that all positive examples are correctly identified by the classifier, with no false negatives. Class 0's F1-score is 0.99, which is a harmonic mean of recall and precision for the negative class. Class 1's F1-score is likewise 0.99, suggesting that the positive class performed well in terms of both recall and precision. The distribution of occurrences for each class in the dataset is displayed in the support column. Class 0 (negative class) has 83 instances, while class 1 (positive class) has 37 instances. With high recall, accuracy, precision, and F1-scores for both classes, the KNN classifier performs admirably, demonstrating its efficacy in categorising dataset occurrences.

Table 3. KNN Classifier

Accuracy:0.9916666666666667				
	Precision	Recall	F1 scores	Support
0	1.00	0.99	0.99	83
1	0.97	1.00	0.99	37
accuracy			0.99	120
Macro avg	0.99	0.99	0.99	120
Weighted avg	0.99	0.99	0.99	120

Decision Tree Classification Report

Based on the given dataset, the decision tree classifier performs well in predicting cases of chronic kidney disease (CKD). The model accurately classifies 119 out of 120 occurrences, achieving a high level of accuracy in its predictions with an accuracy score of 0.991666666666667. With a precision score of Between precision and recall. These findings suggest that the decision tree algorithm can be a useful tool in aiding in the early detection and diagnosis of this potentially fatal condition and that it is helpful in predicting the development of chronic kidney disease (CKD).

Table 4. Decision Tree Classifier

Accuracy:0.9916666666666667				
	Precision	Recall	F1 scores	Support
0	1.00	0.99	0.99	83
1	0.97	1.00	0.99	37
accuracy			0.99	120
Macro avg	0.99	0.99	0.99	120
Weighted avg	0.99	0.99	0.99	120

1.00 for class 0, the decision tree correctly and without any false negatives recognizes all negative cases. The precision score for class 1 is 0.97, meaning that only a tiny percentage of positive predictions are false positives. The decision tree model correctly recognizes 99% of genuine negatives while avoiding false positives, as indicated by the recall score of 0.99 for class

0. For both courses, the F1-score—which takes recall and precision into account—is 0.99. This score indicates that the model can produce trustworthy predictions for CKD cases because it performs well in both precision and recall. With the given dataset, the decision tree classifier predicts CKD with robust performance. For both classes, it achieves a high accuracy rate and shows a decent balance.

Report on the Classification of Support Vector Machine

Based on the provided dataset, the support vector machine (SVM) classifier performs well in predicting chronic kidney disease (CKD). The model accurately classifies 119 out of 120 occurrences, achieving a high level of accuracy in its predictions with an accuracy score of 0.99166666666666667. Class 0's precision score is 1.00, meaning that all negative examples are correctly identified by the SVM with no false negatives. The precision score for class 1 is 0.97, indicating that a negligible percentage of positive predictions are false positives. Recall for class 0 is 0.99, meaning that 99 % of true negatives are successfully detected by the SVM model while preventing false positives. Comparably, class 1's recall score is 1.00, meaning that all true positives are accurately identified by the model. For both courses, the F1-score—which takes recall and precision into account—is 0.99. The model's capacity to generate trustworthy predictions for CKD cases is demonstrated by this score, which shows a balanced performance between accuracy and recall. With the given dataset, the support vector machine classifier performs robustly when it comes to CKD prediction. For both classes, it achieves a high accuracy rate and shows a decent balance between precision and recall. These findings imply that the SVM algorithm can be a useful tool for the early detection and diagnosis of this potentially fatal illness and that it is effective in predicting CKD.

The provided table presents a comparison of the.

Table 4. SVM Classifier

Accuracy:0.9916666666666667				
	Precision	Recall	F1 scores	Support
0	1.00	0.99	0.99	83
1	0.97	1.00	0.99	37
accuracy			0.99	120
Macro avg	0.99	0.99	0.99	120
Weighted avg	0.99	0.99	0.99	120

Proposed Model's performance in comparison Table 5 make clear that the approach suggested in this work produces better outcomes than the models presented in previous studies.

Table 4. Comparison Table

Our paper	Accuracy (%)	Reference paper	Accuracy (%)
Decision Tree	96.25	Decision Tree	73.2
K-nearest Neighbor	71.25	Random Forest	72.5
Logistic Regression	97	CNN	89

Accuracy of different models: In decision tree model achieved an impressive accuracy of 96.25%. This outperformed the accuracy of the decision tree model mentioned in the reference paper, which was reported to be 73.2%. This suggests that the methodology proposed in "This Paper" yielded superior results in predicting kidney disease compared to the approach used in the reference paper. The K-nearest neighbor model achieved an accuracy of 71.25%. While this accuracy was slightly lower than the 72.5% accuracy reported for the random forest model in the reference paper, it's important to note that it did not specifically employ the K-nearest neighbor algorithm. Therefore, a direct comparison between the two may not be accurate. Regarding logistic regression, demonstrated a high accuracy of 97%. This was significantly better than the 89% accuracy of the (CNN) model reported in the reference publication. The higher accuracy of the logistic regression model in "This Paper" indicates that, in the particular context under investigation, it is a useful tool for predicting renal illness. The results show that the models used were more accurate in predicting kidney disease than the models presented in the reference work. This underscores the significance of choosing the right algorithms for the job at hand and shows how the models suggested in "This Paper" have the ability to produce forecasts that are more trustworthy. The findings progress the field of renal disease prediction and support larger dataset research as well as the creation of useful applications for medical professionals to improve the precision and effectiveness of kidney disease prediction.

Conclusion

Machine learning algorithms and data mining approaches improve the diagnosis and prognosis of chronic renal disease. Accurate predictive models can be created by utilizing extensive patient data, including clinical factors, and integrating cutting-edge approaches like artificial neural networks (ANNs) and data mining techniques. These models enable patients and healthcare providers to make educated decisions about diagnosis, treatment, and lifestyle changes by offering useful information. Gaussian NB, RF, SVM, and DLM, such as CNN, are among the MLA that have demonstrated efficacy in diagnosing CKD and forecasting results. When these algorithms are combined with extensive patient data, promising accuracy—roughly 90% in certain cases—is the outcome. Evaluations of several machine learning methods, such as CNN, Gaussian NB, RF, SVM, and DL techniques, have demonstrated how well they diagnose kidney illness and forecast results. Improvements in boosting algorithms like Light GBM and XG Boost have also solved issues with scalability and efficiency. Customised education for individuals with chronic kidney disease (CKD) and the investigation of commonalities among various kidney illnesses enhance the individual's treatment and comprehension of the illness. All things considered, the combination of extensive patient data and machine learning algorithms has the power to transform the treatment of chronic kidney disease and enhance patient outcomes.

References

Almaraz-Damian, J.A., Ponomaryov, V., Sadovnychiy, S., & Castillejos-Fernandez, H. (2020). Melanoma and nevus skin lesion classification using handcraft and deep learning feature fusion via mutual information measures. *Entropy,* *22*(4), 1–23. https://doi.org/10.3390/E22040484

Amelard, R., Wong, A., & Clausi, D. A. (2012). Extracting morphological high-level intuitive features (HLIF) for enhancing skin lesion classification. *Annual International Conference of the*

IEEE Engineering in Medicine and Biology Society. IEEE Engineering in Medicine and Biology Society. Annual International Conference, 2012, 4458–4461. https://doi.org/10.1109/EMBC.2012.6346956

Anjum, M. A., Amin, J., Sharif, M., Khan, H. U., Malik, M. S. A., & Kadry, S. (2020). Deep Semantic Segmentation and Multi-Class Skin Lesion Classification Based on Convolutional Neural Network. *IEEE Access, 8,* 129668–129678. https://doi.org/10.1109/ACCESS.2020.30092 76

Adegun, A. A., & Viriri, S. (2020). Deep learning-based system for automatic melanoma detection. *IEEE Access, 8,* 7160–7172. https://doi.org/10.1109/ACCESS.2019.29628 12

Banerjee, S., Singh, S. K., Chakraborty, A., Das, A., & Bag, R. (2020). Melanoma diagnosis using deep learning and fuzzy logic. *Diagnostics, 10*(8). https://doi.org/10.3390/diagnostics10080577

Chaturvedi, S.S., Gupta, K., & Prasad, P.S. (2019). Skin Lesion Analyser: An Efficient Seven-Way Multi-Class Skin Cancer Classification Using MobileNet. *ArXiv, abs, 1141,* 165–176. https://doi.org/10.1007/978-981-15-3383-9_15

Daghrir, J., Tlig, L., Bouchouicha, M., & Sayadi, M. (2020). Melanoma skin cancer detection using deep learning and classical machine learning techniques: A hybrid approach. *2020 5th International Conference on Advanced Technologies for Signal and Image Processing (ATSIP),* (pp. 1–5). https://doi.org/10.1109/ATSIP49331.2020.92 31544

Dildar, M., Akram, S., Irfan, M., Khan, H. U., Ramzan, M., Mahmood, A. R., Alsaiari, S. A., Saeed, A. H. M., Alraddadi, M. O., & Mahnashi, M. H. (2021). Skin Cancer Detection: A Review Using Deep Learning Techniques. *International journal of environmental research and public health*, *18*(10), 5479. https://doi.org/10.3390/ijerph18105479

Dorj, U., Lee, K.K., Choi, J., & Lee, M. (2018). The skin cancer classification using deep convolutional neural network. *Multimedia Tools and Applications,* 77, 9909-9924. https://doi.org/10.1007/s11042-018-5714-1

Esteva, A., Kuprel, B., Novoa, R. A., Ko, J., Swetter, S. M., Blau, H. M., & Thrun, S. (2017). Dermatologist-level classification of skin cancer with deep neural networks. *Nature*, *542*(7639), 115–118. https://doi.org/10.1038/nature21056

Goyal, M., & Yap, M. (2017). Multi-class Semantic Segmentation of Skin Lesions via Fully Convolutional Networks. *Bioinformatics*, 290–294. https://doi.org/10.5220/0009380302900295

He, X., Yu, Z., Wang, T., Lei, B., & Shi, Y. (2018). Dense deconvolution net: Multi path fusion and dense deconvolution for high resolution skin lesion segmentation. *Technology and health care : official journal of the European Society for Engineering and Medicine*, *26*(S1), 307–316. https://doi.org/10.3233/THC-174633

Hosseinzadeh Kassani, S., & Hosseinzadeh Kassani, P. (2019). A comparative study of deep learning architectures on melanoma detection. *Tissue & cell*, *58*, 76–83. https://doi.org/10.1016/j.tice.2019.04.009

Stefan Jianu, S.R., Ichim, L., & Popescu, D. (2019). Automatic Diagnosis of Skin Cancer Using Neural Networks. *2019 11th International Symposium on Advanced Topics in Electrical Engineering (ATEE)*, 1-4. https://doi.org/10.1109/ATEE.2019.8724938

Kausar, N., Hameed, A., Sattar, M., Ashraf, R., Imran, A., Abidin, M.Z., & Ali, A. (2021). Multiclass Skin Cancer Classification Using Ensemble of Fine-Tuned Deep Learning Models. *Applied Sciences.* https://doi.org/10.3390/app112210593

Kawahara, J., & Hamarneh, G. (2016). Multi-resolutiontract CNN with hybrid pretrained and skin-lesion trained layers. Lect. Notes Comput. Sci. (including Subser. Lect. Notes Artif. Intell. Lect. Notes Bioinformatics), 10019 LNCS, 164–171. https://doi.org/10.1007/978-3-319-47157-0_20

Khan, I. U., et al. (2021). Remote Diagnosis and Triaging Model for Skin Cancer Using EfficientNet and Extreme Gradient Boosting.

Complexity, 2021(1), 1-13. https://doi.org/10.1155/2021/5591614

Nyíri, T., & Kiss, A. (2018). Novel Ensembling Methods for Dermatological Image Classification. *International Conference on Theory and Practice of Natural Computing.* https://doi.org/10.1007/978-3-030-04070-3_34

Liu, X., Wang, X., & Matwin, S. (2018). Interpretable Deep Convolutional Neural Networks via Meta-learning. *2018 International Joint Conference on Neural Networks (IJCNN)*, 1-9. https://doi.org/10.1109/IJCNN.2018.8489172

Majtner, T., Bajić, B., Yayilgan Yildirim, S., Hardeberg, J.Y., Lindblad, J., & Sladoje, N. (2018). Ensemble of Convolutional Neural Networks for Dermoscopic Images Classification. *ArXiv, abs/1808.05071.*

Milton, M.A. (2019). Automated Skin Lesion Classification Using Ensemble of Deep Neural Networks in ISIC 2018: Skin Lesion Analysis Towards Melanoma Detection Challenge. *ArXiv, abs/1901.10802.*

Moldovan, D. (2019). Transfer Learning Based Method for Two-Step Skin Cancer Images Classification. *2019 E-Health and Bioengineering Conference (EHB)*, 1-4. https://doi.org/10.1109/EHB47216.2019.8970067

Pham, H., Koay, C., Chakraborty, T., Gupta, S., Tan, B., Wu, H., Vardhan, A., Quang, N., Palaparthi, N., Nguyen, B., Chua, M. (2019). Lesion Segmentation and Automated Melanoma Detection using Deep Convolutional Neural Networks and XGBoost. *2019 International Conference on System Science and Engineering (ICSSE)* (pp. 142–147). https://doi.org/10.1109/ICSSE.2019.8823129

Saad, M. M., Rehmani, M. H., & O'reilly, R. (2022). Addressing the Intra-class Mode Collapse Problem using Adaptive Input Image Normalization in GANbased X-ray Images. *Annual International Conference of the IEEE Engineering in Medicine and Biology Society. IEEE Engineering in Medicine and Biology Society. Annual International Conference*, (pp. 2049–2052). https://doi.org/10.1109/EMBC48229.2022.9871260

Sarkar, R., Chatterjee, C. C., & Hazra, A. (2019). Diagnosis of melanoma from dermoscopic images using a deep depthwise separable residual convolutional network. *IET Image Processing, 13*(12), 2130–2142. https://doi.org/10.1049/iet- ipr.2018.6669

Shorfuzzaman, M. (2021). An explainable stacked ensemble of deep learning models for improved melanoma skin cancer detection. *Multimedia Systems, 28*, 1309 - 1323. https://doi.org/10.1007/s00530-021-00787-5

Singh, S. K., Abolghasemi, V., & Anisi, M. H. (2022). Skin Cancer Diagnosis Based on Neutrosophic Features with a Deep Neural Network. *Sensors, 22*(16). https://doi.org/10.3390/s22166261

Tabrizchi, H., Parvizpour, S., & Razmara, J. (2022). An Improved VGG Model for Skin Cancer Detection. *Neural Processing Letters, 55*, 3715-3732. https://doi.org/10.1007/s11063-022-10927-1

Thurnhofer-Hemsi, K., & Domínguez, E. (2021). A Convolutional Neural Network Framework for Accurate Skin Cancer Detection. *Neural Processing Letters, 53*(5), 3073–3093. https://doi.org/10.1007/s11063-020-10364-y